

**Annex XLVII: Molecular beacon internal hybridization probes for specific detection of tuf sequences.**

		Originating DNA fragment	
SEQ ID NO.	Nucleotide sequence <sup>a</sup>	SEQ ID NO.	Nucleotide position
<b>Bacterial species:           <i>Chlamydia pneumoniae</i></b>			
2091	5'- <u>CGC GAC</u> TTG AGA TGG AAC TTA GTG AGC TTC TTG <u>GTC GCG</u>	20	157-183
2092	5'- <u>CGC GAC</u> GAA AGA ACT TCC TGA AGG TCG TGC AGG <u>TCC AG</u>	20	491-516
<b>Bacterial species:           <i>Chlamydia trachomatis</i></b>			
2213	5'- <u>CGT GCC</u> ATT GAC ATG ATT TCC GAA GAA GAC GCT GAA <u>GGC ACG</u>	1739 <sup>b</sup>	412-441
<b>Bacterial species:           <i>Enterococcus faecalis</i></b>			
1236	5'- <u>GCG AGC</u> CGT GGT GAA GTT CGC GTT GGT <u>GGC TCG C</u>	883	370-391
<b>Bacterial species:           <i>Enterococcus faecium</i></b>			
1235	5'- <u>GCG AGC</u> CGA AGT TGA AGT TGT TGG TAT TGC TGG <u>CTC GC</u>	64	412-437
<b>Bacterial species:           <i>Legionella pneumophila</i></b>			
2084 <sup>c</sup>	5'- <u>CAC GCG</u> TCA ACA CCC GTA CAA GTC GTC TTT TGC <u>GCG TG</u>	112	461-486
<b>Bacterial species:           <i>Mycoplasma pneumoniae</i></b>			
2096 <sup>c</sup>	5'- <u>CGC GAC</u> CGG TAC CAC GGC CAG TAA TCG TGT <u>CGC G</u>	2097 <sup>b</sup>	658-679
<b>Bacterial species:           <i>Neisseria gonorrhoeae</i></b>			
2177	5'- <u>GGC ACG GAC</u> AAA CCA TTC CTG CTG CCT ATC GAA ACG TGT TCC <u>CGT GCC</u>	126	323-357
2178	5'- <u>GGC ACG</u> ACA AAC CAT TCC TGC TGC CTA TCG AAC <u>GTG CC</u>	126	323-348
2179	5'- <u>GGC AGC</u> TCT ACT TCC GTA CCA CTG ACG TAA CCG <u>GCT GCC</u>	126	692-718

<sup>a</sup> Underlined nucleotides indicate the molecular beacon's stem.

<sup>b</sup> Sequence from databases.

<sup>c</sup> This sequence is from the complementary DNA strand of the sequence of the originating fragment given in the Sequence Listing.

**Annex XLVII: Molecular beacon internal hybridization probes for specific detection of *tuf* sequences (continued).**

		Originating DNA fragment	
SEQ ID NO.	Nucleotide sequence <sup>a</sup>	SEQ ID NO.	Nucleotide position
<b><u>Bacterial species:</u>                   <i>Pseudomonas aeruginosa</i></b>			
2122	5'- <u>CCG AGC</u> GAA TGT AGG AGT CCA GGG TCT CTG <u>CTC</u> GG	153,880,2138 <sup>b,c</sup>	280-302 <sup>d</sup>
<b><u>Bacterial species:</u>                   <i>Staphylococcus aureus</i></b>			
2186	5'- <u>ACG CGC</u> TCA AAG CAG AAG TAT ACG TAT TAT CAA AAG ACG <u>CGC</u> GT	1728	615-646
<b><u>Bacterial group:</u>                   <i>Staphylococcus</i> sp. other than <i>S. aureus</i></b>			
1233	5'- <u>GCG AGC</u> GTT ACT GGT GTA GAA ATG TTC CGG <u>CTC</u> GC	878	372-394
<b><u>Fungal species:</u>                   <i>Candida albicans</i></b>			
2073	5'- <u>CCG AGC</u> AAC ATG ATT GAA CCA TCC ACC AAC TGG <u>CTC</u> GG	408	404-429
<b><u>Fungal species:</u>                   <i>Candida dubliniensis</i></b>			
2074	5'- <u>CCG AGC</u> AAC ATG ATT GAA GCT TCC ACC AAC TGG <u>CTC</u> GG	414	416-441
<b><u>Fungal species:</u>                   <i>Candida glabrata</i></b>			
2110 <sup>b</sup>	5'- <u>GCG GGC</u> CCT TAA CGA TTT CAG CGA ATC TGG ATT CAG <u>CCC</u> GC	417	307-335
2111	5'-GCG GGC ATG TTG AAG CCA CCA CCA ACG CTT CCT GGC CCG C	417	419-447
<b><u>Fungal species:</u>                   <i>Candida krusei</i></b>			
2112 <sup>b</sup>	5'- <u>GCG GGC</u> TTG ATG AAG TTT GGG TTT CCT TGA CAA TTG <u>CCC</u> GC	422	318-347
2113	5'- <u>GCG GGC</u> ACA AGG GTT GGA CTA AGG AAA CCA AGG CAG <u>CCC</u> GC	422	419-447
2114	5'- <u>GCG GGC</u> ATC GAT GCT ATT GAA CCA CCT GTC AGA CCG <u>CCC</u> GC	422	505-533

<sup>a</sup> Underlined nucleotides indicate the molecular beacon's stem.

<sup>b</sup> Sequence from databases.

<sup>c</sup> These sequences were aligned to derive the corresponding primer.

<sup>d</sup> The nucleotide positions refer to the *P. aeruginosa tuf* sequence fragment (SEQ ID NO. 153).



**Annex XLVII: Molecular beacon internal hybridization probes for specific detection of *tuf* sequences (continued).**

SEQ ID NO.	Nucleotide sequence <sup>a</sup>	Originating DNA fragment	
		SEQ ID NO.	Nucleotide position
<b><u>Fungal species:</u>                      <i>Candida lusitanae</i></b>			
2115 <sup>b</sup>	5'- <u>GCG</u> <u>GGC</u> GGT AAG TCC ACC GGT AAG ACC TTG TTG <u>GCC</u> <u>CGC</u>	424	304-330
2116	5'- <u>GCG</u> <u>GGC</u> GTA AGT CAC CGG TAA GAC CTT GTT GGC <u>CCG</u> C	424	476-502
2117	5'- <u>GCG</u> <u>GGC</u> GAC GCC ATT GAG CCA CCT TCG AGA <u>GCC</u> <u>CGC</u>	424	512-535
<b><u>Fungal species:</u>                      <i>Candida parapsilosis</i></b>			
2118 <sup>b</sup>	5'- <u>GCG</u> <u>GGC</u> TCC TTG ACA ATT TCT TCG TAT CTG TTC TTG <u>GCC</u> <u>CGC</u>	426	301-330
<b><u>Fungal species:</u>                      <i>Candida tropicalis</i></b>			
2119	5'- <u>GCG</u> <u>GGC</u> TTA CAA CCC TAA GGC TGT TCC ATT CGT TGC <u>CCG</u> C	429	357-384
2120	5'- <u>GCG</u> <u>GGC</u> AGA AAC CAA GGC TGG TAA GGT TAC CGG <u>AGC</u> <u>CCG</u> C	429	459-487
<b><u>Fungal species:</u>                      <i>Cryptococcus neoformans</i></b>			
2106	5'- <u>GCG</u> <u>AGC</u> AGA GCA CGC CCT CCT CGC <u>CGC</u> . TCG C	623,1985,1986 <sup>c</sup>	226-244 <sup>d</sup>
2107	5'- <u>GCG</u> <u>AGC</u> TCC CCA TCT CTG GTT GGC <u>ACG</u> CTC GC	623,1985,1986 <sup>c</sup>	390-408 <sup>d</sup>
<b><u>Bacterial genus:</u>                      <i>Legionella</i> sp.</b>			
2083	5'- <u>CCG</u> <u>CCG</u> ATG TTC CGT AAA TTA CTT GAI GAA GGT CGA GCC <u>GGC</u> GG	111-112 <sup>a</sup>	488-519 <sup>e</sup>

<sup>a</sup> Underlined nucleotides indicate the molecular beacon's stem.

<sup>b</sup> This sequence is from the complementary DNA strand of the sequence of the originating fragment given in the Sequence Listing.

<sup>c</sup> These sequences were aligned to derive the corresponding primer.

<sup>d</sup> The nucleotide positions refer to the *C. neoformans* *tuf* (EF-1) sequence fragment (SEQ ID NO. 623).

<sup>e</sup> The nucleotide positions refer to the *L. pneumophila* *tuf* (EF-1) sequence fragment (SEQ ID NO. 112).

**Annex XLVII: Molecular beacon internal hybridization probes for specific detection of *tuf* sequences (continued).**

		Originating DNA fragment	
SEQ ID NO.	Nucleotide sequence <sup>a</sup>	SEQ ID NO.	Nucleotide position
<u>Fungal genus:</u> <i>Candida sp.</i>			
2108	5'- <u>GCG</u> <u>GGC</u> AAC TTC RTC AAG AAG GTT GGT TAC AAC CCG <u>CCC</u> <u>GC</u>	414,417, 422,424, 426,429,624 <sup>b</sup>	52-80 <sup>c</sup>
2109	5'- <u>GCG</u> <u>GGC</u> CCA ATC TCT GGT TGG AAY GGT GAC AAG <u>CCC</u> <u>GC</u>	Same as SEQ ID NO. 2108	100-125 <sup>c</sup>
<u>Bacterial group:</u> <i>Pseudomonads</i>			
2121	5'- <u>CGA</u> <u>CCG</u> CIA GCC GCA CAC CAA GTT <u>CCG</u> <u>GTC</u> <u>G</u>	153-155, 205,880,2137 <sup>d</sup> , 2138 <sup>d,b</sup>	598-616 <sup>e</sup>

<sup>a</sup> Underlined nucleotides indicate the molecular beacon's stem.

<sup>b</sup> These sequences were aligned to derive the corresponding primer.

<sup>c</sup> The nucleotide positions refer to the *C. albicans tuf* (EF-1) sequence fragment (SEQ ID NO. 624).

<sup>d</sup> Sequence from databases.

<sup>e</sup> The nucleotide positions refer to the *P. aeruginosa tuf* sequence fragment (SEQ ID NO. 153).

**Annex XLVIII: Molecular beacon internal hybridization probes for specific detection of *ddl* and *mtl* gene sequences.**

		Originating DNA fragment	
SEQ ID NO.	Nucleotide sequence <sup>a</sup>	SEQ ID NO.	Nucleotide position
<hr/>			
<u>Bacterial species:</u> <i>E. faecium (ddl)</i>			
1237	5'-GCG AGC CGC GAA ATC GAA GTT GCT GTA TTA GGG CTC GC	1242 <sup>b</sup>	334-359
<hr/>			
<u>Bacterial species:</u> <i>E. faecalis (mtl)</i>			
1238	5'-GCG AGC GGC GTT AAT TTT GGC ACC GAA GAA GAG CTC GC	1243 <sup>b</sup>	631-656
<hr/>			

<sup>a</sup> Underlined nucleotides indicate the molecular beacon's stem.

<sup>b</sup> Sequence from databases.

**Annex XLIX: Internal hybridization probe for specific detection  
of *S. aureus* sequences of unknown coding potential.**

		Originating DNA fragment	
SEQ ID NO.	Nucleotide sequence	SEQ ID NO.	Nucleotide position
<hr/>			
<u>Bacterial species:</u>		<i>Staphylococcus aureus</i>	
1234	5'-ACT AAA TAA ACG CTC ATT CG	1244	35-54

**Annex L: Specific and ubiquitous primers for nucleic acid amplification (antimicrobial agents resistance genes sequences).**

SEQ ID NO.	Nucleotide sequence	Originating DNA fragment	
		SEQ ID NO.	Nucleotide position
<u>Resistance gene:</u> <i>aac(2')-Ia</i>			
1344	5'-AGC AGC AAC GAT GTT ACG CAG CAG	1348 <sup>a</sup>	163-186
1345 <sup>b</sup>	5'-CCC GCC GAG CAT TTC AAC TAT TG	1348 <sup>a</sup>	392-414
1346	5'-GAT GTT ACG CAG CAG GGC AGT C	1348 <sup>a</sup>	172-193
1347 <sup>b</sup>	5'-ACC AAG CAG GTT CGC AGT CAA GTA	1348 <sup>a</sup>	467-490
<u>Resistance gene:</u> <i>aac(3')-Ib</i>			
1349	5'-CAG CCG ACC AAT GAG TAT CTT GCC	1351 <sup>a</sup>	178-201
1350 <sup>b</sup>	5'-TAA TCA GGG CAG TTG CGA CTC CTA	1351 <sup>a</sup>	356-379
<u>Resistance gene:</u> <i>aac(3')-IIb</i>			
1352	5'-CCA CGC TGA CAG AGC CGC ACC G	1356 <sup>a</sup>	383-404
1353 <sup>b</sup>	5'-GGC CAG CTC CCA TCG GAC CCT G	1356 <sup>a</sup>	585-606
1354	5'-CAC GCT GAC AGA GCC GCA CCG	1356 <sup>a</sup>	384-404
1355 <sup>b</sup>	5'-ATG CCG TTG CTG TCG AAA TCC TCG	1356 <sup>a</sup>	606-629
<u>Resistance gene:</u> <i>aac(3')-IVa</i>			
1357	5'-GCC CAT CCA TTT GCC TTT GC	1361 <sup>a</sup>	295-314
1358 <sup>b</sup>	5'-GCG TAC CAA CTT GCC ATC CTG AAG	1361 <sup>a</sup>	517-540
1359	5'-TGC CCC TGC CAC CTC ACT C	1361 <sup>a</sup>	356-374
1360 <sup>b</sup>	5'-CGT ACC AAC TTG CCA TCC TGA AGA	1361 <sup>a</sup>	516-539
<u>Resistance gene:</u> <i>aac(3')-VIa</i>			
1362	5'-CGC CGC CAT CGC CCA AAG CTG G	1366 <sup>a</sup>	285-306
1363 <sup>b</sup>	5'-CGG CAT AAT GGA GCG CGG TGA CTG	1366 <sup>a</sup>	551-574
1364	5'-TTT CTC GCC CAC GCA GGA AAA ATC	1366 <sup>a</sup>	502-525
1365 <sup>b</sup>	5'-CAT CCT CGA CGA ATA TGC CGC G	1366 <sup>a</sup>	681-702
<u>Resistance gene:</u> <i>aac(6')-Ia</i>			
1367	5'-CAA ATA TAC TAA CAG AAG CGT TCA	1371 <sup>a</sup>	56-79
1368 <sup>b</sup>	5'-AGG ATC TTG CCA ATA CCT TTA T	1371 <sup>a</sup>	269-290
1379	5'-AAA CCT TTG TTT CGG TCT GCT AAT	1371 <sup>a</sup>	153-176
1380 <sup>b</sup>	5'-AAG CGA TTC CAA TAA TAC CTT GCT	1371 <sup>a</sup>	320-343

<sup>a</sup> Sequence from databases.

<sup>b</sup> These sequences are from the complementary DNA strand of the sequence of the originating fragment given in the Sequence Listing.

**Ann x L: Specific and ubiquitous primers for nucleic acid amplification (antimicrobial agents resistance genes sequences) (continued).**

SEQ ID NO.	Nucleotide sequence	Originating DNA fragment	
		SEQ ID NO.	Nucleotide position
<u>Resistance gene:</u> <i>aac(6')-Ic</i>			
1372	5'-GCT TTC GTT GCC TTT GCC GAG GTC	1376 <sup>a</sup>	157-180
1373 <sup>b</sup>	5'-CAC CCC TGT TGC TTC GCC CAC TC	1376 <sup>a</sup>	304-326
1374	5'-AGA TAT TGG CTT CGC CGC ACC ACA	1376 <sup>a</sup>	104-127
1375 <sup>b</sup>	5'-CCC TGT TGC TTC GCC CAC TCC TG	1376 <sup>a</sup>	301-323
<u>Resistance gene:</u> <i>ant(3')-Ia</i>			
1377	5'-GCC GTG GGT CGA TGT TTG ATG TTA	1381 <sup>a</sup>	100-123
1378 <sup>b</sup>	5'-GCT CGA TGA CGC CAA CTA CCT CTG	1381 <sup>a</sup>	221-244
1379	5'-AGC AGC AAC GAT GTT ACG CAG CAG	1381 <sup>a</sup>	127-150
1380 <sup>b</sup>	5'-CGC TCG ATG ACG CCA ACT ACC TCT	1381 <sup>a</sup>	222-245
<u>Resistance gene:</u> <i>ant(4')-Ia</i>			
1382	5'-TAG ATA TGA TAG GCG GTA AAA AGC	1386 <sup>a</sup>	149-172
1383 <sup>b</sup>	5'-CCC AAA TTC GAG TAA GAG GTA TT	1386 <sup>a</sup>	386-408
1384	5'-GAT ATG ATA GGC GGT AAA AAG C	1386 <sup>a</sup>	151-172
1385 <sup>b</sup>	5'-TCC CAA ATT CGA GTA AGA GGT A	1386 <sup>a</sup>	388-409
<u>Resistance gene:</u> <i>aph(3')-Ia</i>			
1387	5'-TTA TGC CTC TTC CGA CCA TCA AGC	1391 <sup>a</sup>	233-256
1338 <sup>b</sup>	5'-TAC GCT CGT CAT CAA AAT CAC TCG	1391 <sup>a</sup>	488-511
1389	5'-GAA TAA CGG TTT GGT TGA TGC GAG	1391 <sup>a</sup>	468-491
1390 <sup>b</sup>	5'-ATG GCA AGA TCC TGG TAT CGG TCT	1391 <sup>a</sup>	669-692
<u>Resistance gene:</u> <i>aph(3')-IIa</i>			
1392	5'-TGG GTG GAG AGG CTA TTC GGC TAT	1396 <sup>a</sup>	43-66
1393 <sup>b</sup>	5'-CAG TCC CTT CCC GCT TCA GTG AC	1396 <sup>a</sup>	250-272
1394	5'-GAC GTT GTC ACT GAA GCG GGA AGG	1396 <sup>a</sup>	244-267
1395 <sup>b</sup>	5'-CTT GGT GGT CGA ATG GGC AGG TAG	1396 <sup>a</sup>	386-409

<sup>a</sup> Sequence from databases.

<sup>b</sup> These sequences are from the complementary DNA strand of the sequence of the originating fragment given in the Sequence Listing.

**Annex L: Specific and ubiquitous primers for nucleic acid amplification (antimicrobial agents resistance genes sequences) (continued).**

SEQ ID NO.	Nucleotide sequence	Originating DNA fragment	
		SEQ ID NO.	Nucleotide position
<u>Resistance gene:</u> <i>aph(3')-IIIa</i>			
1397	5'-GTG GGA GAA AAT GAA AAC CTA T	1401a	103-124
1398b	5'-ATG GAG TGA AAG AGC CTG AT	1401a	355-374
1399	5'-ACC TAT GAT GTG GAA CGG GAA AAG	1401a	160-183
1400b	5'-CGA TGG AGT GAA AGA GCC TGA TG	1401a	354-376
<u>Resistance gene:</u> <i>aph(3')-VIa</i>			
1402	5'-TAT TCA ACA ATT TAT CGG AAA CAG	1406a	18-41
1403b	5'-TCA GAG AGC CAA CTC AAC ATT TT	1406a	175-197
1404	5'-AAA CAG CGT TTT AGA GCC AAA TAA	1406a	36-59
1405b	5'-TTC TCA GAG AGC CAA CTC AAC ATT	1406a	177-200
<u>Resistance gene:</u> <i>blaCARB</i>			
1407	5'-CCC TGT AAT AGA AAA GCA AGT AGG	1411a	351-374
1408b	5'-TTG TCG TAT CCC TCA AAT CAC C	1411a	556-577
1409	5'-TGG GAT TAC AAT GGC AAT CAG CG	1411a	205-227
1410b	5'-GGG GAA TAG GTC ACA AGA TCT GCT T	1411a	329-353
<u>Resistance gene:</u> <i>blaCMY-2</i>			
1412	5'-GAG AAA ACG CTC CAG CAG GGC	1416a	793-813
1413b	5'-CAT GAG GCT TTC ACT GCG GGG	1416a	975-995
1414	5'-TAT CGT TAA TCG CAC CAT CAC	1416a	90-110
1415b	5'-ATG CAG TAA TGC GGC TTT ATC	1416a	439-459
<u>Resistance genes:</u> <i>blaCTX-M-1, blaCTX-M-2</i>			
1417	5'-TGG TTA ACT AYA ATC CSA TTG CGG A	1423a	314-338
1418b	5'-ATG CTT TAC CCA GCG TCA GAT T	1423a	583-604
<u>Resistance gene:</u> <i>blaCTX-M-1</i>			
1419	5'-CGA TGA ATA AGC TGA TTT CTC ACG	1423a	410-433
1420b	5'-TGC TTT ACC CAG CGT CAG ATT ACG	1423a	580-603
1421	5'-AAT TAG AGC GGC AGT CGG GAG GAA	1423a	116-139
1422b	5'-GAA ATC AGC TTA TTC ATC GCC ACG	1423a	405-428

<sup>a</sup> Sequence from databases.

<sup>b</sup> These sequences are from the complementary DNA strand of the sequence of the originating fragment given in the Sequence Listing.

**Annex I: Specific and ubiquitous primers for nucleic acid amplification (antimicrobial agents resistance genes sequences) (continued).**

SEQ ID NO.	Nucleotide sequence	Originating DNA fragment	
		SEQ ID NO.	Nucleotide position
<u>Resistance gene:</u> <i>blaCTX-M-2</i>			
1424	5'-GTT AAC GGT GAT GGC GAC GCT AC	1428 <sup>a</sup>	30-52
1425 <sup>b</sup>	5'-GAA TTA TCG GCG GTG TTA ATC AGC	1428 <sup>a</sup>	153-176
1426	5'-CAC GCT CAA TAC CGC CAT TCC A	1428 <sup>a</sup>	510-531
1427 <sup>b</sup>	5'-TTA TCG CCC ACT ACC CAT GAT TTC	1428 <sup>a</sup>	687-710
<u>Resistance gene:</u> <i>blaIMP</i>			
1429	5'-TTT ACG GCT AAA GAT ACT GAA AAG T	1433 <sup>a</sup>	205-229
1430 <sup>b</sup>	5'-GTT TAA TAA AAC AAC CAC CGA ATA AT	1433 <sup>a</sup>	513-538
1431	5'-TAA TTG ACA CTC CAT TTA CGG CTA A	1433 <sup>a</sup>	191-215
1432 <sup>b</sup>	5'-ACC GAA TAA TAT TTT CCT TTC AGG CA	1433 <sup>a</sup>	497-522
<u>Resistance gene:</u> <i>blaOXA2</i>			
1434	5'-CAC AAT CAA GAC CAA GAT TTG CGA T	1438 <sup>a</sup>	319-343
1435 <sup>b</sup>	5'-GAA AGG GCA GCT CGT TAC GAT AGA G	1438 <sup>a</sup>	532-556
<u>Resistance gene:</u> <i>blaOXA10</i>			
1436	5'-CAG CAT CAA CAT TTA AGA TCC CCA	1439 <sup>a</sup>	194-217
1437 <sup>b</sup>	5'-CTC CAC TTG ATT AAC TGC GGA AAT TC	1439 <sup>a</sup>	479-504
<u>Resistance gene:</u> <i>blaPER-1</i>			
1440	5'-AGA CCG TTA TCG TAA ACA GGG CTA AG	1442 <sup>a</sup>	281-306
1441 <sup>b</sup>	5'-TTT TTT GCT CAA ACT TTT TCA GGA TC	1442 <sup>a</sup>	579-604
<u>Resistance gene:</u> <i>blaPER-2</i>			
1443	5'-CTT CTG CTC TGC TGA TGC TTG GC	1445 <sup>a</sup>	32-54
1444 <sup>b</sup>	5'-GGC GAC CAG GTA TTT TGT AAT ACT GC	1445 <sup>a</sup>	304-329
<u>Resistance genes:</u> <i>blaPER-1, blaPER-2</i>			
1446	5'-GGC CTG YGA TTT GTT ATT TGA ACT GGT	1442 <sup>a</sup>	414-440
1447 <sup>b</sup>	5'-CGC TST GGT CCT GTG GTG GTT TC	1442 <sup>a</sup>	652-674
1448	5'-GAT CAG GTG CAR TAT CAA AAC TGG AC	1442 <sup>a</sup>	532-557
1449 <sup>b</sup>	5'-AGC WGG TAA CAA YCC TTT TAA CCG CT	1442 <sup>a</sup>	671-696

<sup>a</sup> Sequence from databases.

<sup>b</sup> These sequences are from the complementary DNA strand of the sequence of the originating fragment given in the Sequence Listing.



**Annex L: Specific and ubiquitous primers for nucleic acid amplification (antimicrobial agents resistance genes sequences) (continued).**

SEQ ID NO.	Nucleotide sequence	Originating DNA fragment	
		SEQ ID NO.	Nucleotide position
<u>Resistance gene:</u> <i>blaSHV</i>			
1883	5'-AGC CGC TTG AGC AAA TTA AAC TA	1900 <sup>a</sup>	71-93
1884 <sup>b</sup>	5'-GTA TCC CGC AGA TAA ATC ACC AC	1900 <sup>a</sup>	763-785
1885	5'-AGC GAA AAA CAC CTT GCC GAC	1900 <sup>a</sup>	313-333
1884 <sup>b</sup>	5'-GTA TCC CGC AGA TAA ATC ACC AC	1900 <sup>a</sup>	763-785
<u>Resistance gene:</u> <i>blaTEM</i>			
1906	5'-CCT TAT TCC CTT TTT TGC GG	1927 <sup>a</sup>	27-46
1907 <sup>b</sup>	5'-CAC CTA TCT CAG CGA TCT GTC T	1927 <sup>a</sup>	817-838
1908	5'-AAC AGC GGT AAG ATC CTT GAG AG	1927 <sup>a</sup>	148-170
1907 <sup>b</sup>	5'-CAC CTA TCT CAG CGA TCT GTC T	1927 <sup>a</sup>	817-838
<u>Resistance gene:</u> <i>catI</i>			
2145	5'-GCA AGA TGT GGC GTG TTA CGG T	2147 <sup>a</sup>	363-384
2146 <sup>b</sup>	5'-GGG GCG AAG AAG TTG TCC ATA TT	2147 <sup>a</sup>	484-506
<u>Resistance gene:</u> <i>catII</i>			
2148	5'-CAG ATT AAA TGC GGA TTC AGC C	2150 <sup>a</sup>	67-88
2149 <sup>b</sup>	5'-ATC AGG TAA ATC ATC AGC GGA TA	2150 <sup>a</sup>	151-173
<u>Resistance gene:</u> <i>catIII</i>			
2151	5'-ATA TTT CAG CAT TAC CTT GGG TT	2153 <sup>a</sup>	419-441
2152 <sup>b</sup>	5'-TAC ACA ACT CTT GTA GCC GAT TA	2153 <sup>a</sup>	603-625
<u>Resistance gene:</u> <i>catP</i>			
2154	5'-CGC CAT TCA GAG TTT AGG AC	2156 <sup>a</sup>	178-197
2155 <sup>b</sup>	5'-TTC CAT ACC GTT GCG TAT CAC TT	2156 <sup>a</sup>	339-361
<u>Resistance gene:</u> <i>cat</i>			
2157	5'-CCA CAG AAA TTG ATA TTA GTG TTT TAT	2159 <sup>a</sup>	89-115
2158 <sup>b</sup>	5'-TCG CTA TTG TAA CCA GTT CTA	2159 <sup>a</sup>	201-221
2160	5'-TTT TGA ACA CTA TTT TAA CCA GC	2162 <sup>a</sup>	48-70
2161 <sup>b</sup>	5'-GAT TTA ACT TAT CCC AAT AAC CT	2162 <sup>a</sup>	231-253

<sup>a</sup> Sequence from databases.

<sup>b</sup> These sequences are from the complementary DNA strand of the sequence of the originating fragment given in the Sequence Listing.

**Annex L: Specific and ubiquitous primers for nucleic acid amplification (antimicrobial agents resistance genes sequences) (continued).**

SEQ ID NO.	Nucleotide sequence	Originating DNA fragment	
		SEQ ID NO.	Nucleotide position
<u>Resistance gene:</u> <i>dhfrA</i>			
1450	5'-ACC ACT GGG AAT ACA CTT GTA ATG GC	1452 <sup>a</sup>	106-131
1451 <sup>b</sup>	5'-ATC TAC CTG GTC AAT CAT TGC TTC GT	1452 <sup>a</sup>	296-321
<u>Resistance gene:</u> <i>dhfrIa</i>			
1457	5'-CAA AGG TGA ACA GCT CCT GTT T	1461 <sup>a</sup>	75-96
1458 <sup>b</sup>	5'-TCC GTT ATT TTC TTT AGG TTG GTT AAA	1461 <sup>a</sup>	249-275
1459	5'-AAG GTG AAC AGC TCC TGT TT	1461 <sup>a</sup>	77-96
1560 <sup>b</sup>	5'-GAT CAC TAC GTT CTC ATT GTC A	1461 <sup>a</sup>	207-228
<u>Resistance genes:</u> <i>dhfrIa</i> , <i>dhfrXV</i>			
1453	5'-ATC GAA GAA TGG AGT TAT CGG RAA TG	1461 <sup>a</sup>	27-52
1454 <sup>b</sup>	5'-CCT AAA AYT RCT GGG GAT TTC WGG A	1461 <sup>a</sup>	384-408
1455	5'-CAG GTG GTG GGG AGA TAT ACA AAA	1461 <sup>a</sup>	290-313
1456 <sup>b</sup>	5'-TAT GTT AGA SRC GAA GTC TTG GKT AA	1461 <sup>a</sup>	416-441
<u>Resistance gene:</u> <i>dhfrIb</i>			
1466	5'-AAG CAT TGA CCT ACA ATC AGT GT	1470 <sup>a</sup>	98-120
1467 <sup>b</sup>	5'-AAT ACA ACT ACA TTG TCA TCA TTT GAT	1470 <sup>a</sup>	204-230
1468	5'-CGT TAC CCG CTC AGG TTG GAC ATC AA	1470 <sup>a</sup>	183-208
1469 <sup>b</sup>	5'-CAT CCC CCT CTG GCT CGA TGT CG	1470 <sup>a</sup>	354-376
<u>Resistance gene:</u> <i>dhfrV</i>			
1471	5'-GAT AAT GAC AAC GTA ATA GTA TTC CC	1475 <sup>a</sup>	208-233
1472 <sup>b</sup>	5'-GCT CAA TAT CAA TCG TCG ATA TA	1475 <sup>a</sup>	342-364
1473	5'-TTA AAG CCT TGA CGT ACA ACC AGT GG	1475 <sup>a</sup>	95-120
1474 <sup>b</sup>	5'-TGG GCA ATG TTT CTC TGT AAA TCT CC	1475 <sup>a</sup>	300-325
<u>Resistance genes:</u> <i>dhfrIb</i> , <i>dhfrV</i>			
1462	5'-GCA CTC CCY AAT AGG AAA TAC GC	1470 <sup>a</sup>	157-179
1463 <sup>b</sup>	5'-AGT GTT GCT CAA AAA CAA CTT CG	1470 <sup>a</sup>	405-427
1464	5'-ACG TTY GAA TCT ATG GGM GCA CT	1470 <sup>a</sup>	139-161
1465 <sup>b</sup>	5'-GTC GAT AAG TGG AGC GTA GAG GC	1470 <sup>a</sup>	328-350

<sup>a</sup> Sequence from databases.

<sup>b</sup> These sequences are from the complementary DNA strand of the sequence of the originating fragment given in the Sequence Listing.

**Annex L: Specific and ubiquitous primers for nucleic acid amplification (antimicrobial agents resistance genes sequences) (continued).**

SEQ ID NO.	Nucleotide sequence	Originating DNA fragment	
		SEQ ID NO.	Nucleotide position
<b><u>Resistance gene:</u>                    <i>dhfrVI</i></b>			
1476	5'-GGC GAG CAG CTC CTA TTC AAA G	1480a	79-100
1477 <sup>b</sup>	5'-TAG GTA AGC TAA TGC CGA TTC AAC A	1480a	237-261
1478	5'-GAG AAT GGA GTA ATT GGC TCT GGA TT	1480a	31-56
1479 <sup>b</sup>	5'-GCG AAA TAC ACA ACA TCA GGG TCA T	1480a	209-233
<b><u>Resistance gene:</u>                    <i>dhfrVII</i></b>			
1485	5'-AAA ATG GCG TAA TCG GTA ATG GC	1489a	32-54
1486 <sup>b</sup>	5'-CAT TTG AGC TTG AAA TTC CTT TCC TC	1489a	189-214
1487	5'-AAT CGA AAA TAT GCA GTA GTG TCG AG	1489a	166-191
1488 <sup>b</sup>	5'-AGA CTA TTG TAG ATT TGA CCG CCA	1489a	294-317
<b><u>Resistance genes:</u>                    <i>dhfrVII, dhfrXVII</i></b>			
1481	5'-RTT ACA GAT CAT KTA TAT GTC TCT	1489a	268-291
1482 <sup>b</sup>	5'-TAA TTT ATA TTA GAC AWA AAA AAC TG	1489a	421-446
1483	5'-CAR YGT CAG AAA ATG GCG TAA TC	1489a	23-45
1484 <sup>b</sup>	5'-TKC AAA GCR WTT TCT ATT GAA GGA AA	1489a	229-254
<b><u>Resistance gene:</u>                    <i>dhfrVIII</i></b>			
1490	5'-GAC CTA TGA GAG CTT GCC CGT CAA A	1494a	144-168
1491 <sup>b</sup>	5'-TCG CCT TCG TAC AGT CGC TTA ACA AA	1494a	376-401
1492	5'-CAT TTT AGC TGC CAC CGC CAA TGG TT	1494a	18-43
1493 <sup>b</sup>	5'-GCG TCG CTG ACG TTG TTC ACG AAG A	1494a	245-269
<b><u>Resistance gene:</u>                    <i>dhfrIX</i></b>			
1495	5'-TCT CTA AAC ATG ATT GTC GCT GTC	1499a	7-30
1496 <sup>b</sup>	5'-CAG TGA GGC AAA AGT TTT TCT ACC	1499a	133-156
1497	5'-CGG ACG ACT TCA TGT GGT AGT CAG T	1499a	171-195
1498 <sup>b</sup>	5'-TTT GTT TTC AGT AAT GGT CGG GAC CT	1499a	446-471

<sup>a</sup> Sequence from databases.

<sup>b</sup> These sequences are from the complementary DNA strand of the sequence of the originating fragment given in the Sequence Listing.

**Annex L: Specific and ubiquitous primers for nucleic acid amplification (antimicrobial agents resistance genes sequences) (continued).**

SEQ ID NO.	Nucleotide sequence	Originating DNA fragment	
		SEQ ID NO.	Nucleotide position
<u>Resistance gene:</u> <i>dhfrXII</i>			
1500	5'-ATC GGG TTA TTG GCA ATG GTC CTA	1504 <sup>a</sup>	50-73
1501 <sup>b</sup>	5'-GCG GTA GTT AGC TTG GCG TGA GAT T	1504 <sup>a</sup>	201-225
1502	5'-GCG GGC GGA GCT GAG ATA TAC A	1504 <sup>a</sup>	304-325
1503 <sup>b</sup>	5'-AAC GGA GTG GGT GTA CGG AAT TAC AG	1504 <sup>a</sup>	452-477
<u>Resistance gene:</u> <i>dhfrXIII</i>			
1505	5'-ATT TTT CGC AGG CTC ACC GAG AGC	1507 <sup>a</sup>	106-129
1506 <sup>b</sup>	5'-CGG ATG AGA CAA CCT CGA ATT CTG CTG	1507 <sup>a</sup>	413-439
<u>Resistance gene:</u> <i>dhfrXV</i>			
1508	5'-AGA ATG TAT TGG TAT TTC CAT CTA TCG	1512 <sup>a</sup>	215-241
1509 <sup>b</sup>	5'-CAA TGT CGA TTG TTG AAA TAT GTA AA	1512 <sup>a</sup>	336-361
1510	5'-TGG AGT GCC AAA GGG GAA CAA T	1512 <sup>a</sup>	67-88
1511 <sup>b</sup>	5'-CAG ACA CAA TCA CAT GAT CCG TTA TCG	1512 <sup>a</sup>	266-292
<u>Resistance gene:</u> <i>dhfrXVII</i>			
1513	5'-TTC AAG CTC AAA TGA AAA CGT CC	1517 <sup>a</sup>	201-223
1514 <sup>b</sup>	5'-GAA ATT CTC AGG CAT TAT AGG GAA T	1517 <sup>a</sup>	381-405
1515	5'-GTG GTC AGT AAA AGG TGA GCA AC	1517 <sup>a</sup>	66-88
1516 <sup>b</sup>	5'-TCT TTC AAA GCA TTT TCT ATT GAA GG	1517 <sup>a</sup>	232-257
<u>Resistance gene:</u> <i>emhR</i>			
2102	5'-CAC CTT CAC CCT GAC CGA CG	2105 <sup>a</sup>	822-841
2103 <sup>b</sup>	5'-CGA ACC AGC GGA AAT AGT TGG AC	2105 <sup>a</sup>	948-970
<u>Resistance genes:</u> <i>ereA, ereA2</i>			
1528	5'-AAC TTG AGC GAT TTT CGG ATA CCC TG	1530 <sup>a</sup>	80-105
1529 <sup>b</sup>	5'-TTG CCG ATG AAA TAA CCG CCG ACT	1530 <sup>a</sup>	317-340

<sup>a</sup> Sequence from databases.

<sup>b</sup> These sequences are from the complementary DNA strand of the sequence of the originating fragment given in the Sequence Listing.

**Annex L: Specific and ubiquitous primers for nucleic acid amplification (antimicrobial agents resistance genes sequences) (continued).**

		Originating DNA fragment	
SEQ ID NO.	Nucleotide sequence	SEQ ID NO.	Nucleotide position
<u>Resistance gene:</u> <i>ereB</i>			
1531	5'-TCT TTT TGT TAC GAC ATA CGC TTT T	1535a	152-176
1532 <sup>b</sup>	5'-AGT GCT TCT TTA TCC GCT GTT CTA	1535a	456-479
1533	5'-CAG CGG ATA AAG AAG CAC TAC ACA TT	1535a	461-486
1534 <sup>b</sup>	5'-CCT CCT GAA ATA AAG CCC GAC AT	1535a	727-749
<u>Resistance gene:</u> <i>gyrA</i>			
1340	5'-GAA CAA GGT ATG ACA CCG GAT AAA T	1299a	163-188
1341 <sup>b</sup>	5'-GAT AAC TGA AAT CCT GAG CCA TAC G	1299a	274-299
1936	5'-TAC CAC CCG CAC GGC	1954a	205-219
1937 <sup>b</sup>	5'-CGG AGT CGC CGT CGA TG	1954a	309-325
1942	5'-GAC TGG AAC AAA GCC TAT AAA AAA TCA	1954a	148-174
1937 <sup>b</sup>	5'-CGG AGT CGC CGT CGA TG	1954a	309-325
2040	5'-TGT GAC CCC AGA CAA ACC C	2054a	33-51
2041 <sup>b</sup>	5'-GTT GAG CGG CAG CAC TAT CT	2054a	207-226
<u>Resistance gene:</u> <i>inhA</i>			
2098	5'-CTG AGT CAC ACC GAC AAA CGT C	2101a	910-931
2099 <sup>b</sup>	5'-CCA GGA CTG AAC GGG ATA CGA A	2101a	1074-1095
<u>Resistance genes:</u> <i>linA, linA'</i>			
1536 <sup>a</sup>	5'-AGA TGT ATT AAC TGG AAA ACA ACA A	1540 <sup>a</sup>	99-123
1537 <sup>b</sup>	5'-CTT TGT AAT TAG TTT CTG AAA ACC A	1540a	352-376
1538	5'-TTA GAA GAT ATA GGA TAC AAA ATA GAA G	1540a	187-214
1539 <sup>b</sup>	5'-GAA TGA AAA AGA AGT TGA GCT T	1540a	404-425
<u>Resistance gene:</u> <i>linB</i>			
1541	5'-TGA TAA TCT TAT ACG TGG GGA ATT T	1545a	246-270
1542 <sup>b</sup>	5'-ATA ATT TTC TAA TTG CCC TGT TTC AT	1545a	359-384
1543	5'-GGG CAA TTA GAA AAT TAT TTA TCA GA	1545a	367-392
1544 <sup>b</sup>	5'-TTT TAC TCA TGT TTA GCC AAT TAT CA	1545a	579-604

<sup>a</sup> Sequence from databases.

<sup>b</sup> These sequences are from the complementary DNA strand of the sequence of the originating fragment given in the Sequence Listing.

**Annex L: Specific and ubiquitous primers for nucleic acid amplification (antimicrobial agents resistance genes sequences) (continued).**

		Originating DNA fragment	
SEQ ID NO.	Nucleotide sequence	SEQ ID NO.	Nucleotide position
<b><u>Resistance gene:</u>                  <i>mefA</i></b>			
1546	5'-CAA GAA GGA ATG GCT GTA CTA C	1548 <sup>a</sup>	625-646
1547 <sup>b</sup>	5'-TAA TTC CCA AAT AAC CCT AAT AAT AGA	1548 <sup>a</sup>	816-842
<b><u>Resistance gene:</u>                  <i>mefE</i></b>			
1549	5'-GCT TAT TAT TAG GAA GAT TAG GGG GC	1551 <sup>a</sup>	815-840
1550 <sup>b</sup>	5'-TAG CAA GTG ACA TGA TAC TTC CGA	1551 <sup>a</sup>	1052-1075
<b><u>Resistance genes:</u>                  <i>mefA</i>, <i>mefE</i></b>			
1552	5'-GGC AAG CAG TAT CAT TAA TCA CTA	1548 <sup>a</sup>	50-73
1553 <sup>b</sup>	5'-CAA TGC TAC GGA TAA ACA ATA CTA TC	1548 <sup>a</sup>	318-343
1554	5'-AGA AAA TTA AGC CTG AAT ATT TAG GAC	1548 <sup>a</sup>	1010-1035
1555 <sup>b</sup>	5'-TAG TAA AAA CCA ATG ATT TAC ACC G	1548 <sup>a</sup>	1119-1143
<b><u>Resistance genes:</u>                  <i>mphA</i>, <i>mphK</i></b>			
1556	5'-ACT GTA CGC ACT TGC AGC CCG ACA T	1560 <sup>a</sup>	33-57
1557 <sup>b</sup>	5'-GAA CGG CAG GCG ATT CTT GAG CAT	1560 <sup>a</sup>	214-237
1558	5'-GTG GTG GTG CAT GGC GAT CTC T	1560 <sup>a</sup>	583-604
1559 <sup>b</sup>	5'-GCC GCA GCG AGG TAC TCT TCG TTA	1560 <sup>a</sup>	855-878
<b><u>Resistance gene:</u>                  <i>mupA</i></b>			
2142	5'-GCC TTA ATT TCG GAT AGT GC	2144 <sup>a</sup>	1831-1850
2143 <sup>b</sup>	5'-GAG AAA GAG CCC AAT TAT CTA ATG T	2144 <sup>a</sup>	2002-2026
<b><u>Resistance gene:</u>                  <i>parC</i></b>			
1342	5'-GAT GTT ATT GGT CAA TAT CAT CCA	1321 <sup>a</sup>	205-229
1343 <sup>b</sup>	5'-AAG AAA CTG TCT CTT TAT TAA TAT CAC GT	1321 <sup>a</sup>	396-425
1934	5'-GAA CGC CAG CGC GAA ATT CAA AAA G	1781	67-91
1935 <sup>b</sup>	5'-AGC TCG GCA TAC TTC GAC AGG	1781	277-297
2044	5'-ACC GTA AGT CGG CCA AGT CA	2055 <sup>a</sup>	176-195
2045 <sup>b</sup>	5'-GTT CTT TCT CCG TAT CGT C	2055 <sup>a</sup>	436-454

<sup>a</sup> Sequence from databases.

<sup>b</sup> These sequences are from the complementary DNA strand of the sequence of the originating fragment given in the Sequence Listing.

**Annex L: Sp cific and ubiquitous primers for nucleic acid amplification (antimicrobial agents r sistance genes sequences) (continued).**

		Originating DNA fragment	
SEQ ID NO.	Nucleotide sequence	SEQ ID NO.	Nucleotide position
<b><u>Resistance gene:</u>                    <i>ppflo-like</i></b>			
2163	5'-ACC TTC ATC CTA CCG ATG TGG GTT	2165 <sup>a</sup>	922-945
2164 <sup>b</sup>	5'-CAA CGA CAC CAG CAC TGC CAT TG	2165 <sup>a</sup>	1136-1158
<b><u>Resistance gene:</u>                    <i>rpoB</i></b>			
2065	5'-CCA GGA CGT GGA GGC GAT CAC A	2072 <sup>a</sup>	1218-1239
2066 <sup>b</sup>	5'-CAC CGA CAG CGA GCC GAT CAG A	2072 <sup>a</sup>	1485-1506
<b><u>Resistance gene:</u>                    <i>satG</i></b>			
1581	5'-AAT TGG GGA CTA CAC CTA TTA TGA TG	1585 <sup>a</sup>	93-118
1582 <sup>b</sup>	5'-GGC AAA TCA GTC AGT TCA GGA GT	1585 <sup>a</sup>	310-332
1583	5'-CGA TTG GCA ACA ATA CAC TCC TG	1585 <sup>a</sup>	294-316
1584 <sup>b</sup>	5'-TCA CCT ATT TTT ACG CCT GGT AGG AC	1585 <sup>a</sup>	388-413
<b><u>Resistance gene:</u>                    <i>sulII</i></b>			
1961	5'-GCT CAA GGC AGA TGG CAT TCC C	1965 <sup>a</sup>	222-243
1962 <sup>b</sup>	5'-GGA CAA GGC GGT TGC GTT TGA T	1965 <sup>a</sup>	496-517
1963	5'-CAT TCC CGT CTC GCT CGA CAG T	1965 <sup>a</sup>	237-258
1964 <sup>b</sup>	5'-ATC TGC CTG CCC GTC TTG C	1965 <sup>a</sup>	393-411
<b><u>Resistance gene:</u>                    <i>tetB</i></b>			
1966	5'-CAT GCC AGT CTT GCC AAC G	1970 <sup>a</sup>	66-84
1967 <sup>b</sup>	5'-CAG CAA TAA GTA ATC CAG CGA TG	1970 <sup>a</sup>	242-264
1968	5'-GGA GAG ATT TCA CCG CAT AG	1970 <sup>a</sup>	457-476
1969 <sup>b</sup>	5'-AGC CAA CCA TCA TGC TAT TCC A	1970 <sup>a</sup>	721-742
<b><u>Resistance gene:</u>                    <i>tetM</i></b>			
1586	5'-ATT CCC ACA ATC TTT TTT ATC AAT AA	1590 <sup>a</sup>	361-386
1587 <sup>b</sup>	5'-CAT TGT TCA GAT TCG GTA AAG TTC	1590 <sup>a</sup>	501-524
1588	5'-GTT TTT GAA GTT AAA TAG TGT TCT T	1590 <sup>a</sup>	957-981
1589 <sup>b</sup>	5'-CTT CCA TTT GTA CTT TCC CTA	1590 <sup>a</sup>	1172-1192

<sup>a</sup> Sequence from databases.

<sup>b</sup> These sequences are from the complementary DNA strand of the sequence of the originating fragment given in the Sequence Listing.

**Annex L: Specific and ubiquitous primers for nucleic acid amplification (antimicrobial agents resistance genes sequences) (continued).**

SEQ ID NO.	Nucleotide sequence	Originating DNA fragment	
		SEQ ID NO.	Nucleotide position
<u>Resistance gene:</u> <b>vatB</b>			
1609	5'-GCC CTG ATC CAA ATA GCA TAT A	1613 <sup>a</sup>	11-32
1610 <sup>b</sup>	5'-CCT GGC ATA ACA GTA ACA TTC TG	1613 <sup>a</sup>	379-401
1611	5'-TGG GAA AAA GCA ACT CCA TCT C	1613 <sup>a</sup>	301-322
1612 <sup>b</sup>	5'-ACA ACT GAA TTC GCA GCA ACA AT	1613 <sup>a</sup>	424-446
<u>Resistance gene:</u> <b>vatC</b>			
1614	5'-CCA ATC CAG AAG AAA TAT ACC C	1618 <sup>a</sup>	26-47
1615 <sup>b</sup>	5'-ATT AGT TTA TCC CCA ATC AAT TCA	1618 <sup>a</sup>	177-200
1616	5'-ATA ATG AAT GGG GCT AAT CAT CGT AT	1618 <sup>a</sup>	241-266
1617 <sup>b</sup>	5'-GCC AAC AAC TGA ATA AGG ATC AAC	1618 <sup>a</sup>	463-486
<u>Resistance gene:</u> <b>vga</b>			
1619	5'-AAG GCA AAA TAA AAG GAG CAA AGC	1623 <sup>a</sup>	641-664
1620 <sup>b</sup>	5'-TGT ACC CGA GAC ATC TTC ACC AC	1623 <sup>a</sup>	821-843
1621	5'-AAT TGA AGG ACG GGT ATT GTG GAA AG	1623 <sup>a</sup>	843-868
1622 <sup>b</sup>	5'-CGA TTT TGA CAG ATG GCG ATA ATG AA	1623 <sup>a</sup>	975-1000
<u>Resistance gene:</u> <b>vgaB</b>			
1624	5'-TTC TTT AAT GCT CGT AGA TGA ACC TA	1628 <sup>a</sup>	354-379
1625 <sup>b</sup>	5'-TTT TCG TAT TCT TCT TGT TGC TTT C	1628 <sup>a</sup>	578-602
1626	5'-AGG AAT GAT TAA GCC CCC TTC AAA AA	1628 <sup>a</sup>	663-688
1627 <sup>b</sup>	5'-TTA CAT TGC GAC CAT GAA ATT GCT CT	1628 <sup>a</sup>	849-874
<u>Resistance genes:</u> <b>vgb, vgh</b>			
1629	5'-AAG GGG AAA GTT TGG ATT ACA CAA CA	1633 <sup>a</sup>	73-98
1630 <sup>b</sup>	5'-GAA CCA CAG GGC ATT ATC AGA ACC	1633 <sup>a</sup>	445-468
1631	5'-CGA CGA TGC TTT ATG GTT TGT	1633 <sup>a</sup>	576-596
1632 <sup>b</sup>	5'-GTT AAT TTG CCT ATC TTG TCA CAC TC	1633 <sup>a</sup>	850-875

<sup>a</sup> Sequence from databases.

<sup>b</sup> These sequences are from the complementary DNA strand of the sequence of the originating fragment given in the Sequence Listing.



**Annex L: Specific and ubiquitous primers for nucleic acid amplification (antimicrobial agents resistance genes sequences) (continued).**

SEQ ID NO.	Nucleotide sequence	Originating DNA fragment	
		SEQ ID NO.	Nucleotide position
<b><u>Resistance gene:</u>                    <i>vgbB</i></b>			
1634	5'-TTA ACT TGT CTA TTC CCG ATT CAG G	1882 <sup>a</sup>	23-47
1635 <sup>b</sup>	5'-GCT GTG GCA ATG GAT ATT CTG TA	1882 <sup>a</sup>	267-289
1636	5'-TTC CTA CCC CTG ATG CTA AAG TGA	1882 <sup>a</sup>	155-178
1637 <sup>b</sup>	5'-CAA AGT GCG TTA TCC GAA CCT AA	1882 <sup>a</sup>	442-464
<b>Sequencing primers</b>			
<b><u>Resistance gene:</u>                    <i>gyrA</i></b>			
1290	5'-GAY TAY GCI ATG ISI GTI ATH GT	1299 <sup>a</sup>	70-83
1292 <sup>b</sup>	5'-ARI SCY TCI ARI ATR TGI GC	1299 <sup>a</sup>	1132-1152
1291	5'-GCI YTI CCI GAY GTI MGI GAY GG	1299 <sup>a</sup>	100-123
1292 <sup>b</sup>	5'-ARI SCY TCI ARI ATR TGI GC	1299 <sup>a</sup>	1132-1152
1293	5'-ATG GCT GAA TTA CCT CAA TC	1299 <sup>a</sup>	1-21
1294 <sup>b</sup>	5'-ATG ATT GTT GTA TAT CTT CTT CAA C	1299 <sup>a</sup>	2626-2651
1295 <sup>b</sup>	5'-CAG AAA GTT TGA AGC GTT GT	1299 <sup>a</sup>	1255-1275
1296	5'-AAC GAT TCG TGA GTC AGA TA	1299 <sup>a</sup>	1188-1208
1297	5'-CGG TCA ACA TTG AGG AAG AGC T	1300 <sup>a</sup>	29-51
1298 <sup>b</sup>	5'-ACG AAA TCG ACC GTC TCT TTT TC	1300 <sup>a</sup>	415-437
<b><u>Resistance gene:</u>                    <i>gyrB</i></b>			
1301	5'-GTI MGI AWT MGI CCI GSI ATG TA	1307 <sup>a</sup>	82-105
1302 <sup>b</sup>	5'-TAI ADI GGI GGI KKI GCI ATR TA	1307 <sup>a</sup>	1600-1623
1303	5'-GGI GAI GAI DYI MGI GAR GG	1307 <sup>a</sup>	955-975
1304 <sup>b</sup>	5'-CIA RYT TIK YIT TIG TYT G	1307 <sup>a</sup>	1024-1043
1305	5'-ATG GTG ACT GCA TTG TCA GAT G	1307 <sup>a</sup>	1-23
1306 <sup>b</sup>	5'-GTC TAC GGT TTT CTA CAA CGT C	1307 <sup>a</sup>	1858-1888

<sup>a</sup> Sequence from databases.

<sup>b</sup> These sequences are from the complementary DNA strand of the sequence of the originating fragment given in the Sequence Listing.

**Annex L: Specific and ubiquitous primers for nucleic acid amplification (antimicrobial agents resistance genes sequences) (continued).**

SEQ ID NO.	Nucleotide sequence	Originating DNA fragment	
		SEQ ID NO.	Nucleotide position
Sequencing primers (continued)			
<u>Resistance gene:</u> <i>parC</i>			
1308	5'-ATG TAY GTI ATI ATG GAY MGI GC	1320 <sup>a</sup>	67-90
1309 <sup>b</sup>	5'-ATI ATY TTR TTI CCY TTI CCY TT	1320 <sup>a</sup>	1993-2016
1310	5'-ATI ATI TSI ATI ACY TCR TC	1320 <sup>a</sup>	1112-1132
1311 <sup>b</sup>	5'-GAR ATG AAR ATI MGI GGI GAR CA	1320 <sup>a</sup>	1288-1311
1312	5'-AAR TAY ATI ATI CAR GAR MGI GC	1321 <sup>a</sup>	67-90
1313 <sup>b</sup>	5'-AMI AYI CKR TGI GGI TTI TTY TT	1321 <sup>a</sup>	2212-2235
1314	5'-TAI GAI TTY ACI GAI SMI CAR GC	1321 <sup>a</sup>	1228-1251
1315 <sup>b</sup>	5'-ACI ATI GCI TCI GCY TGI KSY TC	1321 <sup>a</sup>	1240-1263
1316	5'-GTG AGT GAA ATA ATT CAA GAT T	1321 <sup>a</sup>	1-23
1317 <sup>b</sup>	5'-CAC CAA AAT CAT CTG TAT CTA C	1321 <sup>a</sup>	2356-2378
1318	5'-ACC TAY TCS ATG TAC GTR ATC ATG GA	1320 <sup>a</sup>	58-84
1319 <sup>b</sup>	5'-AGR TCG TCI ACC ATC GGY AGY TT	1320 <sup>a</sup>	832-855
<u>Resistance gene:</u> <i>parE</i>			
1322	5'-RTI GAI AAY ISI GTI GAY GAR G	1328 <sup>a</sup>	133-155
1325 <sup>b</sup>	5'-RTT CAT YTC ICC IAR ICC YTT	1328 <sup>a</sup>	1732-1752
1323	5'-ACI AWR SAI GGI GGI ACI CAY G	1328 <sup>a</sup>	829-850
1324 <sup>b</sup>	5'-CCI CCI GCI SWR TCI CCY TC	1328 <sup>a</sup>	1280-1302
1326	5'-TGA TTC AAT ACA GGT TTT AGA G	1328 <sup>a</sup>	27-49
1327 <sup>b</sup>	5'-CTA GAT TTC CTC CTC ATC AAA T	1328 <sup>a</sup>	1971-1993

<sup>a</sup> Sequence from databases.

<sup>b</sup> These sequences are from the complementary DNA strand of the sequence of the originating fragment given in the Sequence Listing.

**Annex LI: Internal hybridization probes for specific detection of antimicrobial agents resistance genes sequences (continued).**

		Originating DNA fragment	
SEQ ID NO.	Nucleotide sequence	SEQ ID NO.	Nucleotide position
<u>Resistance gene:</u> <i>blaTEM</i> (continued)			
2007	5'-TGG AGC CAG TGA GCG TGG	2010 <sup>a</sup>	699-716
2008	5'-TCT GGA GCC GAT GAG CGT G	1929 <sup>a</sup>	697-715
2009	5'-CTG GAG CCA GTA AGC GTG G	2011 <sup>a</sup>	698-716
2141	5'-CAC CAG TCA CAG AAA AGC	1927 <sup>a</sup>	311-328
<u>Resistance gene:</u> <i>dhfrIa</i>			
2253	5'-CAT TAC CCA ACC GAA AGT A	1461 <sup>a</sup>	158-176
<u>Resistance gene:</u> <i>embB</i>			
2104	5'-CTG GGC ATG GCI CGA GTC	2105 <sup>a</sup>	910-927
<u>Resistance gene:</u> <i>gyrA</i>			
1333	5'-TCA TGG TGA CTT ATC TAT TTA TG	1299 <sup>a</sup>	240-263
1334	5'-CAT CTA TTT ATA AAG CAA TGG TA	1299 <sup>a</sup>	251-274
1335	5'-CTA TTT ATG GAG CAA TGG T	1299 <sup>a</sup>	254-273
1940	5'-GTA TCG TTG GTG ACG TAA T	1299 <sup>a</sup>	206-224
1943	5'-GCT GGT GGA CGG CCA G	1954 <sup>a</sup>	279-294
1945	5'-CGG CGA CTA CGC GGT AT	1954 <sup>a</sup>	216-232
1946	5'-CGG CGA CTT CGC GGT AT	1954 <sup>a</sup>	216-232
1947	5'-CGG TAT ACG GCA CCA TCG T	1954 <sup>a</sup>	227-245
1948	5'-GCG GTA TAC AAC ACC ATC G	1954 <sup>a</sup>	226-244
1949	5'-CGG TAT ACG CCA CCA TCG T	1954 <sup>a</sup>	227-245
2042	5'-CAC GGG GAT TTC TCT ATT TA	2054 <sup>a</sup>	103-122
2043	5'-CAC GGG GAT TAC TCT ATT TA	2054 <sup>a</sup>	103-122
<u>Resistance gene:</u> <i>inhA</i>			
2100	5'-GCG AGA CGA TAG GTT GTC	2101 <sup>a</sup>	1017-1034
<u>Resistance gene:</u> <i>parC</i>			
1336	5'-TGG AGA CTA CTC AGT GT	1321 <sup>a</sup>	232-249
1337	5'-TGG AGA CTT CTC AGT GT	1321 <sup>a</sup>	232-249
1338	5'-GTG TAC GGA GCA ATG	1321 <sup>a</sup>	245-260
1339	5'-CCA GCG GAA ATG CGT	1321 <sup>a</sup>	342-357
1941	5'-GCA ATG GTC CGT TTA AGT	1321 <sup>a</sup>	253-270
1944	5'-TTT CGC CGC CAT GCG TTA C	1781	247-265
1950	5'-GGC GAC ATC GCC TGC	1781	137-151
1951	5'-GGC GAC AGA GCC TGC TA	1781	137-153

<sup>a</sup> Sequence from databases.

**Annex LI: Internal hybridization probes for specific detection of antimicrobial agents resistance genes sequences.**

SEQ ID NO.	Nucleotide sequence	Originating DNA fragment	
		SEQ ID NO.	Nucleotide position
<b>Resistance gene:                   aph3'VIa</b>			
2252	5'-CCA CAT ACA GTG TCT CTC	1406 <sup>a</sup>	149-166
<b>Resistance gene:                   blaSHV</b>			
1886	5'-GAC GCC CGC GCC ACC ACT	1900 <sup>a</sup>	484-501
1887	5'-GAC GCC CGC GAC ACC ACT A	1899 <sup>a</sup>	514-532
1888	5'-GAC GCC CGC AAC ACC ACT A	1901 <sup>a</sup>	514-532
1889	5'-GTT CGC AAC TGC AGC TGC TG	1899 <sup>a</sup>	593-612
1890	5'-TTC GCA ACG GCA GCT GCT G	1899 <sup>a</sup>	594-612
1891	5'-CCG GAG CTG CCG AIC GGG	1902 <sup>a</sup>	692-709
1892	5'-CGG AGC TGC CAA RCG GGG	1903 <sup>a</sup>	693-710
1893	5'-GGA GCT GGC GAR CGG GGT	1899 <sup>a</sup>	694-711
1894	5'-GAC CGG AGC TAG CGA RCG	1904 <sup>a</sup>	690-707
1895	5'-CGG AGC TAG CAA RCG GGG T	1905 <sup>a</sup>	693-711
1896	5'-GAA ACG GAA CTG AAT GAG GCG	1899 <sup>a</sup>	484-504
1897	5'-CAT TAC CAT GGG CGA TAA CAG	1899 <sup>a</sup>	366-386
1898	5'-CCA TTA CCA TGA GCG ATA ACAG	1899 <sup>a</sup>	365-386
<b>Resistance gene:                   blaTEM</b>			
1909	5'-ATG ACT TGG TTA AGT ACT CAC C	1928 <sup>a</sup>	293-314
1910	5'-ATG ACT TGG TTG AGT ACT CAC C	1927 <sup>a</sup>	293-314
1911	5'-CCA TAA CCA TGG GTG ATA ACA C	1928 <sup>a</sup>	371-392
1912	5'-CCA TAA CCA TGA GTG ATA ACA C	1927 <sup>a</sup>	371-392
1913	5'-CGC CTT GAT CAT TGG GAA CC	1928 <sup>a</sup>	475-494
1914	5'-CGC CTT GAT CGT TGG GAA CC	1927 <sup>a</sup>	475-494
1915	5'-CGC CTT GAT AGT TGG GAA CC	1929 <sup>a</sup>	475-494
1916	5'-CGT GGG TCT TGC GGT ATC AT	1927 <sup>a</sup>	712-731
1917	5'-CGT GGG TCT GGC GGT ATC AT	1930 <sup>a</sup>	712-731
1918	5'-GTG GGT CTC ACG GTA TCA TTG	1927 <sup>a</sup>	713-733
1919	5'-CGT GGG TCT CTC GGT ATC ATT	1931 <sup>a</sup>	712-732
1920	5'-CGT GGI TCT CGC GGT ATC AT	1927 <sup>a</sup>	712-731
1921	5'-CGT GGG TCT AGC GGT ATC ATT	1932 <sup>a</sup>	713-733
1922	5'-GTT TTC CAA TGA TTA GCA CTT TTA	1927 <sup>a</sup>	188-211
1923	5'-GTT TTC CAA TGA TAA GCA CTT TTA	1927 <sup>a</sup>	188-211
1924	5'-GTT TTC CAA TGC TGA GCA CTT TT	1932 <sup>a</sup>	188-210
1925	5'-CGT TTT CCA ATG ATG AGC ACT TT	1927 <sup>a</sup>	187-209
1926	5'-GTT TTC CAA TGG TGA GCA CTT TT	1933 <sup>a</sup>	188-210
2006	5'-TGG AGC CGG TGA GCG TGG	1927 <sup>a</sup>	699-716

<sup>a</sup> Sequence from databases.

**Annex LI: Internal hybridization probes for specific detection of antimicrobial agents resistance genes sequences (continued).**

SEQ ID NO.	Nucleotide sequence	Originating DNA fragment	
		SEQ ID NO.	Nucleotide position
<u>Resistance gene:</u> <i>parC</i> (continued)			
1952	5'-CCT GCT ATG GAG CGA TGG T	1781	147-165
1953	5'-CGC CTG CTA TAA AGC GAT GGT	1781	145-165
2046	5'-ACG GGG ATT TTT CTA TCT AT	2055 <sup>a</sup>	227-246
<u>Resistance gene:</u> <i>rpoB</i>			
2067	5'-AGC TGA GCC AAT TCA TGG	2072 <sup>a</sup>	1304-1321
2068	5'-ATT CAT GGA CCA GAA CAA C	2072 <sup>a</sup>	1314-1332
2069	5'-CGC TGT CGG GGT TGA CCC	2072 <sup>a</sup>	1334-1351
2070	5'-GTT GAC CCA CAA GCG CCG	2072 <sup>a</sup>	1344-1361
2071	5'-CGA CTG TCG GCG CTG GGG	2072 <sup>a</sup>	1360-1377
<u>Resistance gene:</u> <i>tetM</i>			
2254	5'-ACC TGA ACA GAG AGA AAT G	1590 <sup>a</sup>	1062-1080

<sup>a</sup> Sequence from databases.

**Annex LII: Molecular beacon internal hybridization probes for specific detection of atpD sequences.**

		Originating DNA fragment	
SEQ ID NO.	Nucleotide sequence <sup>a</sup>	SEQ ID NO.	Nucleotide position
<b><u>Bacterial species:</u>           <i>Bacteroides fragilis</i></b>			
2136	5'- <u>CCA</u> <u>ACG</u> <u>CGT</u> CCT CAA TCA TTT CTA ACT TCT ATG GCC GGC <u>GTT</u> <u>GG</u>	929	353-382
<b><u>Bacterial species:</u>           <i>Bordetella pertussis</i></b>			
2182	5'- <u>GCG</u> <u>CGC</u> CAA CGA CTT CTA CCA CGA AAT GGA AGA GTC <u>GCG</u> <u>CGC</u>	1672	576-605
<b><u>Bacterial group:</u>           <i>Campylobacter jejuni</i> and <i>C. coli</i></b>			
2133	5'- <u>CCA</u> <u>CGC</u> ACA WAA ACT TGT TTT AGA AGT AGC AGC WCA <u>GCG</u> <u>TGG</u>	1576, 1600,1849, 1863,2139 <sup>b,c</sup>	44-73 <sup>d</sup>
<b><u>Fungal species:</u>           <i>Candida glabrata</i></b>			
2078	5'- <u>CCG</u> <u>AGC</u> CTT GGT CTT CGG CCA AAT GAA <u>CGC</u> <u>TCG</u> <u>G</u>	463	442-463
<b><u>Fungal species:</u>           <i>Candida krusei</i></b>			
2075	5'- <u>CCG</u> <u>AGC</u> CAG GTT CTG AAG TCT CTG CAT TAT TAG GTG <u>CTC</u> <u>GG</u>	468	720-748
<b><u>Fungal species:</u>           <i>Candida lusitanae</i></b>			
2080	5'- <u>CCG</u> <u>AGC</u> CGA AGA GGG CCA AGA TGT <u>CGC</u> <u>TCG</u> <u>G</u>	470	520-538
<b><u>Fungal species:</u>           <i>Candida parapsilosis</i></b>			
2079	5'- <u>CCG</u> <u>AGC</u> GTT CAG TTA CTT CAG TCC AAG CCG <u>GCT</u> <u>CGG</u>	472	837-860
<b><u>Fungal species:</u>           <i>Candida tropicalis</i></b>			
2077	5'- <u>CCG</u> <u>AGC</u> AAC CGA TCC AGC TCC AGC TAC <u>GCT</u> <u>CGG</u>	475	877-897
<b><u>Bacterial species:</u>           <i>Klebsiella pneumoniae</i></b>			
2281	5'- <u>CCC</u> <u>CCA</u> GCT GGG CGG CGG TAT CGA <u>TGG</u> <u>GGG</u>	317	40-59

<sup>a</sup> Underlined nucleotides indicate the molecular beacon's stem.

<sup>b</sup> Sequence from databases.

<sup>c</sup> These sequences were aligned to derive the corresponding primer.

<sup>d</sup> The nucleotide positions refer to the *C. jejuni* atpD sequence fragment (SEQ ID NO. 1576).

**Annex LII: Molecular beacon internal hybridization probes for specific detection of *atpD* sequences (continued).**

		Originating DNA fragment	
SEQ ID NO.	Nucleotide sequence <sup>a</sup>	SEQ ID NO.	Nucleotide position
<u>Fungal genus:</u> <i>Candida sp.</i>			
2076	5'- <u>CCG</u> <u>AGC</u> YGA YAA CAT TTT CAG ATT CAC CCA RGC <u>GCT</u> <u>CGG</u>	460-478, 663 <sup>b</sup>	697-723 <sup>c</sup>

<sup>a</sup> Underlined nucleotides indicate the molecular beacon's stem.

<sup>b</sup> These sequences were aligned to derive the corresponding primer.

<sup>c</sup> The nucleotide positions refer to the *C. albicans atpD* sequence fragment (SEQ ID NO. 460).

**Annex LIII: Internal hybridization probes for specific detection of *atpD* sequences.**

SEQ ID NO.	Nucleotide sequence	Originating DNA fragment	
		SEQ ID NO.	Nucleotide position
<hr/>			
<u>Bacterial species:</u> <i>Acinetobacter baumannii</i>			
2169	5'-CCC GTT TGC GAA AGG TGG	243	304-321
<hr/>			
<u>Bacterial species:</u> <i>Klebsiella pneumoniae</i>			
2167	5'-CAG CAG CTG GGC GGC GGT	317	36-53
<hr/>			



**Annex LIV: Internal hybridization probes for specific detection of *ddl* and *mt1* sequences.**

SEQ ID NO.	Nucleotide sequence	Originating DNA fragment	
		SEQ ID NO.	Nucleotide position
<u>Bacterial species:</u> <i>Enterococcus faecium (ddl)</i>			
2286	5'-AGT TGC TGT ATT AGG AAA TG	2288 <sup>a</sup>	784-803
2287	5'-TCG AAG TTG CTG TAT TAG GA	2288 <sup>a</sup>	780-799
<u>Bacterial species:</u> <i>Enterococcus faecalis mt1)</i>			
2289	5'-CAC CGA AGA AGA TGA AAA AA	1243 <sup>a</sup>	264-283
2290	5'-TGG CAC CGA AGA AGA TGA	1243 <sup>a</sup>	261-278
2291	5'-ATT TTG GCA CCG AAG AAG A	1243 <sup>a</sup>	257-275

<sup>a</sup> Sequence from databases.

**What is claimed is:**

1. A method for generating a repertory of nucleic acids of *tuf*, *fus*, *atpD* and/or *recA* genes from which are derived probes or primers, or both, useful for the detection of one, more than one related microorganisms, or substantially all microorganisms of a group selected from algae, archaea, bacteria, fungi and parasites, which comprises the step of:

- amplifying the nucleic acids of a plurality of determined algal, archaeal, bacterial, fungal and parasitical species with any combination of the primer pairs defined in SEQ ID NOs.: 543, 556-574, 636-655, 664, 681-683, 694, 696-697, 699-700, 708, 812-815, 911-917, 919-922, 935-938, 1203-1207, 1212-1213, 1221-1229, 1605-1606, 1974-1984, 1999-2003, 2282-2285.

2. A method for generating a repertory of nucleic acid sequences, which comprises the steps of:

- reproducing the method of claim 1, and
- adding the step of:
  - sequencing said nucleic acids.

3. A method for generating sequences of probes, or primers, or both, useful for the detection of one, more than one related microorganisms, or substantially all microorganisms of a group selected from algae, archaea, bacteria, fungi and parasites, which comprises the steps of:

- reproducing the method of claim 2, and
- adding the steps of:
  - aligning a subset of nucleic acid sequences of said repertory,
  - locating nucleic acid stretches that are present in the nucleic acids of strains or representatives of said one, more than one related microorganisms, or substantially all microorganisms of said group, and not present in the nucleic acid sequences of other microorganisms, and

- deriving consensus nucleic acid sequences useful as probes or primers from said stretches.

4. A bank of nucleic acids comprising the repertory of nucleic acids obtained from the method of claim 1.

5. A bank of nucleic acid sequences comprising the repertory of nucleic acid sequences obtained from the method of claim 2.

6. A method for generating sequences of probes, or primers, or both, useful for the detection of one, more than one related microorganisms, or substantially all microorganisms of a group selected from algae, archaea, bacteria, fungi and parasites, which comprises the steps of.

- aligning a subset of nucleic acid sequences of the bank as defined in claim 5,
- locating nucleic acid sequence stretches that are present in the nucleic acid sequences of strains or representatives of said one, more than one related microorganisms, or substantially all microorganisms of said group, and not present in the nucleic acid sequences of other microorganisms, and
- deriving consensus nucleic acid sequences useful as probes or primers from said stretches.

7. A method for generating probes, or primers or both, useful for the detection of one, more than one related microorganisms, or substantially all microorganisms of a group selected from algae, archaea, bacteria, fungi and parasites, which comprises the steps of:

- reproducing the method of claim 3 or 6, and
- adding the step of:
  - synthesising said probes or primers upon the nucleic acid sequences thereof.

8. A nucleic acid used for universal detection of any one of alga, archaeon, bacterium, fungus and parasite which is obtained from the method of claim 7.

9. A nucleic acid used for universal detection as set forth in claim 8, which has a nucleic acid sequence of at least 12 nucleotides capable of hybridizing with said any one of alga, archaeon, bacterium, fungus and parasite and with any one of SEQ ID NOs.: 543, 556-574, 636-655, 658-661, 664, 681-683, 694, 696, 697, 699, 700, 708, 812-815, 911-917, 919-922, 935-938, 1203-1207, 1212-1213, 1221-1229, 1605-1606, 1974-1984, 1999-2003, 2282-2285.

10. A nucleic acid used for the specific and ubiquitous detection and for identification of any one of a algal, archaeal, bacterial, fungal and parasitital species, genus, family and group, which is obtained from the method of claim 7.

11. A nucleic acid as set forth in claim 10 having any one of the nucleotide sequences which are defined in SEQ ID NOs.:

539, 540	for the detection and/or identification of <i>Mycobacteriaceae</i> family
541, 542, 544, 2121	for the detection and/or identification of Pseudomonads group
545, 546	for the detection and/or identification of <i>Corynebacterium</i> sp.
547, 548, 1202	for the detection and/or identification of <i>Streptococcus</i> sp.
549, 550, 582, 583, 625, 626, 627, 628, 1199	for the detection and/or identification of <i>Streptococcus agalactiae</i>
551, 552, 2166, 2173, 2174, 2175, 2176, 2177, 2178, 2179	for the detection and/or identification of <i>Neisseria gonorrhoeae</i>
553, 575, 605, 606, 707, 1175, 1176	for the detection and/or identification of <i>Staphylococcus</i> sp.
554, 555, 2213	for the detection and/or identification of <i>Chlamydia trachomatis</i>

576, 631, 632, 633, 634, 635, 1163, 1164, 1167, 2076, 2108, 2109	for the detection and/or identification of <i>Candida</i> sp.
577, 1156, 1160 2073	for the detection and/or identification of <i>Candida albicans</i>
578, 1166, 1168, 2074	for the detection and/or identification of <i>Candida dubliniensis</i>
579, 2168	for the detection and/or identification of <i>Escherichia coli</i>
580, 603, 1174, 1236, 1238, 2289, 2290, 2291	for the detection and/or identification of <i>Enterococcus faecalis</i>
581	for the detection and/or identification of <i>Haemophilus influenzae</i>
584, 585, 586, 587, 588, 1232, 1234, 2186	for the detection and/or identification of <i>Staphylococcus aureus</i>
589, 590, 591, 592, 593	for the detection and/or identification of <i>Staphylococcus epidermidis</i>
594, 595	for the detection and/or identification of <i>Staphylococcus haemolyticus</i>
596, 597, 598	for the detection and/or identification of <i>Staphylococcus hominis</i>
599, 600, 601, 695, 1208, 1209	for the detection and/or identification of <i>Staphylococcus saprophyticus</i>
602, 1235, 1237, 1696, 1697, 1698, 1699, 1700, 1701, 2286, 2287	for the detection and/or identification of <i>Enterococcus faecium</i>
604	for the detection and/or identification of <i>Enterococcus gallinarum</i>
620, 1122	for the detection and/or identification of <i>Enterococcus casseliflavus</i> , <i>E. flavescens</i> and <i>E. gallinarum</i>
629, 630, 2085, 2086, 2087, 2088, 2089, 2090, 2091, 2092	for the detection and/or identification of <i>Chlamydia pneumoniae</i>

636, 637, 638, 639, for the detection and/or identification of at least the following:  
640, 641, 642

*Abiotrophia adiacens*, *Abiotrophia defectiva*, *Acinetobacter baumannii*, *Acinetobacter lwoffii*, *Aerococcus viridans*, *Bacillus anthracis*, *Bacillus cereus*, *Bacillus subtilis*, *Brucella abortus*, *Burkholderia cepacia*, *Citrobacter diversus*, *Citrobacter freundii*, *Enterobacter aerogenes*, *Enterobacter agglomerans*, *Enterobacter cloacae*, *Enterococcus avium*, *Enterococcus casseliflavus*, *Enterococcus dispar*, *Enterococcus durans*, *Enterococcus faecalis*, *Enterococcus faecium*, *Enterococcus flavescens*, *Enterococcus gallinarum*, *Enterococcus mundtii*, *Enterococcus raffinosus*, *Enterococcus solitarius*, *Escherichia coli*, *Gemella morbillorum*, *Haemophilus ducreyi*, *Haemophilus haemolyticus*, *Haemophilus influenzae*, *Haemophilus parahaemolyticus*, *Haemophilus parainfluenzae*, *Hafnia alvei*, *Kingella kingae*, *Klebsiella oxytoca*, *Klebsiella pneumoniae*, *Legionella pneumophila*, *Megamonas hypermegale*, *Moraxella atlantiae*, *Moraxella catarrhalis*, *Morganella morganii*, *Neisseria gonorrhoeae*, *Neisseria meningitidis*, *Pasteurella aerogenes*, *Pasteurella multocida*, *Peptostreptococcus magnus*, *Proteus mirabilis*, *Providencia alcalifaciens*, *Providencia rettgeri*, *Providencia rustigianii*, *Providencia stuartii*, *Pseudomonas aeruginosa*, *Pseudomonas fluorescens*, *Pseudomonas stutzeri*, *Salmonella bongori*, *Salmonella choleraesuis*, *Salmonella enteritidis*, *Salmonella gallinarum*, *Salmonella typhimurium*, *Serratia liquefaciens*, *Serratia marcescens*, *Shigella flexneri*, *Shigella sonnei*, *Staphylococcus aureus*, *Staphylococcus capitis*, *Staphylococcus epidermidis*, *Staphylococcus haemolyticus*, *Staphylococcus hominis*, *Staphylococcus lugdunensis*, *Staphylococcus saprophyticus*, *Staphylococcus simulans*, *Staphylococcus warneri*, *Stenotrophomonas maltophilia*, *Streptococcus acidominimus*, *Streptococcus agalactiae*, *Streptococcus anginosus*, *Streptococcus bovis*, *Streptococcus constellatus*, *Streptococcus cricetus*, *Streptococcus cristatus*, *Streptococcus dysgalactiae*, *Streptococcus equi*, *Streptococcus ferus*, *Streptococcus gordonii*, *Streptococcus intermedius*, *Streptococcus macacae*, *Streptococcus mitis*, *Streptococcus mutans*, *Streptococcus oralis*, *Streptococcus parasanguinis*, *Streptococcus parauberis*, *Streptococcus pneumoniae*, *Streptococcus pyogenes*, *Streptococcus rattii*, *Streptococcus salivarius*, *Streptococcus sanguinis*, *Streptococcus sobrinus*, *Streptococcus uberis*, *Streptococcus vestibularis*, *Vibrio cholerae*, *Yersinia enterocolitica*, *Yersinia pestis*, *Yersinia pseudotuberculosis*.

656, 657, 271, for the detection and/or identification of *Enterococcus* sp.

1136, 1137

701, 702

for the detection and/or identification of *Leishmania* sp.

703, 704, 705, 706, 793	for the detection and/or identification of <i>Entamoeba</i> sp.
794, 795	for the detection and/or identification of <i>Trypanosoma cruzi</i>
796, 797, 808, 809, 810, 811	for the detection and/or identification of <i>Clostridium</i> sp.
798, 799, 800, 801, 802, 803, 804, 805, 806, 807	for the detection and/or identification of <i>Cryptosporidium parvum</i>
816, 817, 818, 819	for the detection and/or identification of <i>Giardia</i> sp.
820, 821, 822	for the detection and/or identification of <i>Trypanosoma brucei</i>
823, 824	for the detection and/or identification of <i>Trypanosoma</i> sp.
825, 826	for the detection and/or identification of <i>Bordetella</i> sp.
923, 924, 925, 926, 927, 928	for the detection and/or identification of <i>Trypanosomatidae</i> family
933, 934	for the detection and/or identification of <i>Enterobacteriaceae</i> group
994, 995, 996, 997, 998, 999, 1000, 1001, 1200, 1210, 1211	for the detection and/or identification of <i>Streptococcus pyogenes</i>
1157, 2079, 2118	for the detection and/or identification of <i>Candida parapsilosis</i>
1158, 1159, 2078, 2110, 2111	for the detection and/or identification of <i>Candida glabrata</i>
1160, 2077, 2119, 2120	for the detection and/or identification of <i>Candida tropicalis</i>
1161, 2075, 2112, 2113, 2114	for the detection and/or identification of <i>Candida krusei</i>
1162	for the detection and/or identification of <i>Candida guilliermondii</i>
1162, 2080, 2115, 2116, 2117	for the detection and/or identification of <i>Candida lusitanae</i>
1165	for the detection and/or identification of <i>Candida zeylanoides</i>
1201	for the detection and/or identification of <i>Streptococcus pneumoniae</i>

1233	for the detection and/or identification of <i>Staphylococcus</i> sp. other than <i>S. aureus</i>
1329, 1330, 1331, 1332, 2167, 2281	for the detection and/or identification of <i>Klebsiella pneumoniae</i>
1661, 1665	for the detection and/or identification of <i>Escherichia coli</i> and <i>Shigella</i> sp.
1690, 1691, 1692, 1693, 2169	for the detection and/or identification of <i>Acinetobacter baumannii</i>
1694, 1695, 2122	for the detection and/or identification of <i>Pseudomonas aeruginosa</i>
1971, 1972, 1973	for the detection and/or identification of <i>Cryptococcus</i> sp.
2081, 2082, 2083	for the detection and/or identification of <i>Legionella</i> sp.
2084	for the detection and/or identification of <i>Legionella pneumophila</i>
2093, 2094, 2095, 2096	for the detection and/or identification of <i>Mycoplasma pneumoniae</i>
2106, 2107	for the detection and/or identification of <i>Cryptococcus neoformans</i>
2131, 2132, 2133	for the detection and/or identification of <i>Campylobacter jejuni</i> and <i>C. coli</i>
2134, 2135, 2136	for the detection and/or identification of <i>Bacteroides fragilis</i>
2170	for the detection and/or identification of <i>Abiotrophia adiacens</i>
2171	for the detection and/or identification of <i>Gemella</i> sp.
2172	for the detection and/or identification of <i>Enterococcus</i> sp., <i>Gemella</i> sp., <i>A. adiacens</i>
2180, 2181, 2182	for the detection and/or identification of <i>Bordetella pertussis</i> .

12. A method for detecting the presence in a test sample of a microorganism that is an alga, archaeum, bacterium, fungus or parasite, which comprises:

- a) putting in contact any test sample *tuf* or *atpD* or *recA* nucleic acids and nucleic acid primers and/or probes, said primers and/or probes having



been selected to be sufficiently complementary to hybridize to one or more *tuf* or *atpD* or *recA* nucleic acids that are specific to said group of microorganisms;

b) allowing the primers and/or probes and any test sample *tuf* or *atpD* or *recA* nucleic acids to hybridize under specified conditions such as said primers and/or probes hybridize to the *tuf* or *atpD* or *recA* nucleic acids of said microorganism and does not detectably hybridize to *tuf* or *atpD* or *recA* sequences from other microorganisms; and,

c) testing for hybridization of said primers and/or probes to any test sample *tuf* or *atpD* or *recA* nucleic acids.

13. The method of claim 12 wherein c) is based on a nucleic acid target amplification method.

14. The method of claim 12 wherein c) is based on a signal amplification method.

15. The method of any one of claims 12 to 14 wherein said primers and/or probes that are sufficiently complementary are perfectly complementary.

16. The method of any one of claims 12 to 14 wherein said primers and/or probes that are sufficiently complementary are not perfectly complementary.

17. A method for the specific detection and/or identification of a microorganism that is an algal, archaeal, bacterial, fungal or parasitical species, genus, family or group in any sample, using a panel of probes or amplification primers or both, each individual probe or primer being derived from a nucleic acid which has a nucleotide sequence of at least 12 nucleotides in length capable of hybridizing with the nucleic acids of said microorganism and with a nucleic acid having any one of the nucleotide sequences defined in SEQ ID NOs.:

539, 540	for the detection and/or identification of <i>Mycobacteriaceae</i> family
541, 542, 544, 2121	for the detection and/or identification of <i>Pseudomonads</i> group

- 545, 546 for the detection and/or identification of *Corynebacterium* sp.
- 547, 548, 1202 for the detection and/or identification of *Streptococcus* sp.
- 549, 550, 582, 583, 625, 626, 627, 628, 1199 for the detection and/or identification of *Streptococcus agalactiae*
- 551, 552, 2166, 2173, 2174, 2175, 2176, 2177, 2178, 2179 for the detection and/or identification of *Neisseria gonorrhoeae*
- 553, 575, 605, 606, 707, 1175, 1176 for the detection and/or identification of *Staphylococcus* sp.
- 554, 555, 2213 for the detection and/or identification of *Chlamydia trachomatis*
- 576, 631, 632, 633, 634, 635, 1163, 1164, 1167, 2076, 2108, 2109 for the detection and/or identification of *Candida* sp.
- 577, 1156, 1160 2073 for the detection and/or identification of *Candida albicans*
- 578, 1166, 1168, 2074 for the detection and/or identification of *Candida dubliniensis*
- 579, 2168 for the detection and/or identification of *Escherichia coli*
- 580, 603, 1174, 1236, 1238, 2289, 2290, 2291 for the detection and/or identification of *Enterococcus faecalis*
- 581 for the detection and/or identification of *Haemophilus influenzae*
- 584, 585, 586, 587, 588, 1232, 1234, 2186 for the detection and/or identification of *Staphylococcus aureus*
- 589, 590, 591, 592, 593 for the detection and/or identification of *Staphylococcus epidermidis*
- 594, 595 for the detection and/or identification of *Staphylococcus haemolyticus*
- 596, 597, 598 for the detection and/or identification of *Staphylococcus hominis*

- 599, 600, 601, 695, 1208, 1209 for the detection and/or identification of *Staphylococcus saprophyticus*
- 602, 1235, 1237, 1696, 1697, 1698, 1699, 1700, 1701, 2286, 2287 for the detection and/or identification of *Enterococcus faecium*
- 604 for the detection and/or identification of *Enterococcus gallinarum*
- 620, 1122 for the detection and/or identification of *Enterococcus casseliflavus*, *E. flavescens* and *E. gallinarum*
- 629, 630, 2085, 2086, 2087, 2088, 2089, 2090, 2091, 2092 for the detection and/or identification of *Chlamydia pneumoniae*
- 636, 637, 638, 639, 640, 641, 642 for the detection and/or identification of at least the following: *Abiotrophia adiacens*, *Abiotrophia defectiva*, *Acinetobacter baumannii*, *Acinetobacter lwoffii*, *Aerococcus viridans*, *Bacillus anthracis*, *Bacillus cereus*, *Bacillus subtilis*, *Brucella abortus*, *Burkholderia cepacia*, *Citrobacter diversus*, *Citrobacter freundii*, *Enterobacter aerogenes*, *Enterobacter agglomerans*, *Enterobacter cloacae*, *Enterococcus avium*, *Enterococcus casseliflavus*, *Enterococcus dispar*, *Enterococcus durans*, *Enterococcus faecalis*, *Enterococcus faecium*, *Enterococcus flavescens*, *Enterococcus gallinarum*, *Enterococcus mundtii*, *Enterococcus raffinosus*, *Enterococcus solitarius*, *Escherichia coli*, *Gemella morbillorum*, *Haemophilus ducreyi*, *Haemophilus haemolyticus*, *Haemophilus influenzae*, *Haemophilus parahaemolyticus*, *Haemophilus parainfluenzae*, *Hafnia alvei*, *Kingella kingae*, *Klebsiella oxytoca*, *Klebsiella pneumoniae*, *Legionella pneumophila*, *Megamonas hypermegale*, *Moraxella atlantae*, *Moraxella catarrhalis*, *Morganella morganii*, *Neisseria gonorrhoeae*, *Neisseria meningitidis*, *Pasteurella aerogenes*, *Pasteurella multocida*, *Peptostreptococcus magnus*, *Proteus mirabilis*, *Providencia alcalifaciens*, *Providencia rettgeri*, *Providencia rustigianii*, *Providencia stuartii*, *Pseudomonas aeruginosa*, *Pseudomonas fluorescens*, *Pseudomonas stutzeri*, *Salmonella bongori*, *Salmonella choleraesuis*, *Salmonella enteritidis*, *Salmonella gallinarum*, *Salmonella typhimurium*, *Serratia liquefaciens*, *Serratia marcescens*, *Shigella flexneri*, *Shigella sonnei*, *Staphylococcus aureus*, *Staphylococcus capitis*, *Staphylococcus epidermidis*, *Staphylococcus haemolyticus*, *Staphylococcus hominis*, *Staphylococcus lugdunensis*, *Staphylococcus saprophyticus*, *Staphylococcus simulans*, *Staphylococcus warneri*, *Stenotrophomonas*

	<i>maltophilia, Streptococcus acidominimus, Streptococcus agalactiae, Streptococcus anginosus, Streptococcus bovis, Streptococcus constellatus, Streptococcus cricetus, Streptococcus cristatus, Streptococcus dysgalactiae, Streptococcus equi, Streptococcus ferus, Streptococcus gordonii, Streptococcus intermedius, Streptococcus macacae, Streptococcus mitis, Streptococcus mutans, Streptococcus oralis, Streptococcus parasanguinis, Streptococcus parauberis, Streptococcus pneumoniae, Streptococcus pyogenes, Streptococcus ratti, Streptococcus salivarius, Streptococcus sanguinis, Streptococcus sobrinus, Streptococcus uberis, Streptococcus vestibularis, Vibrio cholerae, Yersinia enterocolitica, Yersinia pestis, Yersinia pseudotuberculosis.</i>
656, 657, 271, 1136, 1137	for the detection and/or identification of <i>Enterococcus</i> sp.
701, 702	for the detection and/or identification of <i>Leishmania</i> sp.
703, 704, 705, 706, 793	for the detection and/or identification of <i>Entamoeba</i> sp.
794, 795	for the detection and/or identification of <i>Trypanosoma cruzi</i>
796, 797, 808, 809, 810, 811	for the detection and/or identification of <i>Clostridium</i> sp.
798, 799, 800, 801, 802, 803, 804, 805, 806, 807	for the detection and/or identification of <i>Cryptosporidium parvum</i>
816, 817, 818, 819	for the detection and/or identification of <i>Giardia</i> sp.
820, 821, 822	for the detection and/or identification of <i>Trypanosoma brucei</i>
823, 824	for the detection and/or identification of <i>Trypanosoma</i> sp.
825, 826	for the detection and/or identification of <i>Bordetella</i> sp.
923, 924, 925, 926, 927, 928	for the detection and/or identification of <i>Trypanosomatidae</i> family
933, 934	for the detection and/or identification of <i>Enterobacteriaceae</i> group
994, 995, 996, 997, 998, 999, 1000, 1001, 1200, 1210, 1211	for the detection and/or identification of <i>Streptococcus pyogenes</i>
1157, 2079, 2118	for the detection and/or identification of <i>Candida parapsilosis</i>

1158, 1159, 2078, 2110, 2111	for the detection and/or identification of <i>Candida glabrata</i>
1160, 2077, 2119, 2120	for the detection and/or identification of <i>Candida tropicalis</i>
1161, 2075, 2112, 2113, 2114	for the detection and/or identification of <i>Candida krusei</i>
1162	for the detection and/or identification of <i>Candida guilliermondii</i>
1162, 2080, 2115 2116, 2117	for the detection and/or identification of <i>Candida lusitaniae</i>
1165	for the detection and/or identification of <i>Candida zeylanoides</i>
1201	for the detection and/or identification of <i>Streptococcus pneumoniae</i>
1233	for the detection and/or identification of <i>Staphylococcus</i> sp. other than <i>S. aureus</i>
1329, 1330, 1331, 1332, 2167, 2281	for the detection and/or identification of <i>Klebsiella pneumoniae</i>
1661, 1665	for the detection and/or identification of <i>Escherichia coli</i> and <i>Shigella</i> sp.
1690, 1691, 1692, 1693, 2169	for the detection and/or identification of <i>Acinetobacter baumannii</i>
1694, 1695, 2122	for the detection and/or identification of <i>Pseudomonas aeruginosa</i>
1971, 1972, 1973	for the detection and/or identification of <i>Cryptococcus</i> sp.
2081, 2082, 2083	for the detection and/or identification of <i>Legionella</i> sp.
2084	for the detection and/or identification of <i>Legionella pneumophila</i>
2093, 2094, 2095, 2096	for the detection and/or identification of <i>Mycoplasma pneumoniae</i>
2106, 2107	for the detection and/or identification of <i>Cryptococcus neoformans</i>
2131, 2132, 2133	for the detection and/or identification of <i>Campylobacter jejuni</i> and <i>C. coli</i>
2134, 2135, 2136	for the detection and/or identification of <i>Bacteroides fragilis</i>

- 2170 for the detection and/or identification of *Abiotrophia adiacens*  
 2171 for the detection and/or identification of *Gemella* sp.  
 2172 for the detection and/or identification of *Enterococcus* sp.,  
*Gemella* sp., *A. adiacens*  
 2180, 2181, 2182 for the detection and/or identification of *Bordetella pertussis*,

said method comprising the step of contacting the nucleic acids of the sample with said primers or probes under suitable conditions of hybridization or of amplification and detecting the presence of hybridized probes or amplified products as an indication of the presence of said specific algal, archaeal, bacterial, fungal or parasitical species, genus, family or group.

18. A method for the universal detection of any bacterium, fungus or parasite in a sample, using a panel of probes or amplification primers or both, each individual probe or primer being derived from a nucleic acid as defined in claims 8 or 9, the method comprising the step of contacting the nucleic acids of the sample with said primers or probes under suitable conditions of hybridization or of amplification and detecting the presence of any alga, archaeon, bacterium, fungus or parasite.

19. A method as set forth in claim 17 or 18, which further comprises probes or primers, or both, for the detection of at least one antimicrobial agent resistance gene.

20. A method as set forth in claim 17, 18 or 19, which further comprises probes or primers, or both, for the detection of at least one toxin gene.

21. A method as set forth in claim 19 or 20, wherein the probes or primers for the detection of said antimicrobial agent resistance gene or toxin gene have at least 12 nucleotides in length capable of hybridizing with an antimicrobial agent resistance gene and/or toxin gene selected from SEQ ID NOs.:

- 1078, 1079, 1085 for the detection and/or identification of the *E. coli* Shiga-like toxin 2 (*stx*<sub>2</sub>) gene

1080, 1081, 1084, 2012	for the detection and/or identification of the <i>E. coli</i> Shiga-like toxin 1 ( <i>stx<sub>I</sub></i> ) gene
1082, 1083	for the detection and/or identification of <i>E. coli</i> Shiga-like toxins 1 and 2 ( <i>stx</i> ) genes
1086, 1087, 1088, 1089, 1090, 1091, 1092, 1170, 1239, 1240, 2292	for the detection and/or identification of the <i>vanA</i> resistance gene
1095, 1096, 1171, 1241, 2294, 2295	for the detection and/or identification of the <i>vanB</i> resistance gene
1111, 1112, 1113, 1114, 1115, 1116, 1118, 1119, 1120, 1121, 1123, 1124	for the detection and/or identification of the <i>vanAB</i> resistance genes
1103, 1104, 1109, 1110	for the detection and/or identification of the <i>vanC1</i> resistance gene
1105, 1106, 1107, 1108	for the detection and/or identification of the <i>vanC2</i> and <i>vanC3</i> resistance genes
1097, 1098, 1099, 1100, 1101, 1102	for the detection and/or identification of the <i>vanC1</i> , <i>vanC2</i> and <i>vanC3</i> resistance genes
1150, 1153, 1154, 1155	for the detection and/or identification of the <i>vanAXY</i> resistance genes
1094, 1125, 1126, 1127, 1128, 1129, 1130, 1131, 1132, 1133, 1134, 1135, 1192, 1193, 1194, 1195, 1196, 1197, 1214, 1216, 1217, 1218, 1219, 1220, 2015, 2016, 2017, 2018, 2019, 2020, 2021, 2022, 2023, 2024, 2025, 2026, 2027, 2028, 2029, 2030, 2031, 2032, 2033, 2034, 2035, 2036, 2037, 2038, 2039	for the detection and/or identification of the <i>S. pneumoniae</i> <i>pbp1a</i> gene

1142, 1143, 1144, 1145	for the detection and/or identification of the <i>S. pneumoniae</i> <i>pbp2b</i> gene
1146, 1147, 1148, 1149	for the detection and/or identification of the <i>S. pneumoniae</i> <i>pbp2x</i> gene
1177, 1231	for the detection and/or identification of the <i>mecA</i> resistance gene
1290, 1291, 1292, 1293, 1294, 1295, 1296, 1297, 1298, 1333, 1334, 1335, 1340, 1341, 1936, 1937, 1940, 1942, 1943, 1945, 1946, 1947, 1948, 1949, 2040, 2041, 2042, 2043, 2250, 2251	for the detection and/or identification of the <i>gyrA</i> resistance gene
1301, 1302, 1303, 1304, 1305, 1306	for the detection and/or identification of the <i>gyrB</i> resistance gene
1308, 1309, 1310, 1311, 1312, 1313, 1314, 1315, 1316, 1317, 1318, 1319, 1336, 1337, 1338, 1339, 1342, 1343, 1934, 1935, 1938, 1939, 1941, 1944, 1950, 1951, 1952, 1953, 1955, 2044, 2045, 2046	for the detection and/or identification of the <i>parC</i> resistance gene
1322, 1323, 1324, 1325, 1326, 1327	for the detection and/or identification of the <i>parE</i> resistance gene
1344, 1345, 1346, 1347	for the detection and/or identification of the <i>aac(2')-Ia</i> resistance gene
1349, 1350	for the detection and/or identification of the <i>aac(3')-Ib</i> resistance gene
1352, 1353, 1354, 1355	for the detection and/or identification of the <i>aac(3')-IIb</i> resistance gene
1357, 1358, 1359, 1360	for the detection and/or identification of the <i>aac(3')-IVa</i> resistance gene
1362, 1363, 1364, 1365	for the detection and/or identification of the <i>aac(3')-VIa</i> resistance gene



1367, 1368, 1369, 1370	for the detection and/or identification of the <i>aac(6')-Ia</i> resistance gene
1372, 1373, 1374, 1375	for the detection and/or identification of the <i>aac(6')-Ic</i> resistance gene
1377, 1378, 1379, 1380	for the detection and/or identification of the <i>ant(3')-Ia</i> resistance gene
1382, 1383, 1384, 1385	for the detection and/or identification of the <i>ant(4')-Ia</i> resistance gene
1387, 1388, 1389, 1390	for the detection and/or identification of the <i>aph(3')-Ia</i> resistance gene
1392, 1393, 1394, 1395	for the detection and/or identification of the <i>aph(3')-IIa</i> resistance gene
1397, 1398, 1399, 1400	for the detection and/or identification of the <i>aph(3')-IIIa</i> resistance gene
1402, 1403, 1404, 1405, 2252	for the detection and/or identification of the <i>aph(3')-VIa</i> resistance gene
1407, 1408, 1409 1410	for the detection and/or identification of the <i>blaCARB</i> resistance gene
1412, 1413, 1414, 1415	for the detection and/or identification of the <i>blaCMY-2</i> resistance gene
1417, 1418	for the detection and/or identification of the <i>blaCTX-M-1</i> and <i>blaCTX-M-2</i> resistance genes
1419, 1420, 1421, 1422	for the detection and/or identification of the <i>blaCTX-M-1</i> resistance gene
1424, 1425, 1426, 1427	for the detection and/or identification of the <i>blaCTX-M-2</i> resistance gene
1429, 1430, 1431, 1432	for the detection and/or identification of the <i>blaIMP</i> resistance gene
1434, 1435	for the detection and/or identification of the <i>blaOXA2</i> resistance gene
1436, 1437	for the detection and/or identification of the <i>blaOXA10</i> resistance gene
1440, 1441	for the detection and/or identification of the <i>blaPER-1</i> resistance gene

1443, 1444	for the detection and/or identification of the <i>blaPER-2</i> resistance gene
1446, 1447, 1448, 1449	for the detection and/or identification of the <i>blaPER-1</i> and <i>blaPER-2</i> resistance genes
1450, 1451	for the detection and/or identification of the <i>dhfrA</i> resistance gene
1453, 1454, 1455, 1456	for the detection and/or identification of the <i>dhfrIa</i> and <i>dhfrXV</i> resistance genes
1457, 1458, 1459, 1460, 2253	for the detection and/or identification of the <i>dhfrIa</i> resistance gene
1462, 1463, 1464, 1465	for the detection and/or identification of the <i>dhfrIb</i> and <i>dhfrV</i> resistance genes
1466, 1467, 1468, 1469	for the detection and/or identification of the <i>dhfrIb</i> resistance gene
1471, 1472, 1473, 1474	for the detection and/or identification of the <i>dhfrV</i> resistance gene
1476, 1477, 1478, 1479	for the detection and/or identification of the <i>dhfrVI</i> resistance gene
1481, 1482, 1483, 1484	for the detection and/or identification of the <i>dhfrVII</i> and <i>dhfrXVII</i> resistance genes
1485, 1486, 1487, 1488	for the detection and/or identification of the <i>dhfrVII</i> resistance gene
1490, 1491, 1492, 1493	for the detection and/or identification of the <i>dhfrVIII</i> resistance gene
1495, 1496, 1497, 1498	for the detection and/or identification of the <i>dhfrIX</i> resistance gene
1500, 1501, 1502, 1503	for the detection and/or identification of the <i>dhfrXII</i> resistance gene
1505, 1506	for the detection and/or identification of the <i>dhfrXIII</i> resistance gene
1508, 1509, 1510, 1511	for the detection and/or identification of the <i>dhfrXV</i> resistance gene
1513, 1514, 1515, 1516	for the detection and/or identification of the <i>dhfrXVII</i> resistance gene

1528, 1529	for the detection and/or identification of the <i>ereA</i> and <i>ereA2</i> resistance genes
1531, 1532, 1533, 1534	for the detection and/or identification of the <i>ereB</i> resistance gene
1536, 1537, 1538, 1539	for the detection and/or identification of the <i>linA</i> and <i>linA'</i> resistance genes
1541, 1542, 1543, 1544	for the detection and/or identification of the <i>linB</i> resistance gene
1546, 1547	for the detection and/or identification of the <i>mefA</i> resistance gene
1549, 1550	for the detection and/or identification of the <i>mefE</i> resistance gene
1552, 1553, 1554, 1555	for the detection and/or identification of the <i>mefA</i> and <i>mefE</i> resistance genes
1556, 1557, 1558, 1559	for the detection and/or identification of the <i>mphA</i> and <i>mphK</i> resistance genes
1581, 1582, 1583, 1584	for the detection and/or identification of the <i>satG</i> resistance gene
1586, 1587, 1588, 1589, 2254	for the detection and/or identification of the <i>tetM</i> resistance gene
1591, 1592, 1593, 2297	for the detection and/or identification of the <i>vanD</i> resistance gene
1595, 1596, 1597, 1598	for the detection and/or identification of the <i>vanE</i> resistance gene
1609, 1610, 1611, 1612	for the detection and/or identification of the <i>vatB</i> resistance gene
1614, 1615, 1616, 1617	for the detection and/or identification of the <i>vatC</i> resistance gene
1619, 1620, 1621, 1622	for the detection and/or identification of the <i>vga</i> resistance gene
1624, 1625, 1626, 1627	for the detection and/or identification of the <i>vgaB</i> resistance gene
1629, 1630, 1631, 1632	for the detection and/or identification of the <i>vgb</i> and <i>vgh</i> resistance genes

1634, 1635, 1636, 1637	for the detection and/or identification of the <i>vgbB</i> resistance gene
1883, 1884, 1885, 1886, 1887, 1888, 1889, 1890, 1891, 1892, 1893, 1894, 1895, 1896, 1897, 1898	for the detection and/or identification of the <i>blaSHV</i> resistance gene
1906, 1907, 1908, 1909, 1910, 1911, 1912, 1913, 1914, 1915, 1916, 1917, 1918, 1919, 1920, 1921, 1922, 1923, 1924, 1925, 1926, 2006, 2007, 2008, 2009, 2141	for the detection and/or identification of the <i>blaTEM</i> resistance gene
1961, 1962, 1963, 1964	for the detection and/or identification of the <i>sulIII</i> resistance gene
1966, 1967, 1968, 1969	for the detection and/or identification of the <i>tetB</i> resistance gene
2065, 2066, 2067, 2068, 2069, 2070, 2071	for the detection and/or identification of the <i>rhoB</i> resistance gene
2098, 2099, 2100	for the detection and/or identification of the <i>inhA</i> resistance gene
2102, 2103, 2104	for the detection and/or identification of the <i>embB</i> resistance gene
2123, 2124, 2125	for the detection and/or identification of the <i>C. difficile cdtA</i> toxin gene
2126, 2127, 2128	for the detection and/or identification of the <i>C. difficile cdtB</i> toxin gene
2142, 2143	for the detection and/or identification of the <i>mupA</i> resistance gene
2145, 2146	for the detection and/or identification of the <i>catI</i> resistance gene
2148, 2149	for the detection and/or identification of the <i>catII</i> resistance gene

2151, 2152	for the detection and/or identification of the <i>catIII</i> resistance gene
2154, 2155	for the detection and/or identification of the <i>catP</i> resistance gene
2157, 2158, 2160, 2161	for the detection and/or identification of the <i>cat</i> resistance gene
2163, 2164	for the detection and/or identification of the <i>ppflo</i> -like resistance gene.

22. A composition of matter comprising a specific nucleic acid as set forth in claim 10 or 11, which is specific for a bacterial, fungal or parasitical species, genus, family, or group, or a nucleic acid as set forth in claim 8 or 9 which is universal for a bacterium, fungus or parasite, or both specific and universal nucleic acids, in conjunction with a nucleic acid sequence of at least 12 nucleotides capable of hybridizing with an antimicrobial agent resistance gene and/or toxin gene.

23. A composition as set forth in claim 22, wherein the nucleic acid capable of hybridizing with an antimicrobial agent resistance gene and/or toxin gene is any one of:

1078, 1079, 1085	for the detection and/or identification of the <i>E. coli</i> Shiga-like toxin 2 ( <i>stx</i> <sub>2</sub> ) gene
1080, 1081, 1084, 2012	for the detection and/or identification of the <i>E. coli</i> Shiga-like toxin 1 ( <i>stx</i> <sub>1</sub> ) gene
1082, 1083	for the detection and/or identification of <i>E. coli</i> Shiga-like toxins 1 and 2 ( <i>stx</i> ) genes
1086, 1087, 1088, 1089, 1090, 1091, 1092, 1170, 1239, 1240, 2292	for the detection and/or identification of the <i>vanA</i> resistance gene
1095, 1096, 1171, 1241, 2294, 2295	for the detection and/or identification of the <i>vanB</i> resistance gene
1111, 1112, 1113, 1114, 1115, 1116, 1118, 1119, 1120, 1121, 1123, 1124	for the detection and/or identification of the <i>vanAB</i> resistance genes

1103, 1104, 1109, 1110	for the detection and/or identification of the <i>vanC1</i> resistance gene
1105, 1106, 1107, 1108	for the detection and/or identification of the <i>vanC2</i> and <i>vanC3</i> resistance genes
1097, 1098, 1099, 1100, 1101, 1102	for the detection and/or identification of the <i>vanC1</i> , <i>vanC2</i> and <i>vanC3</i> resistance genes
1150, 1153, 1154, 1155	for the detection and/or identification of the <i>vanAXY</i> resistance genes
1094, 1125, 1126, 1127, 1128, 1129, 1130, 1131, 1132, 1133, 1134, 1135, 1192, 1193, 1194, 1195, 1196, 1197, 1214, 1216, 1217, 1218, 1219, 1220, 2015, 2016, 2017, 2018, 2019, 2020, 2021, 2022, 2023, 2024, 2025, 2026, 2027, 2028, 2029, 2030, 2031, 2032, 2033, 2034, 2035, 2036, 2037, 2038, 2039	for the detection and/or identification of the <i>S. pneumoniae pbp1a</i> gene
1142, 1143, 1144, 1145	for the detection and/or identification of the <i>S. pneumoniae pbp2b</i> gene
1146, 1147, 1148, 1149	for the detection and/or identification of the <i>S. pneumoniae pbp2x</i> gene
1177, 1231	for the detection and/or identification of the <i>mecA</i> resistance gene
1290, 1291, 1292, 1293, 1294, 1295, 1296, 1297, 1298, 1333, 1334, 1335, 1340, 1341, 1936, 1937, 1940, 1942, 1943, 1945, 1946, 1947, 1948, 1949, 2040, 2041, 2042, 2043, 2250, 2251	for the detection and/or identification of the <i>gyrA</i> resistance gene

1301, 1302, 1303, 1304, 1305, 1306	for the detection and/or identification of the <i>gyrB</i> resistance gene
1308, 1309, 1310, 1311, 1312, 1313, 1314, 1315, 1316, 1317, 1318, 1319, 1336, 1337, 1338, 1339, 1342, 1343, 1934, 1935, 1938, 1939, 1941, 1944, 1950, 1951, 1952, 1953, 1955, 2044, 2045, 2046	for the detection and/or identification of the <i>parC</i> resistance gene
1322, 1323, 1324, 1325, 1326, 1327	for the detection and/or identification of the <i>parE</i> resistance gene
1344, 1345, 1346, 1347	for the detection and/or identification of the <i>aac(2')-Ia</i> resistance gene
1349, 1350	for the detection and/or identification of the <i>aac(3')-Ib</i> resistance gene
1352, 1353, 1354, 1355	for the detection and/or identification of the <i>aac(3')-IIb</i> resistance gene
1357, 1358, 1359, 1360	for the detection and/or identification of the <i>aac(3')-IVa</i> resistance gene
1362, 1363, 1364, 1365	for the detection and/or identification of the <i>aac(3')-VIa</i> resistance gene
1367, 1368, 1369, 1370	for the detection and/or identification of the <i>aac(6')-Ia</i> resistance gene
1372, 1373, 1374, 1375	for the detection and/or identification of the <i>aac(6')-Ic</i> resistance gene
1377, 1378, 1379, 1380	for the detection and/or identification of the <i>ant(3')-Ia</i> resistance gene
1382, 1383, 1384, 1385	for the detection and/or identification of the <i>ant(4')-Ia</i> resistance gene
1387, 1388, 1389, 1390	for the detection and/or identification of the <i>aph(3')-Ia</i> resistance gene
1392, 1393, 1394, 1395	for the detection and/or identification of the <i>aph(3')-IIa</i> resistance gene
1397, 1398, 1399, 1400	for the detection and/or identification of the <i>aph(3')-IIIa</i> resistance gene

1402, 1403, 1404, 1405, 2252	for the detection and/or identification of the <i>aph(3')-VIa</i> resistance gene
1407, 1408, 1409 1410	for the detection and/or identification of the <i>blaCARB</i> resistance gene
1412, 1413, 1414, 1415	for the detection and/or identification of the <i>blaCMY-2</i> resistance gene
1417, 1418	for the detection and/or identification of the <i>blaCTX-M-1</i> and <i>blaCTX-M-2</i> resistance genes
1419, 1420, 1421, 1422	for the detection and/or identification of the <i>blaCTX-M-1</i> resistance gene
1424, 1425, 1426, 1427	for the detection and/or identification of the <i>blaCTX-M-2</i> resistance gene
1429, 1430, 1431, 1432	for the detection and/or identification of the <i>blaIMP</i> resistance gene
1434, 1435	for the detection and/or identification of the <i>blaOXA2</i> resistance gene
1436, 1437	for the detection and/or identification of the <i>blaOXA10</i> resistance gene
1440, 1441	for the detection and/or identification of the <i>blaPER-1</i> resistance gene
1443, 1444	for the detection and/or identification of the <i>blaPER-2</i> resistance gene
1446, 1447, 1448, 1449	for the detection and/or identification of the <i>blaPER-1</i> and <i>blaPER-2</i> resistance genes
1450, 1451	for the detection and/or identification of the <i>dhfrA</i> resistance gene
1453, 1454, 1455, 1456	for the detection and/or identification of the <i>dhfrIa</i> and <i>dhfrXV</i> resistance genes
1457, 1458, 1459, 1460, 2253	for the detection and/or identification of the <i>dhfrIa</i> resistance gene
1462, 1463, 1464, 1465	for the detection and/or identification of the <i>dhfrIb</i> and <i>dhfrV</i> resistance genes
1466, 1467, 1468, 1469	for the detection and/or identification of the <i>dhfrIb</i> resistance gene



1471, 1472, 1473, 1474	for the detection and/or identification of the <i>dhfrV</i> resistance gene
1476, 1477, 1478, 1479	for the detection and/or identification of the <i>dhfrVI</i> resistance gene
1481, 1482, 1483, 1484	for the detection and/or identification of the <i>dhfrVII</i> and <i>dhfrXVII</i> resistance genes
1485, 1486, 1487, 1488	for the detection and/or identification of the <i>dhfrVII</i> resistance gene
1490, 1491, 1492, 1493	for the detection and/or identification of the <i>dhfrVIII</i> resistance gene
1495, 1496, 1497, 1498	for the detection and/or identification of the <i>dhfrIX</i> resistance gene
1500, 1501, 1502, 1503	for the detection and/or identification of the <i>dhfrXII</i> resistance gene
1505, 1506	for the detection and/or identification of the <i>dhfrXIII</i> resistance gene
1508, 1509, 1510, 1511	for the detection and/or identification of the <i>dhfrXV</i> resistance gene
1513, 1514, 1515, 1516	for the detection and/or identification of the <i>dhfrXVII</i> resistance gene
1528, 1529	for the detection and/or identification of the <i>ereA</i> and <i>ereA2</i> resistance genes
1531, 1532, 1533, 1534	for the detection and/or identification of the <i>ereB</i> resistance gene
1536, 1537, 1538, 1539	for the detection and/or identification of the <i>linA</i> and <i>linA'</i> resistance genes
1541, 1542, 1543, 1544	for the detection and/or identification of the <i>linB</i> resistance gene
1546, 1547	for the detection and/or identification of the <i>mefA</i> resistance gene
1549, 1550	for the detection and/or identification of the <i>mefE</i> resistance gene
1552, 1553, 1554, 1555	for the detection and/or identification of the <i>mefA</i> and <i>mefE</i> resistance genes

1556, 1557, 1558, 1559	for the detection and/or identification of the <i>mphA</i> and <i>mphK</i> resistance genes
1581, 1582, 1583, 1584	for the detection and/or identification of the <i>satG</i> resistance gene
1586, 1587, 1588, 1589, 2254	for the detection and/or identification of the <i>tetM</i> resistance gene
1591, 1592, 1593, 2297	for the detection and/or identification of the <i>vanD</i> resistance gene
1595, 1596, 1597, 1598	for the detection and/or identification of the <i>vanE</i> resistance gene
1609, 1610, 1611, 1612	for the detection and/or identification of the <i>vatB</i> resistance gene
1614, 1615, 1616, 1617	for the detection and/or identification of the <i>vatC</i> resistance gene
1619, 1620, 1621, 1622	for the detection and/or identification of the <i>vga</i> resistance gene
1624, 1625, 1626, 1627	for the detection and/or identification of the <i>vgaB</i> resistance gene
1629, 1630, 1631, 1632	for the detection and/or identification of the <i>vgb</i> and <i>vgh</i> resistance genes
1634, 1635, 1636, 1637	for the detection and/or identification of the <i>vgbB</i> resistance gene
1883, 1884, 1885, 1886, 1887, 1888, 1889, 1890, 1891, 1892, 1893, 1894, 1895, 1896, 1897, 1898	for the detection and/or identification of the <i>blaSHV</i> resistance gene
1906, 1907, 1908, 1909, 1910, 1911, 1912, 1913, 1914, 1915, 1916, 1917, 1918, 1919, 1920, 1921, 1922, 1923, 1924, 1925, 1926, 2006, 2007, 2008, 2009, 2141	for the detection and/or identification of the <i>blaTEM</i> resistance gene
1961, 1962, 1963, 1964	for the detection and/or identification of the <i>sulII</i> resistance gene

1966, 1967, 1968, 1969	for the detection and/or identification of the <i>tetB</i> resistance gene
2065, 2066, 2067, 2068, 2069, 2070, 2071	for the detection and/or identification of the <i>therpoB</i> resistance gene
2098, 2099, 2100	for the detection and/or identification of the <i>inhA</i> resistance gene
2102, 2103, 2104	for the detection and/or identification of the <i>embB</i> resistance gene
2123, 2124, 2125	for the detection and/or identification of the <i>C. difficile cdtA</i> toxin gene
2126, 2127, 2128	for the detection and/or identification of the <i>C. difficile cdtB</i> toxin gene
2142, 2143	for the detection and/or identification of the <i>mupA</i> resistance gene
2145, 2146	for the detection and/or identification of the <i>catI</i> resistance gene
2148, 2149	for the detection and/or identification of the <i>catII</i> resistance gene
2151, 2152	for the detection and/or identification of the <i>catIII</i> resistance gene
2154, 2155	for the detection and/or identification of the <i>catP</i> resistance gene
2157, 2158, 2160, 2161	for the detection and/or identification of the <i>cat</i> resistance gene
2163, 2164	for the detection and/or identification of the <i>ppflo</i> -like resistance gene.

24. A nucleic acid having at least 12 nucleotides in length, capable of hybridizing with the nucleotide sequence of any one of the *tuf* sequences defined in SEQ ID NOs.: 1-73, 75-241, 399-457, 498-529, 612-618, 621-624, 675, 677, 717-736, 779-792, 840-855, 865, 868-888, 897-910, 932, 967-989, 992, 1266-1287, 1518-1526, 1561-1575, 1578-1580, 1662-1664, 1666-1667, 1669-1670, 1673-1683, 1685-1689, 1786-1843, 1874-1881, 1956-1960, 2183-2185, 2187-2188, 2193-2201, 2214-2249, 2255-2272.

25. A nucleic acid having at least 12 nucleotides in length, capable of hybridizing with the nucleotide sequence of any one of the *atpD* sequences defined in SEQ ID NOs.: 242-270, 272-398, 458-497, 530-538, 663, 667, 673, 674, 676, 678-680, 737-778, 827-832, 834-839, 856-862, 866-867, 889-896, 929-931, 941-966, 1245-1254, 1256-1265, 1527, 1576-1577, 1600-1604, 1638-1647, 1649-1660, 1671, 1684, 1844-1848, 1849-1865, 2189-2192.

26. A nucleic acid having at least 12 nucleotides in length, capable of hybridizing with the nucleotide sequence of any one of the *recA* sequences defined in SEQ ID NOs.: 990-991, 1003, 1288-1289, 1714, 1756-1763, 1866-1873 and 2202-2212.

27. A nucleic acid having at least 12 nucleotides in length, capable of selectively hybridizing with the nucleotide sequence of any one of the antimicrobial agent resistance gene sequences defined in SEQ ID NOs.: 1004-1075, 1255, 1607-1608, 1648, 1764-1785, 2013-2014, 2056-2064, 2273-2280.

28. The nucleic acid sequences of the nucleic acids of any one of claims 24 to 27.

29. The use of a nucleic acid having at least 12 nucleotides in length capable of hybridizing with the nucleic acids of any one of the antimicrobial agent resistance genes sequences defined in SEQ ID NOs.: 1004-1075, 1255, 1607-1608, 1648, 1764-1785, 2013-2014, 2056-2064, 2273-2280 for the detection and identification of microbial species.

30. The use of a nucleic acid having at least 12 nucleotides in length capable of hybridizing with the nucleic acids of any one of the toxin genes defined in SEQ ID NOs.: 1078-1085, 2012 and 2123 to 2128 for the detection and identification of microbial species.

31. A repertory of *hexA* nucleic acids used for the detection and/or identification of *Streptococcus pneumoniae*, which repertory is created by amplifying

the nucleic acids of any streptococcal species with any combination of primers SEQ ID NOs.: 1179, 1181 and 1182.

32. A repertory as defined in claim 31, which comprises the nucleic acids having a nucleotide sequence defined in SEQ ID NOs.: 1184 to 1191.

33. A repertory of nucleic acid sequences derived from the repertory of claim 31 or 32.

34. A nucleic acid used for the specific and ubiquitous detection and for identification of *Streptococcus pneumoniae*, which is derived from the repertory of claim 31.

35. A nucleic acid as set forth in claim 34 which has a nucleic acid sequence of at least 12 nucleotides capable of hybridizing with said any *Streptococcus pneumoniae* and with any one of SEQ ID NOs.: 1184 to 1187.

36. A nucleic acid as set forth in claim 34, which has a nucleic acid sequence of at least 12 nucleotides capable of hybridizing with the nucleic acids of *Streptococcus pneumoniae* and with any one of the nucleic acids having SEQ ID NOs.: 1179, 1180, 1181, 1182.

37. A peptide derived from the translation of the nucleic acids from the repertory obtained from the method of claim 1, 31 or 32, or of the nucleic acids defined in any one of claims 24 to 27, 35 and 36.

38. A peptide sequence derived from the peptide of claim 37.

39. A recombinant vector comprising a nucleic acid obtained from the method of claim 1, 31 or 32, or from the nucleic acids defined in any one of claims 24 to 27, 35 and 36.

40. A recombinant vector as defined in claim 39 which is an expression vector.

41. A recombinant host cell comprising the recombinant vector defined in claim 39 or 40.

42. The use of the nucleic acid sequences defined in claim 28 or 33, or obtained from the method of claim 2 and of the protein sequences deduced from said nucleic acid sequences, for the design of a therapeutic agent effective against said microorganisms.

43. The use as defined in claim 42, wherein said therapeutic agent is an antimicrobial agent, a vaccine or a genic therapeutic agent.

44. A method for identification of a microorganism in a test sample, comprising the steps of:

- a) obtaining a nucleic acid sequence for a *tuf*, *atpD*, and/or *recA* genes of said microorganisms, and
- b) comparing said nucleic acid sequence with the nucleic acid sequences of a bank as defined in claim 5, said repertory comprising a nucleic acid sequence obtained from the nucleic acids of said microorganism, whereby said microorganism is identified when said comparison results in a match between said sequences.

1/27

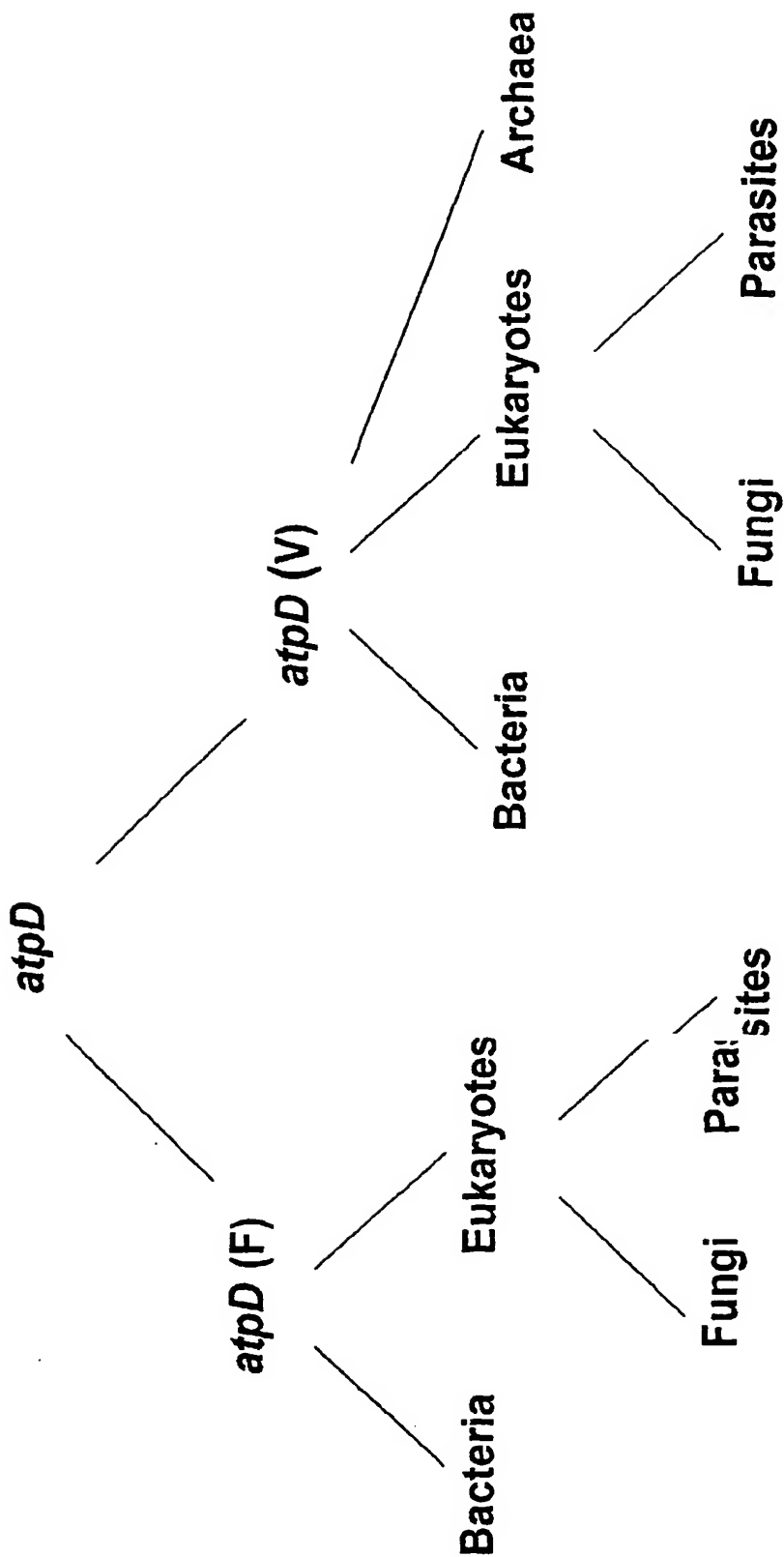


FIG. 1

2 / 27

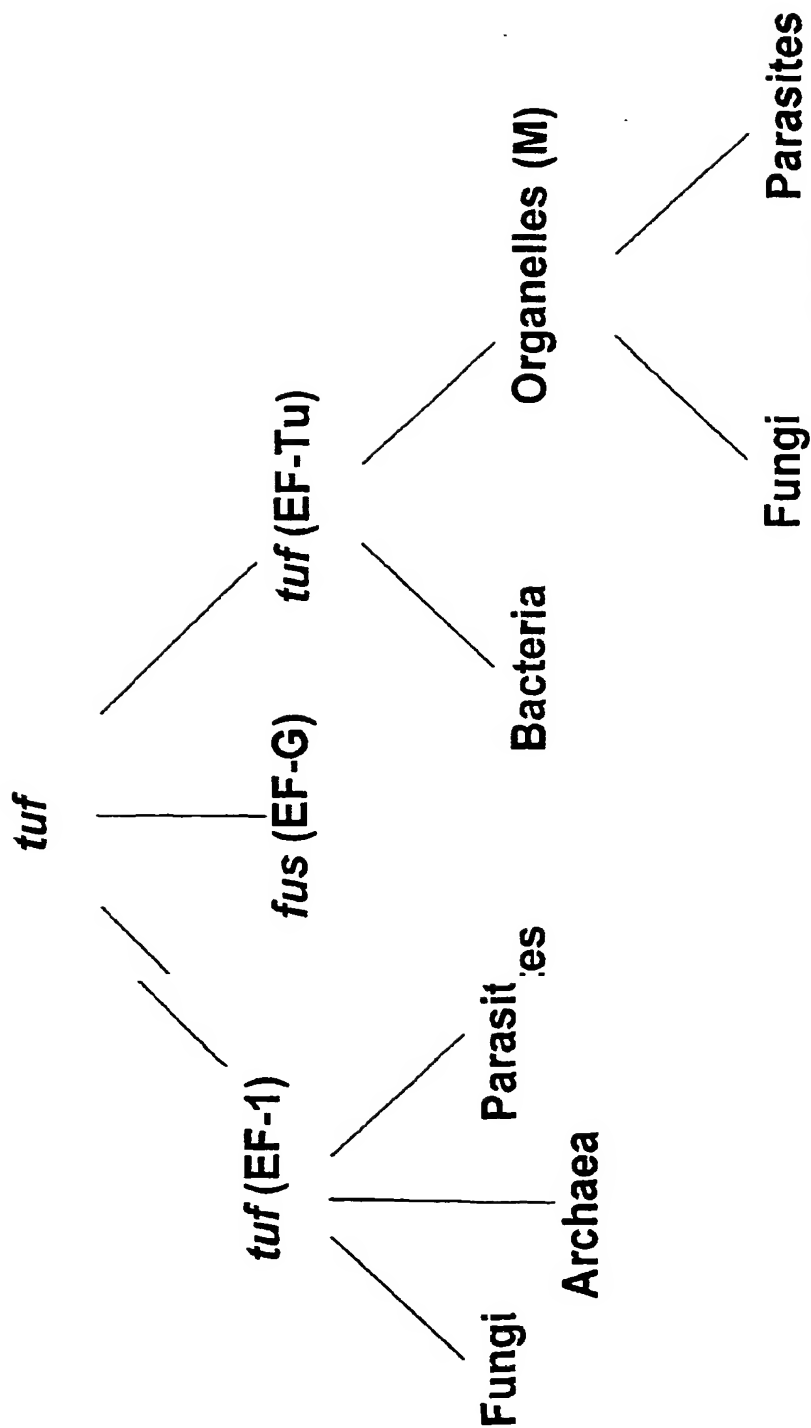
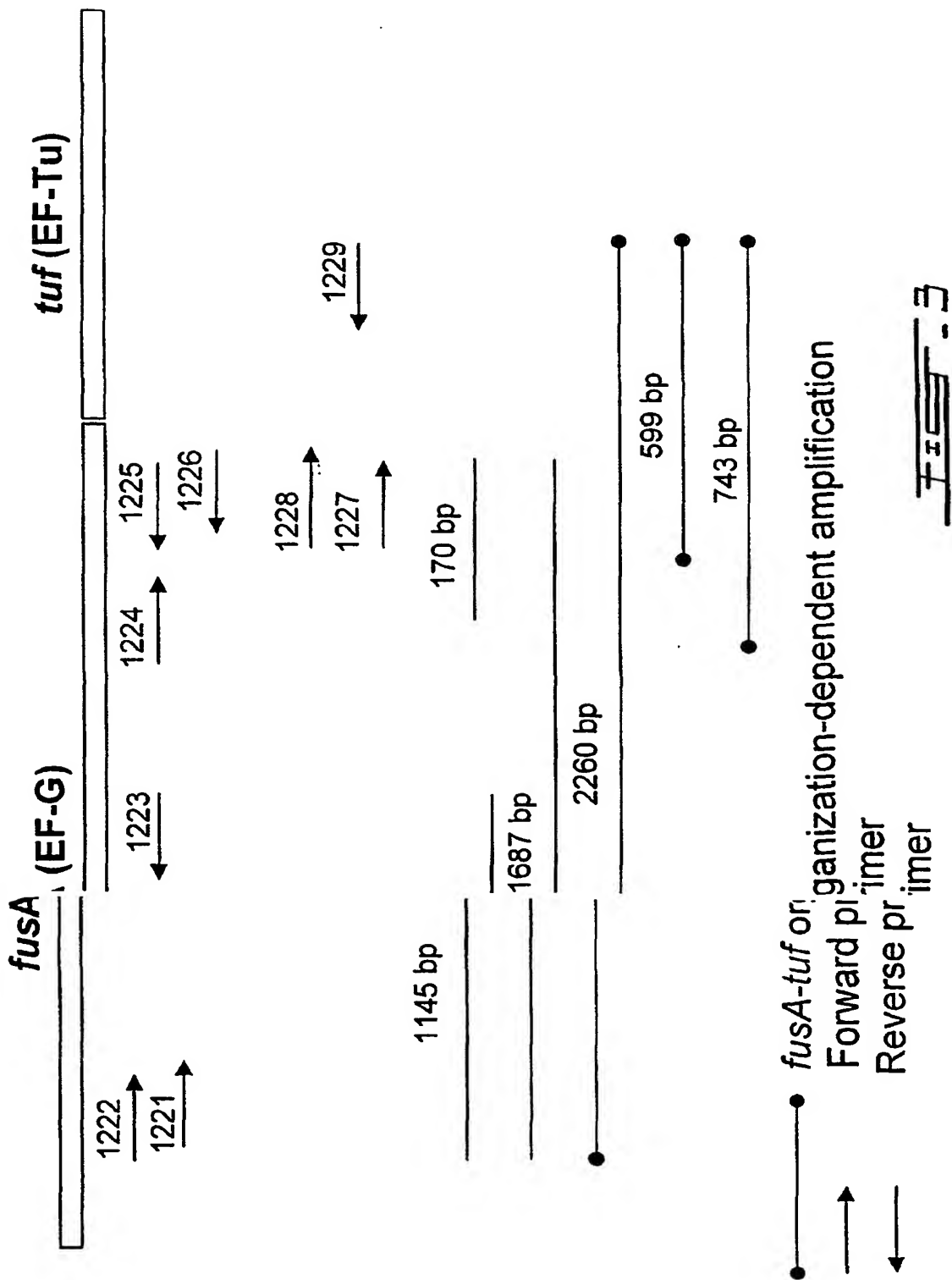


Fig. 2



3/27



4/27

	120	130	140	150	160	170	180	190	200
<i>S. aureus</i>	REHLLSRNVGVPYIVF	TNKM	DWVDEEELLE	VELVEMVRD	LLEYDF	PGDVP	VIAGS	ALKALE	.....
<i>S. epidermidis</i>	REHLLSRNVGVPYIVF	TNKM	DWVDEEELLE	VELVEMVRD	LLEYDF	PGDVP	VIAGS	ALKALE	.....
<i>S. durans</i> (A)	REHLLSRNVGVPYIVF	TNKM	DWVDEEELLE	VELVEMVRD	LLEYDF	PGDVP	VIAGS	ALKALE	.....
<i>S. hirae</i> (A)	REHLLSRNVGVPYIVF	TNKM	DWVDEEELLE	VELVEMVRD	LLEYDF	PGDVP	VIAGS	ALKALE	.....
<i>S. mundtii</i> (A)	REHLLSRNVGVPYIVF	TNKM	DWVDEEELLE	VELVEMVRD	LLEYDF	PGDVP	VIAGS	ALKALE	.....
<i>S. faecium</i> (A)	REHLLSRNVGVPYIVF	TNKM	DWVDEEELLE	VELVEMVRD	LLEYDF	PGDVP	VIAGS	ALKALE	.....
<i>S. cecorum</i>	REHLLSRNVGVPYIVF	TNKM	DWVDEEELLE	VELVEMVRD	LLEYDF	PGDVP	VIAGS	ALKALE	.....
<i>S. columbae</i>	REHLLSRNVGVPYIVF	TNKM	DWVDEEELLE	VELVEMVRD	LLEYDF	PGDVP	VIAGS	ALKALE	.....
<i>S. cassel. flavus</i> (A)	REHLLSRNVGVPYIVF	TNKM	DWVDEEELLE	VELVEMVRD	LLEYDF	PGDVP	VIAGS	ALKALE	.....
<i>S. gallinarum</i> (A)	REHLLSRNVGVPYIVF	TNKM	DWVDEEELLE	VELVEMVRD	LLEYDF	PGDVP	VIAGS	ALKALE	.....
<i>S. faecalis</i>	REHLLSRNVGVPYIVF	TNKM	DWVDEEELLE	VELVEMVRD	LLEYDF	PGDVP	VIAGS	ALKALE	.....
<i>S. avium</i> (A)	REHLLSRNVGVPYIVF	TNKM	DWVDEEELLE	VELVEMVRD	LLEYDF	PGDVP	VIAGS	ALKALE	.....
<i>S. raffinosus</i> (A)	REHLLSRNVGVPYIVF	TNKM	DWVDEEELLE	VELVEMVRD	LLEYDF	PGDVP	VIAGS	ALKALE	.....
<i>S. dispar</i> (A)	REHLLSRNVGVPYIVF	TNKM	DWVDEEELLE	VELVEMVRD	LLEYDF	PGDVP	VIAGS	ALKALE	.....
<i>S. malodoratus</i> (A)	REHLLSRNVGVPYIVF	TNKM	DWVDEEELLE	VELVEMVRD	LLEYDF	PGDVP	VIAGS	ALKALE	.....
<i>S. pseudoavium</i> (A)	REHLLSRNVGVPYIVF	TNKM	DWVDEEELLE	VELVEMVRD	LLEYDF	PGDVP	VIAGS	ALKALE	.....
<i>S. sulfureus</i>	REHLLSRNVGVPYIVF	TNKM	DWVDEEELLE	VELVEMVRD	LLEYDF	PGDVP	VIAGS	ALKALE	.....
<i>S. saccharolyticus</i>	REHLLSRNVGVPYIVF	TNKM	DWVDEEELLE	VELVEMVRD	LLEYDF	PGDVP	VIAGS	ALKALE	.....
<i>S. solitarius</i>	REHLLSRNVGVPYIVF	TNKM	DWVDEEELLE	VELVEMVRD	LLEYDF	PGDVP	VIAGS	ALKALE	.....
	REHLLSRNVGVPYIVF	TNKM	DWVDEEELLE	VELVEMVRD	LLEYDF	PGDVP	VIAGS	ALKALE	.....

FIFTH - 4a

5/27

210	220	230	240	250	260	270	280	290
<i>S. aureus</i>	TPERDNDKPFMMPVEDVI	TPERDNDKPFMMPVEDVI	TPERDNDKPFMMPVEDVI	TPERDNDKPFMMPVEDVI	TPERDNDKPFMMPVEDVI	TPERDNDKPFMMPVEDVI	TPERDNDKPFMMPVEDVI	TPERDNDKPFMMPVEDVI
<i>S. epidermidis</i>	TPERDNDKPFMMPVEDVI	TPERDNDKPFMMPVEDVI	TPERDNDKPFMMPVEDVI	TPERDNDKPFMMPVEDVI	TPERDNDKPFMMPVEDVI	TPERDNDKPFMMPVEDVI	TPERDNDKPFMMPVEDVI	TPERDNDKPFMMPVEDVI
<i>E. durans</i> (A)	TPERDNDKPFMMPVEDVI	TPERDNDKPFMMPVEDVI	TPERDNDKPFMMPVEDVI	TPERDNDKPFMMPVEDVI	TPERDNDKPFMMPVEDVI	TPERDNDKPFMMPVEDVI	TPERDNDKPFMMPVEDVI	TPERDNDKPFMMPVEDVI
<i>E. hirae</i> (A)	TPERDNDKPFMMPVEDVI	TPERDNDKPFMMPVEDVI	TPERDNDKPFMMPVEDVI	TPERDNDKPFMMPVEDVI	TPERDNDKPFMMPVEDVI	TPERDNDKPFMMPVEDVI	TPERDNDKPFMMPVEDVI	TPERDNDKPFMMPVEDVI
<i>E. mundtii</i> (A)	TPERDNDKPFMMPVEDVI	TPERDNDKPFMMPVEDVI	TPERDNDKPFMMPVEDVI	TPERDNDKPFMMPVEDVI	TPERDNDKPFMMPVEDVI	TPERDNDKPFMMPVEDVI	TPERDNDKPFMMPVEDVI	TPERDNDKPFMMPVEDVI
<i>E. faecium</i> (A)	TPERDNDKPFMMPVEDVI	TPERDNDKPFMMPVEDVI	TPERDNDKPFMMPVEDVI	TPERDNDKPFMMPVEDVI	TPERDNDKPFMMPVEDVI	TPERDNDKPFMMPVEDVI	TPERDNDKPFMMPVEDVI	TPERDNDKPFMMPVEDVI
<i>E. cecorum</i>	TPERDNDKPFMMPVEDVI	TPERDNDKPFMMPVEDVI	TPERDNDKPFMMPVEDVI	TPERDNDKPFMMPVEDVI	TPERDNDKPFMMPVEDVI	TPERDNDKPFMMPVEDVI	TPERDNDKPFMMPVEDVI	TPERDNDKPFMMPVEDVI
<i>E. columbae</i>	TPERDNDKPFMMPVEDVI	TPERDNDKPFMMPVEDVI	TPERDNDKPFMMPVEDVI	TPERDNDKPFMMPVEDVI	TPERDNDKPFMMPVEDVI	TPERDNDKPFMMPVEDVI	TPERDNDKPFMMPVEDVI	TPERDNDKPFMMPVEDVI
<i>E. cassel. flavus</i> (A)	TPERDNDKPFMMPVEDVI	TPERDNDKPFMMPVEDVI	TPERDNDKPFMMPVEDVI	TPERDNDKPFMMPVEDVI	TPERDNDKPFMMPVEDVI	TPERDNDKPFMMPVEDVI	TPERDNDKPFMMPVEDVI	TPERDNDKPFMMPVEDVI
<i>E. gallinarum</i> (A)	TPERDNDKPFMMPVEDVI	TPERDNDKPFMMPVEDVI	TPERDNDKPFMMPVEDVI	TPERDNDKPFMMPVEDVI	TPERDNDKPFMMPVEDVI	TPERDNDKPFMMPVEDVI	TPERDNDKPFMMPVEDVI	TPERDNDKPFMMPVEDVI
<i>E. faecalis</i>	TPERDNDKPFMMPVEDVI	TPERDNDKPFMMPVEDVI	TPERDNDKPFMMPVEDVI	TPERDNDKPFMMPVEDVI	TPERDNDKPFMMPVEDVI	TPERDNDKPFMMPVEDVI	TPERDNDKPFMMPVEDVI	TPERDNDKPFMMPVEDVI
<i>E. avium</i> (A)	TPERDNDKPFMMPVEDVI	TPERDNDKPFMMPVEDVI	TPERDNDKPFMMPVEDVI	TPERDNDKPFMMPVEDVI	TPERDNDKPFMMPVEDVI	TPERDNDKPFMMPVEDVI	TPERDNDKPFMMPVEDVI	TPERDNDKPFMMPVEDVI
<i>E. raffinosus</i> (A)	TPERDNDKPFMMPVEDVI	TPERDNDKPFMMPVEDVI	TPERDNDKPFMMPVEDVI	TPERDNDKPFMMPVEDVI	TPERDNDKPFMMPVEDVI	TPERDNDKPFMMPVEDVI	TPERDNDKPFMMPVEDVI	TPERDNDKPFMMPVEDVI
<i>E. dispar</i> (A)	TPERDNDKPFMMPVEDVI	TPERDNDKPFMMPVEDVI	TPERDNDKPFMMPVEDVI	TPERDNDKPFMMPVEDVI	TPERDNDKPFMMPVEDVI	TPERDNDKPFMMPVEDVI	TPERDNDKPFMMPVEDVI	TPERDNDKPFMMPVEDVI
<i>E. malodoratus</i> (A)	TPERDNDKPFMMPVEDVI	TPERDNDKPFMMPVEDVI	TPERDNDKPFMMPVEDVI	TPERDNDKPFMMPVEDVI	TPERDNDKPFMMPVEDVI	TPERDNDKPFMMPVEDVI	TPERDNDKPFMMPVEDVI	TPERDNDKPFMMPVEDVI
<i>E. pseudoavium</i> (A)	TPERDNDKPFMMPVEDVI	TPERDNDKPFMMPVEDVI	TPERDNDKPFMMPVEDVI	TPERDNDKPFMMPVEDVI	TPERDNDKPFMMPVEDVI	TPERDNDKPFMMPVEDVI	TPERDNDKPFMMPVEDVI	TPERDNDKPFMMPVEDVI
<i>E. sulfureus</i>	TPERDNDKPFMMPVEDVI	TPERDNDKPFMMPVEDVI	TPERDNDKPFMMPVEDVI	TPERDNDKPFMMPVEDVI	TPERDNDKPFMMPVEDVI	TPERDNDKPFMMPVEDVI	TPERDNDKPFMMPVEDVI	TPERDNDKPFMMPVEDVI
<i>E. saccharolyticus</i>	TPERDNDKPFMMPVEDVI	TPERDNDKPFMMPVEDVI	TPERDNDKPFMMPVEDVI	TPERDNDKPFMMPVEDVI	TPERDNDKPFMMPVEDVI	TPERDNDKPFMMPVEDVI	TPERDNDKPFMMPVEDVI	TPERDNDKPFMMPVEDVI
<i>E. solitarius</i>	TPERDNDKPFMMPVEDVI	TPERDNDKPFMMPVEDVI	TPERDNDKPFMMPVEDVI	TPERDNDKPFMMPVEDVI	TPERDNDKPFMMPVEDVI	TPERDNDKPFMMPVEDVI	TPERDNDKPFMMPVEDVI	TPERDNDKPFMMPVEDVI



6/27

<i>L. monocytogenes</i>	REHLLSRQVGVPYIV	FANKDNDVDEELLELEVMEIRULLTEYEPFGDDIPVIGSALKALQ	GEADWEAKIDELMEAVDSYIP
<i>E. cassel. flavus (B)</i>	REHLLSRQVGKHLIV	FANKDNDVDEELLELEVMEIRULLTEYEPFGDDIPVIGSALKALQ	GDPAEAAITLMDTVDEYIP
<i>E. gallinarum (B)</i>	REHLLSRQVGKHLIV	FANKDNDVDEELLELEVMEIRULLTEYEPFGDDIPVIGSALKALQ	GDPAEAAITLMDTVDEYIP
<i>E. durans (B)</i>	REHLLSRQVGKHLIV	FANKDNDVDEELLELEVMEIRULLTEYEPFGDDIPVIGSALKALQ	GDPAEAAITLMDTVDEYIP
<i>E. faecium (B)</i>	REHLLSRQVGKHLIV	FANKDNDVDEELLELEVMEIRULLTEYEPFGDDIPVIGSALKALQ	GDPAEAAITLMDTVDEYIP
<i>E. hirae (B)</i>	REHLLSRQVGKHLIV	FANKDNDVDEELLELEVMEIRULLTEYEPFGDDIPVIGSALKALQ	GDPAEAAITLMDTVDEYIP
<i>E. mundtii (B)</i>	REHLLSRQVGKHLIV	FANKDNDVDEELLELEVMEIRULLTEYEPFGDDIPVIGSALKALQ	GDPAEAAITLMDTVDEYIP
<i>E. avium (B)</i>	REHLLSRQVGKHLIV	FANKDNDVDEELLELEVMEIRULLTEYEPFGDDIPVIGSALKALQ	GDPAEAAITLMDTVDEYIP
<i>E. pseudoavium (B)</i>	REHLLSRQVGKHLIV	FANKDNDVDEELLELEVMEIRULLTEYEPFGDDIPVIGSALKALQ	GDPAEAAITLMDTVDEYIP
<i>E. malodoratus (B)</i>	REHLLSRQVGKHLIV	FANKDNDVDEELLELEVMEIRULLTEYEPFGDDIPVIGSALKALQ	GDPAEAAITLMDTVDEYIP
<i>E. raffinosus (B)</i>	REHLLSRQVGKHLIV	FANKDNDVDEELLELEVMEIRULLTEYEPFGDDIPVIGSALKALQ	GDPAEAAITLMDTVDEYIP
<i>E. dispar (B)</i>	REHLLSRQVGKHLIV	FANKDNDVDEELLELEVMEIRULLTEYEPFGDDIPVIGSALKALQ	GDPAEAAITLMDTVDEYIP
<i>S. pneumoniae</i>	REHLLSRQVGKHLIV	FANKDNDVDEELLELEVMEIRULLTEYEPFGDDIPVIGSALKALQ	GDPAEAAITLMDTVDEYIP
<i>S. suis</i>	REHLLSRQVGKHLIV	FANKDNDVDEELLELEVMEIRULLTEYEPFGDDIPVIGSALKALQ	GDPAEAAITLMDTVDEYIP
<i>S. pyogenes</i>	REHLLSRQVGKHLIV	FANKDNDVDEELLELEVMEIRULLTEYEPFGDDIPVIGSALKALQ	GDPAEAAITLMDTVDEYIP
<i>S. mutans</i>	REHLLSRQVGKHLIV	FANKDNDVDEELLELEVMEIRULLTEYEPFGDDIPVIGSALKALQ	GDPAEAAITLMDTVDEYIP
<i>L. lactis</i>	REHLLSRQVGKHLIV	FANKDNDVDEELLELEVMEIRULLTEYEPFGDDIPVIGSALKALQ	GDPAEAAITLMDTVDEYIP
<i>T. aquaticus</i>	REHLLSRQVGKHLIV	FANKDNDVDEELLELEVMEIRULLTEYEPFGDDIPVIGSALKALQ	GDPAEAAITLMDTVDEYIP
<i>E. coli</i>	REHLLSRQVGKHLIV	FANKDNDVDEELLELEVMEIRULLTEYEPFGDDIPVIGSALKALQ	GDPAEAAITLMDTVDEYIP

7/27

<i>L. monocytogenes</i>	TPEROTDKPFWMPVED	VFSTHGRGTWASGRIDRGVAVRGVDEIVGIGIEESKVVVTGVMFRKLLDYAAGDNIGALLRGVAREDIORGQVLA	$\Rightarrow$	a2	b <sub>2</sub>	$\Rightarrow$	c2	$\Rightarrow$	d2	$\Rightarrow$	e2	$\Rightarrow$	f2	g2	$\Rightarrow$	h2	i2	$\Rightarrow$	j2	$\Rightarrow$	k2
<i>E. cassel. flavus (B)</i>	TPEROTDKPILLPIED	VFSTHGRGTWASGRIDRGVAVRGVDEIVGIGIEESKVVVTGVMFRKLLDYAAGDNIGALLRGVAREDIORGQVLA																			
<i>E. gallinarum (B)</i>	TPEROTDKPILLPVED	VFSTHGRGTWASGRIDRGVAVRGVDEIVGIGIEESKVVVTGVMFRKLLDYAAGDNIGALLRGVAREDIORGQVLA																			
<i>E. durans (B)</i>	TPEROTDKPILLPVED	VFSTHGRGTWASGRIDRGVAVRGVDEIVGIGIEESKVVVTGVMFRKLLDYAAGDNIGALLRGVAREDIORGQVLA																			
<i>E. faecium (B)</i>	TPEROTDKPILLPVED	VFSTHGRGTWASGRIDRGVAVRGVDEIVGIGIEESKVVVTGVMFRKLLDYAAGDNIGALLRGVAREDIORGQVLA																			
<i>E. hirae (B)</i>	TPEROTDKPILLPAED	VFSTHGRGTWASGRIDRGVAVRGVDEIVGIGIEESKVVVTGVMFRKLLDYAAGDNIGALLRGVAREDIORGQVLA																			
<i>E. mundtii (B)</i>	TPEROTDKPILLPVED	VFSTHGRGTWASGRIDRGVAVRGVDEIVGIGIEESKVVVTGVMFRKLLDYAAGDNIGALLRGVAREDIORGQVLA																			
<i>E. avium (B)</i>	TPEROTDKPILLPVED	VFSTHGRGTWASGRIDRGVAVRGVDEIVGIGIEESKVVVTGVMFRKLLDYAAGDNIGALLRGVAREDIORGQVLA																			
<i>E. pseudoavium (B)</i>	TPEROTDKPILLPVED	VFSTHGRGTWASGRIDRGVAVRGVDEIVGIGIEESKVVVTGVMFRKLLDYAAGDNIGALLRGVAREDIORGQVLA																			
<i>E. malodoratus (B)</i>	TPEROTDKPILLPVED	VFSTHGRGTWASGRIDRGVAVRGVDEIVGIGIEESKVVVTGVMFRKLLDYAAGDNIGALLRGVAREDIORGQVLA																			
<i>E. raffinosus (B)</i>	TPEROTDKPILLPVED	VFSTHGRGTWASGRIDRGVAVRGVDEIVGIGIEESKVVVTGVMFRKLLDYAAGDNIGALLRGVAREDIORGQVLA																			
<i>E. dispar (B)</i>	TPEROTDKPILLPVED	VFSTHGRGTWASGRIDRGVAVRGVDEIVGIGIEESKVVVTGVMFRKLLDYAAGDNIGALLRGVAREDIORGQVLA																			
<i>S. pneumoniae</i>	EPEROTDKPILLPVED	VFSTHGRGTWASGRIDRGVAVRGVDEIVGIGIEESKVVVTGVMFRKLLDYAAGDNIGALLRGVAREDIORGQVLA																			
<i>S. suis</i>	EPEROTDKPILLPVED	VFSTHGRGTWASGRIDRGVAVRGVDEIVGIGIEESKVVVTGVMFRKLLDYAAGDNIGALLRGVAREDIORGQVLA																			
<i>S. pyogenes</i>	EPEROTDKPILLPVED	VFSTHGRGTWASGRIDRGVAVRGVDEIVGIGIEESKVVVTGVMFRKLLDYAAGDNIGALLRGVAREDIORGQVLA																			
<i>S. mutans</i>	EPEROTDKPILLPVED	VFSTHGRGTWASGRIDRGVAVRGVDEIVGIGIEESKVVVTGVMFRKLLDYAAGDNIGALLRGVAREDIORGQVLA																			
<i>L. lactis</i>	TPEROTDKPILLPVED	VFSTHGRGTWASGRIDRGVAVRGVDEIVGIGIEESKVVVTGVMFRKLLDYAAGDNIGALLRGVAREDIORGQVLA																			
<i>T. aquaticus</i>	TPEROTDKPILLPVED	VFSTHGRGTWASGRIDRGVAVRGVDEIVGIGIEESKVVVTGVMFRKLLDYAAGDNIGALLRGVAREDIORGQVLA																			
<i>E. coli</i>	EPEROTDKPILLPIED	VFSTHGRGTWASGRIDRGVAVRGVDEIVGIGIEESKVVVTGVMFRKLLDYAAGDNIGALLRGVAREDIORGQVLA																			

F=5-4d

8/27

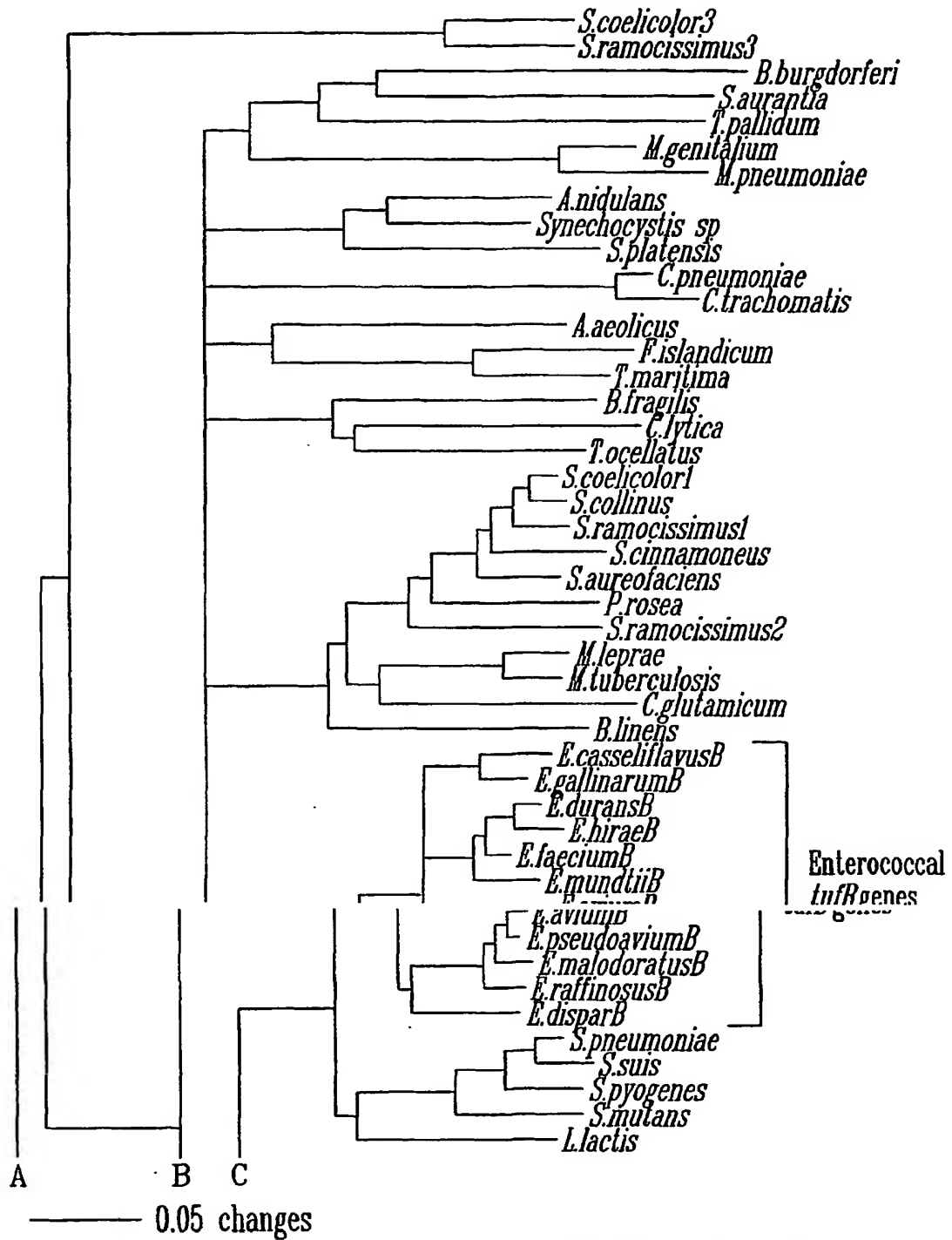
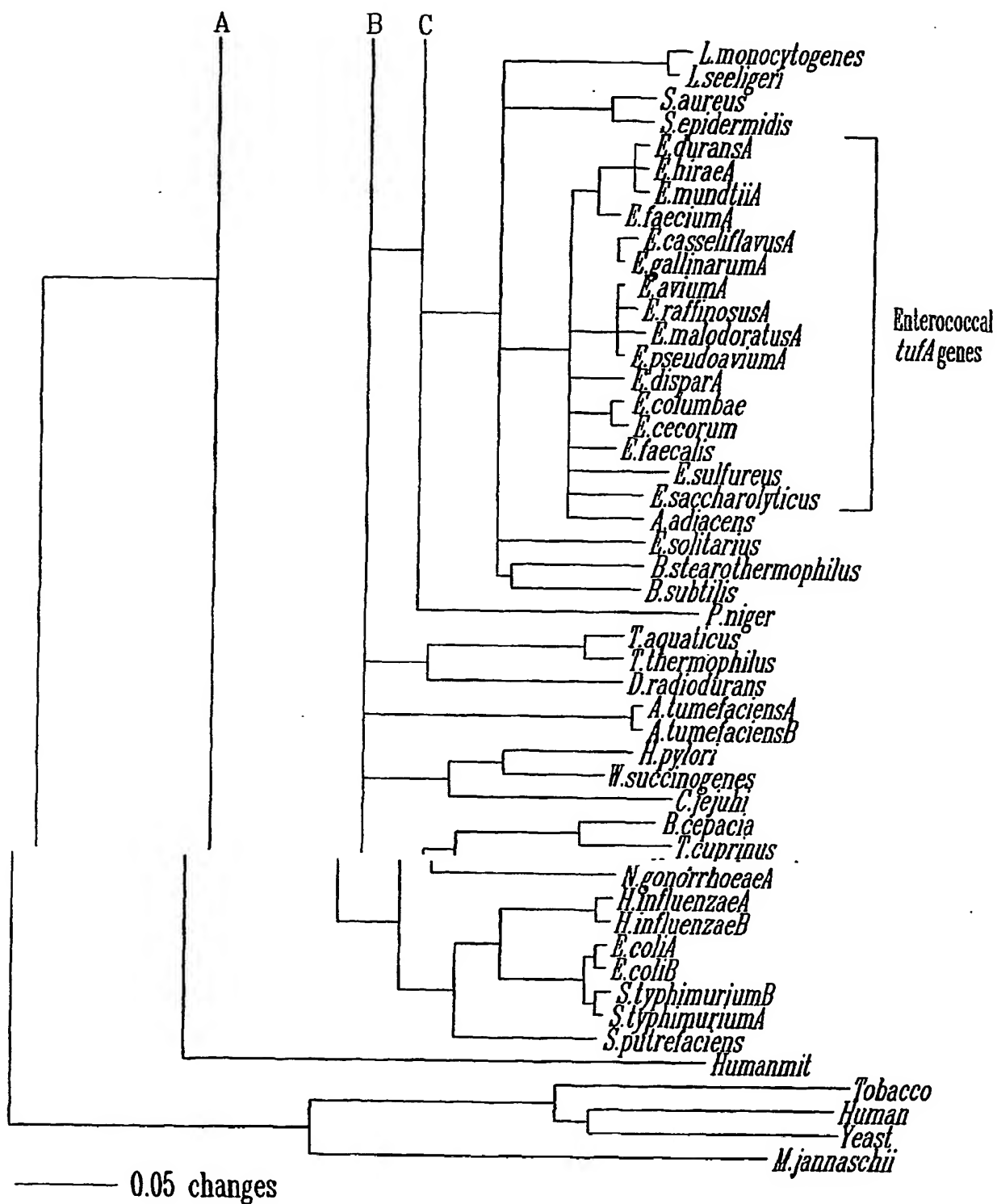


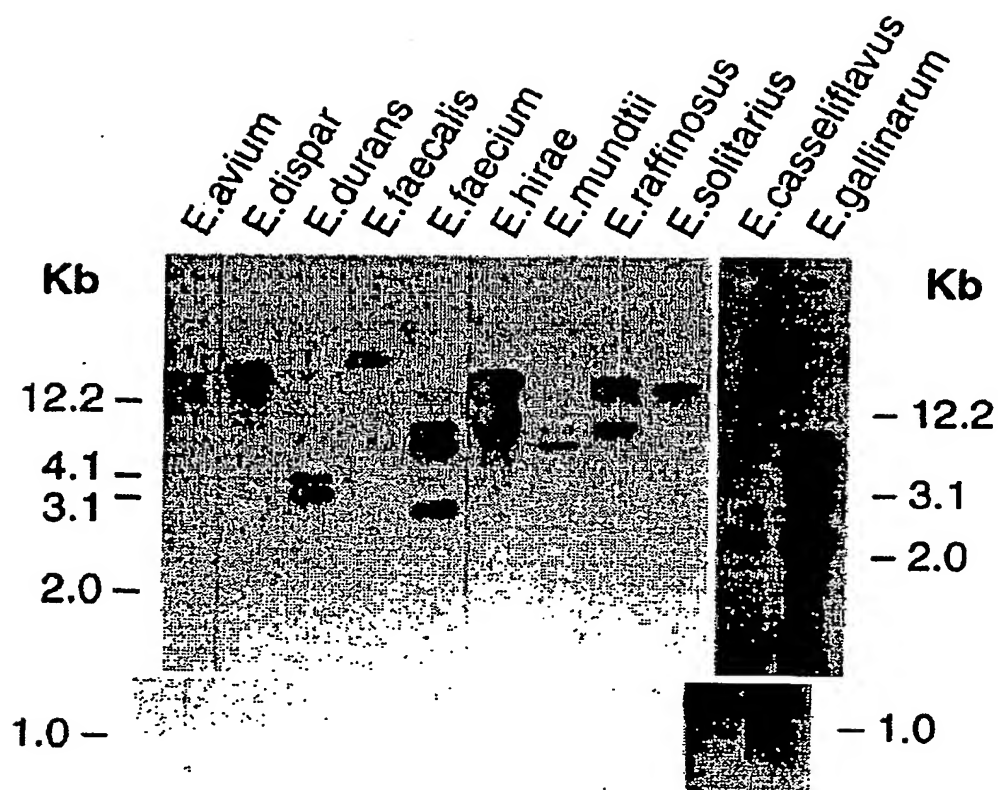
FIG. 5a

9/27



FIS-56

10/27

FIG. 6



11/27

	301	311	321	331
E. coli	GAGATCGGT <sup>1</sup>	AAGAAGAGCG	TTGGG	CGATTCACCG
E. agglomerans	GACATCGGT <sup>1</sup>	AAGAAGAGCG	TTGGG	CGATCCACCG
P. agglomerans	GAGCTGAAA <sup>1</sup>	AAGAAGATGG	CAGCGCAGTA	CTATTCACCG
P. dispersa	GACCTGAAA <sup>1</sup>	AAGAAGACGG	CAGCGCTGTA	CTATTCATCG
T. ptyseos	GACCTGAAG <sup>1</sup>	ACGAAGATGG	TAGCAATGTT	CTATTCACCG
E. coli	~I~G~E~	E~E~R~W~	~A~	I~H~R~
E. agglomerans	~I~G~E~	E~E~R~W~	~A~	I~H~R~
P. agglomerans	~L~K~E~	E~D~G~S~	~V~E~ ~I~A~S~	I~H~R~
P. dispersa	~L~K~E~	E~D~G~S~	~V~E~ ~V~S~S~	I~H~R~
T. ptyseos	~L~K~N~	E~D~G~S~	~N~ ~V~E~ ~V~N~S~	I~H~R~

FIG. 7

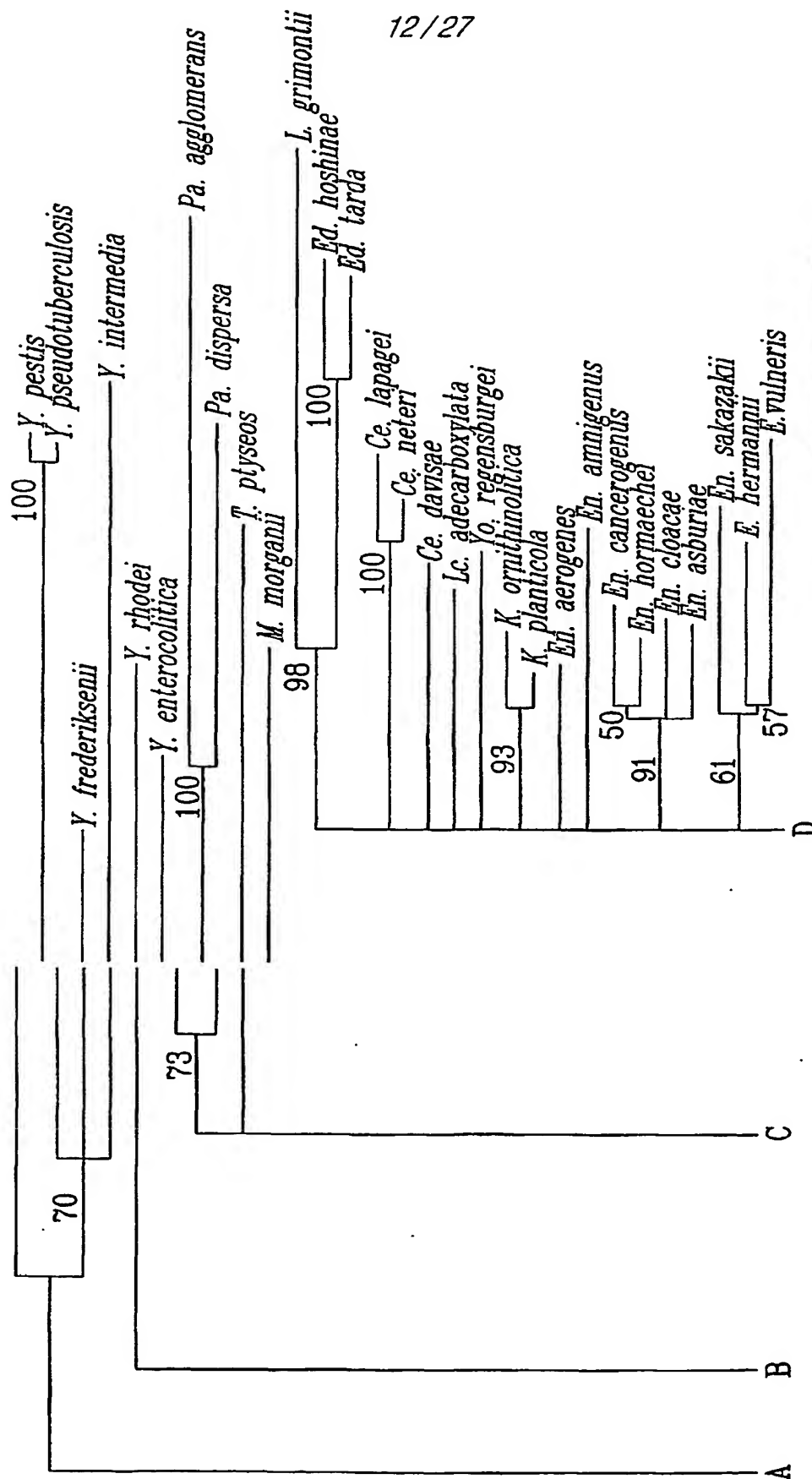
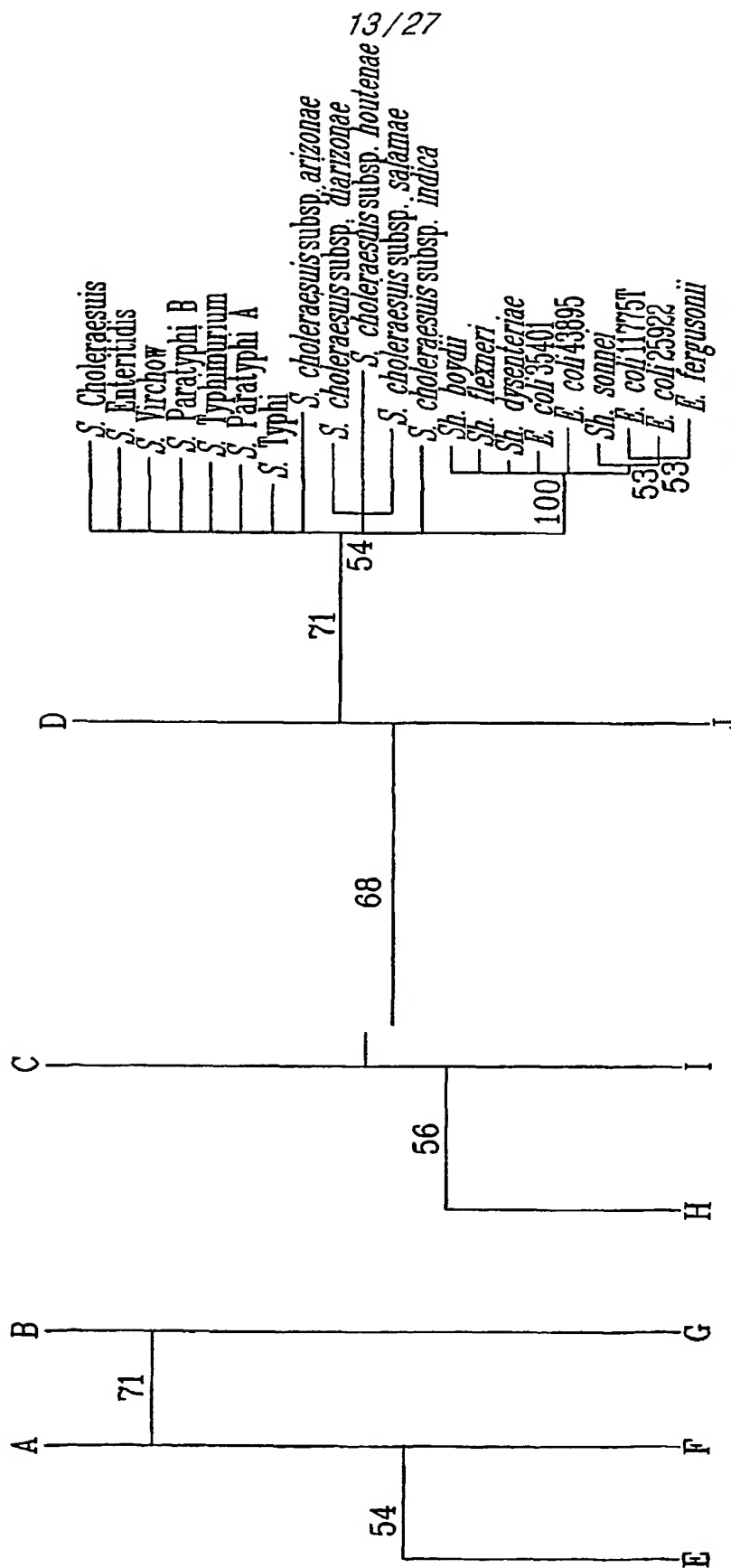


FIG. 1a

13/27



五

14/27

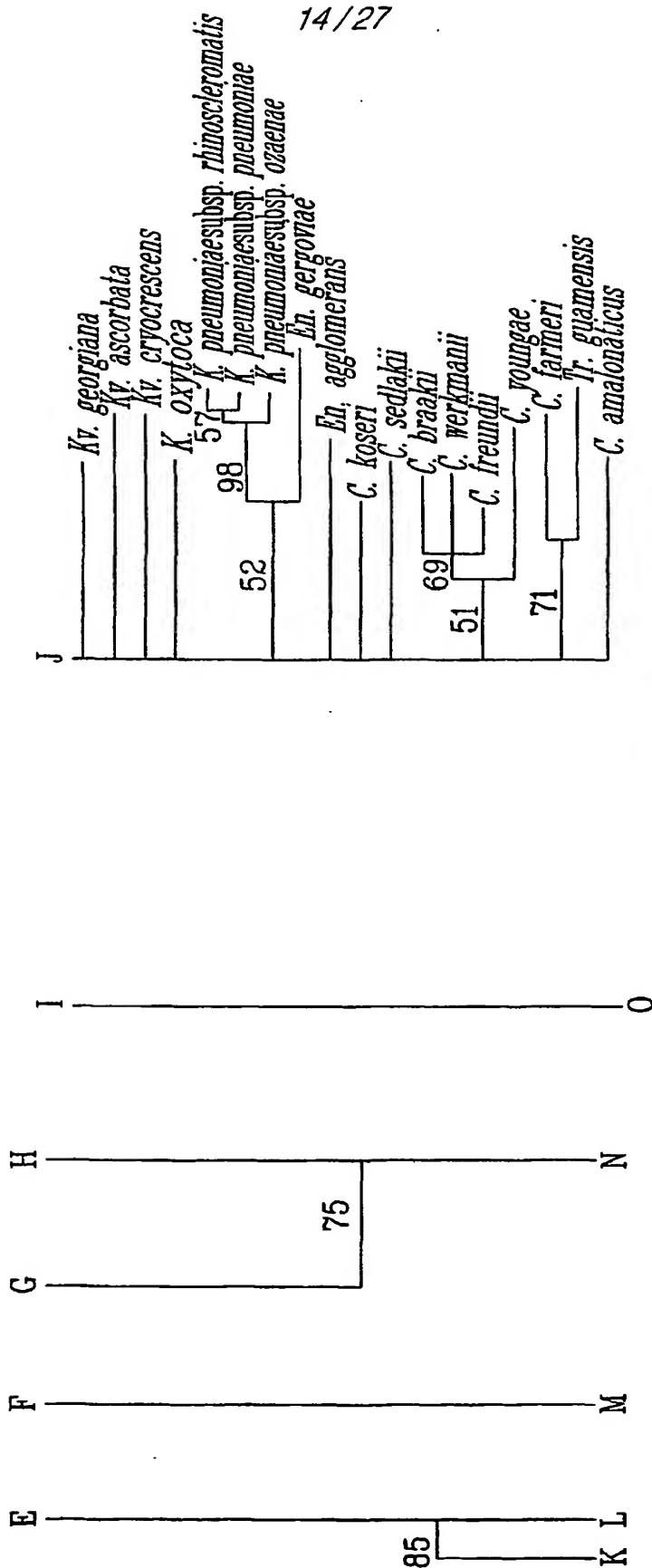


FIG. 1

15/27

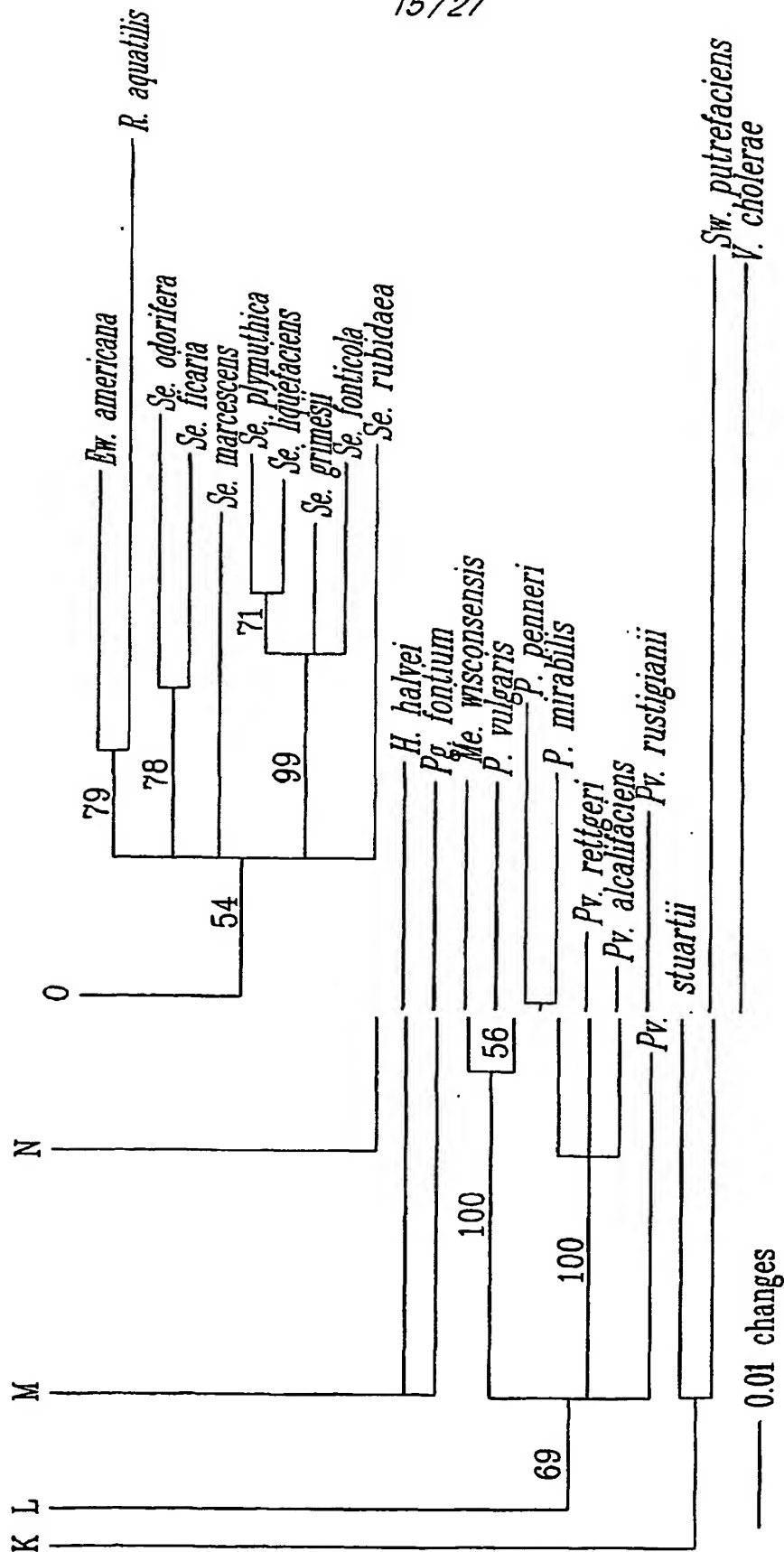
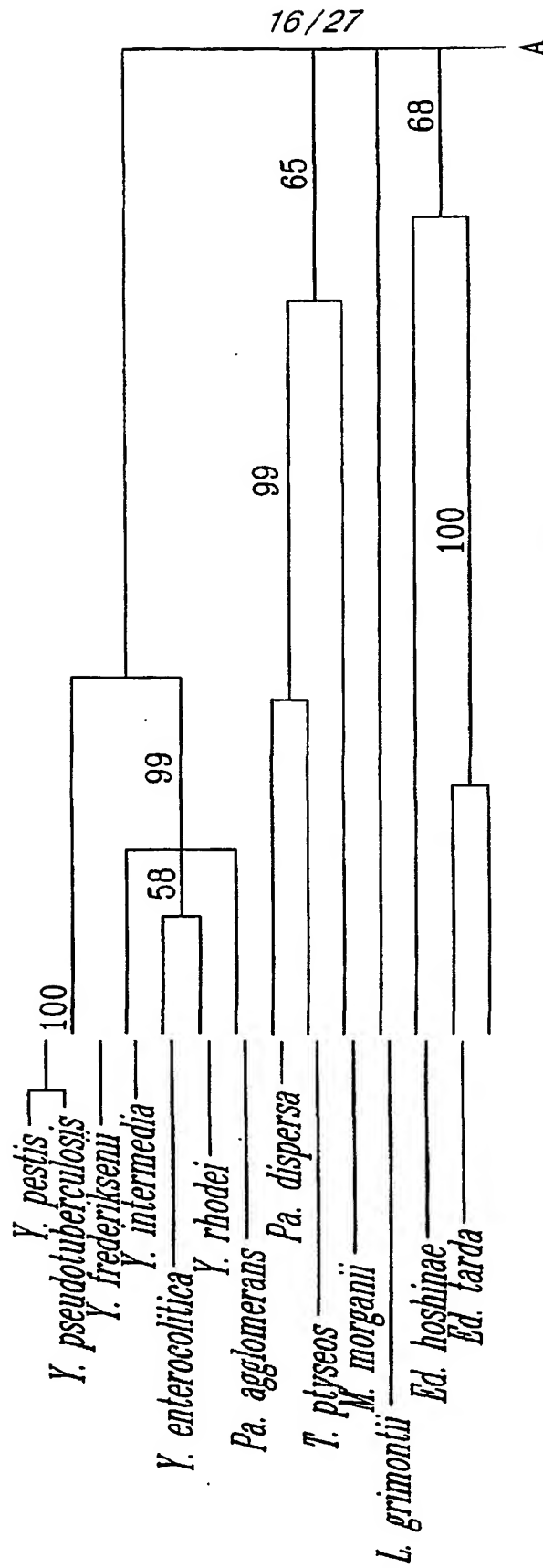
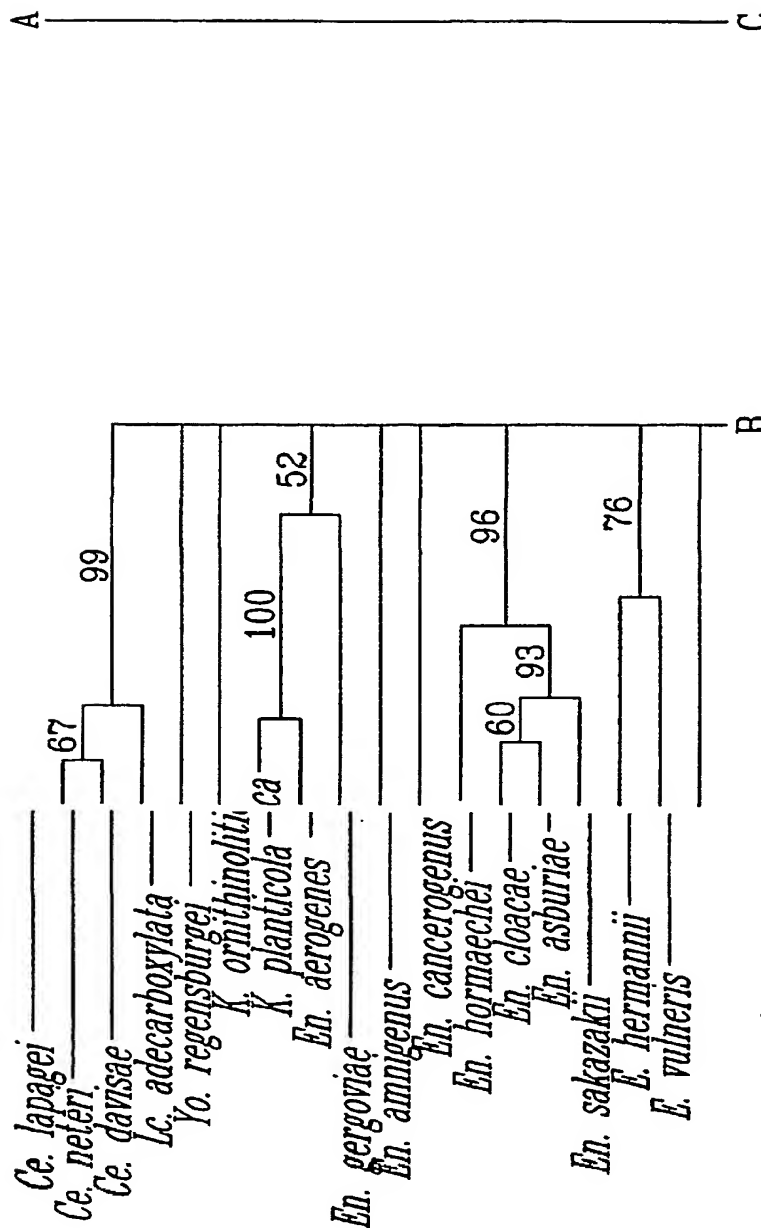


FIG. 8d

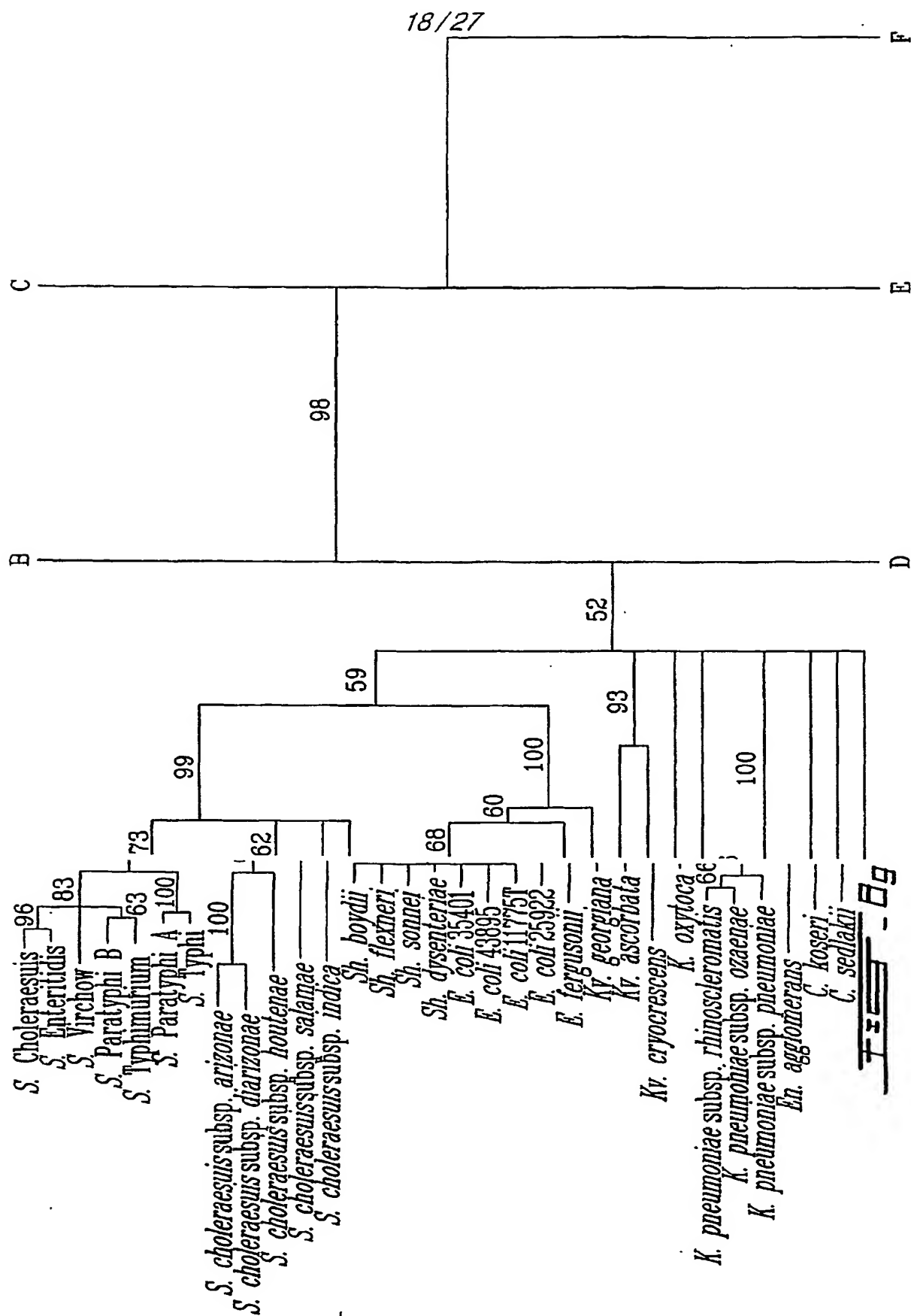


16/27

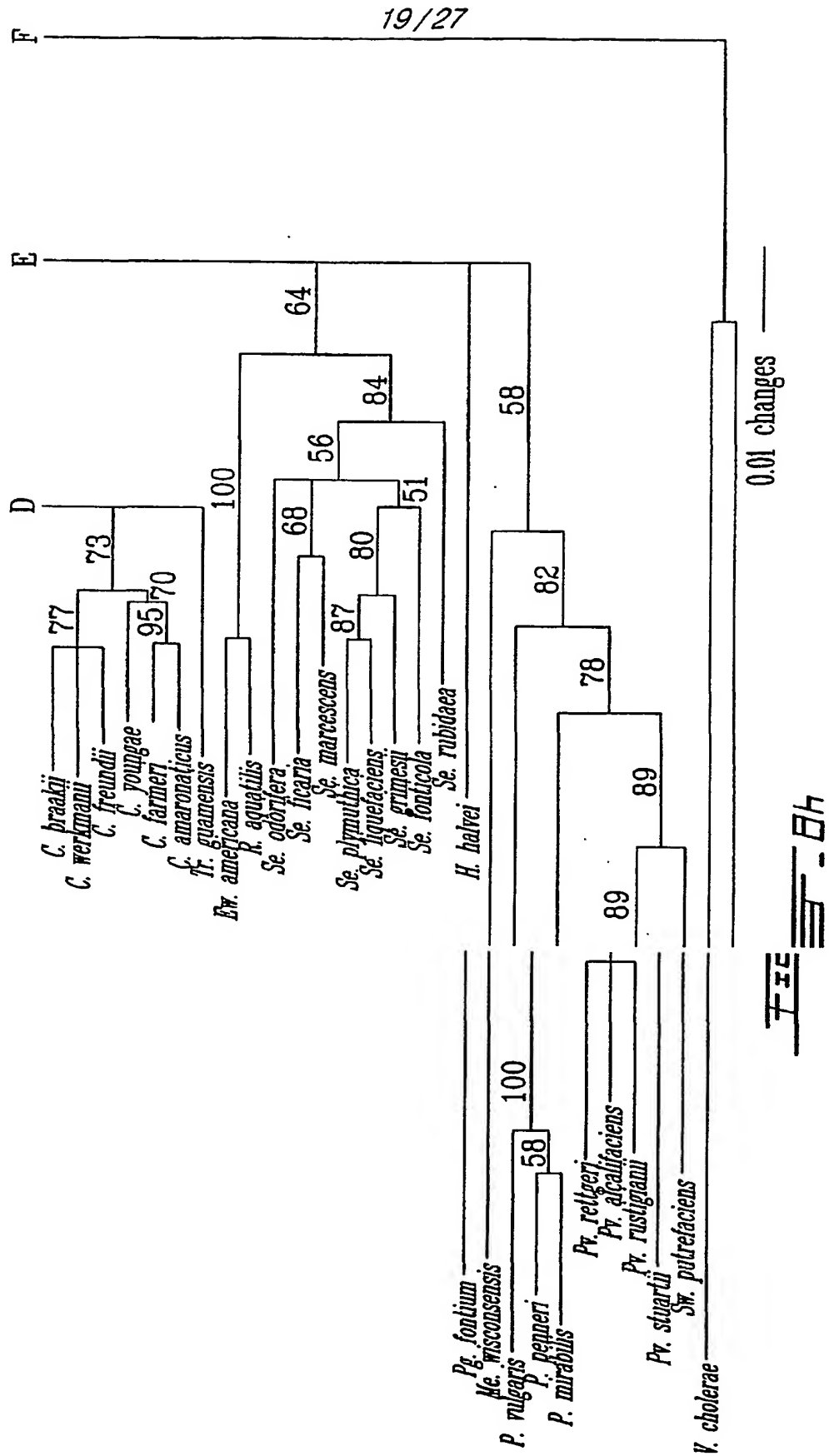
17/27



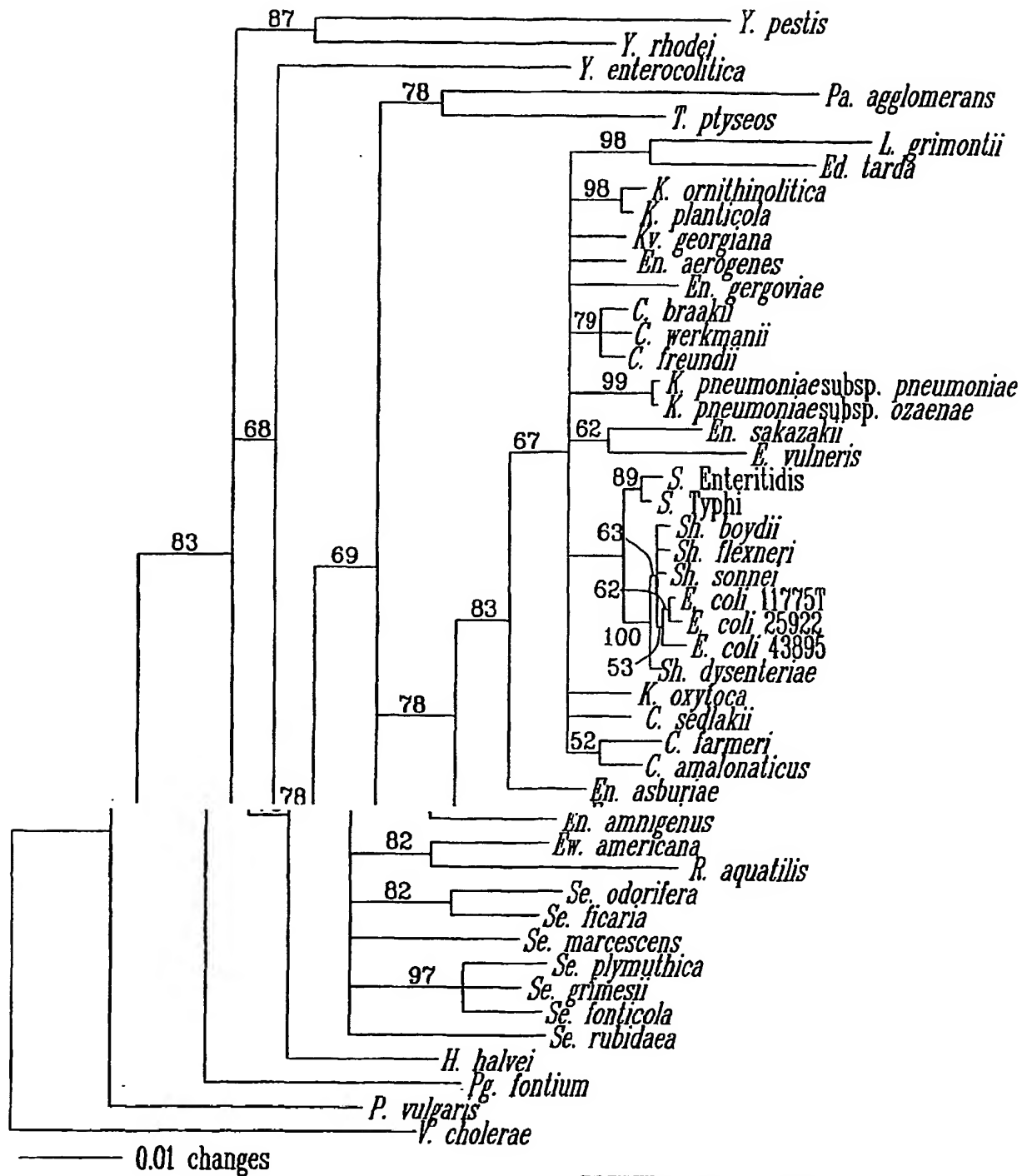
FEF-BF





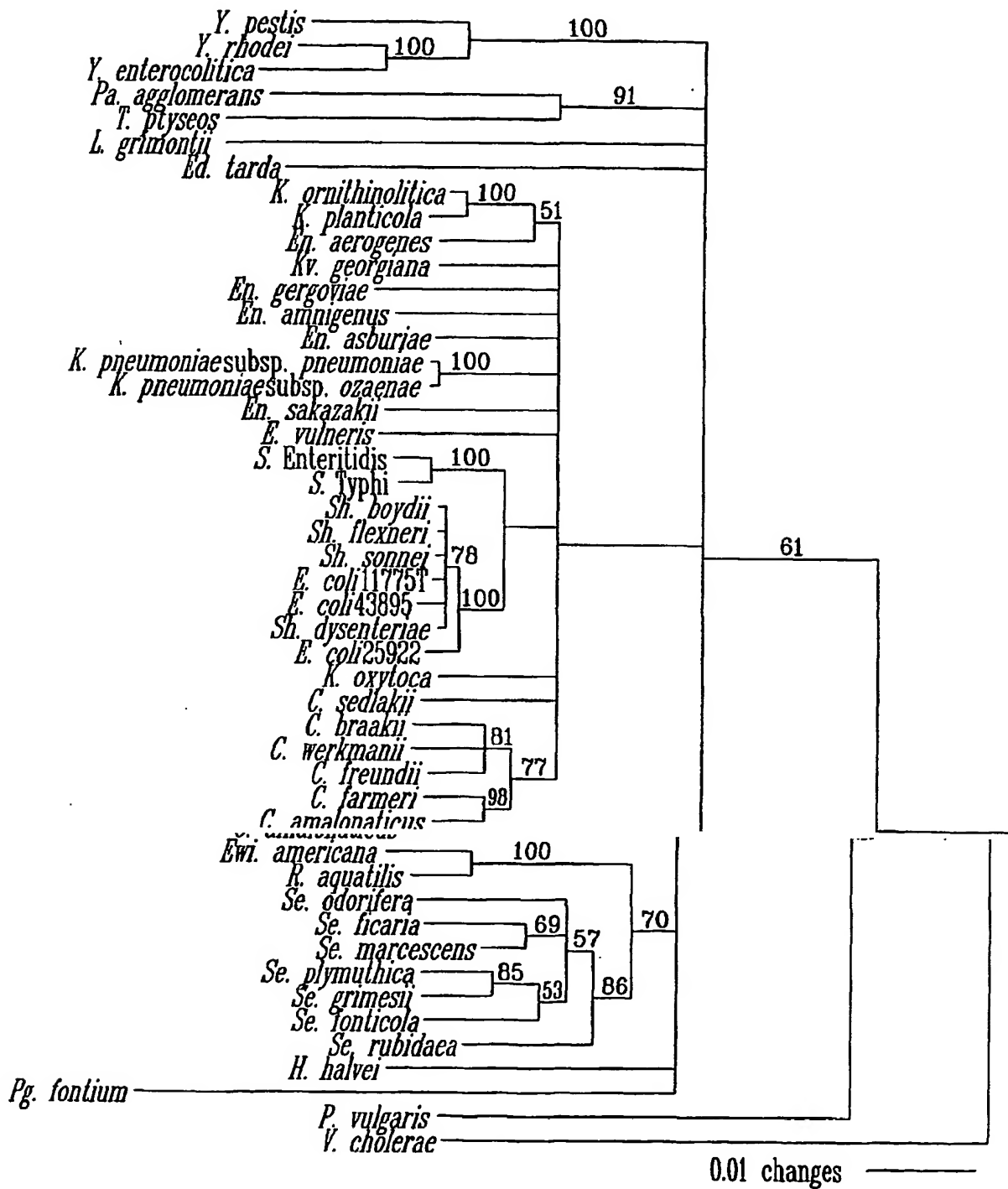


20/27



F I S S - 9 a

21/27



715 - 96

22/27

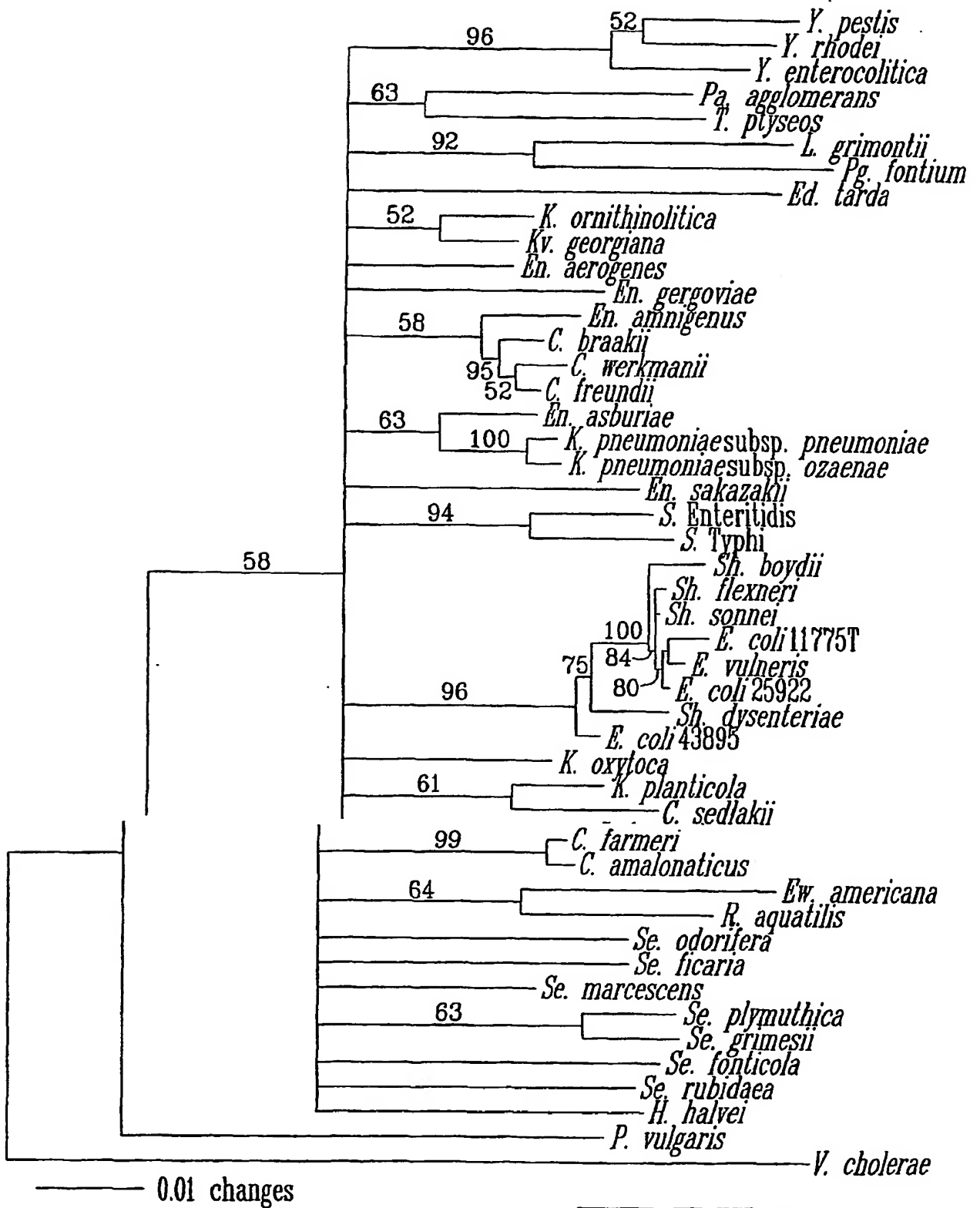
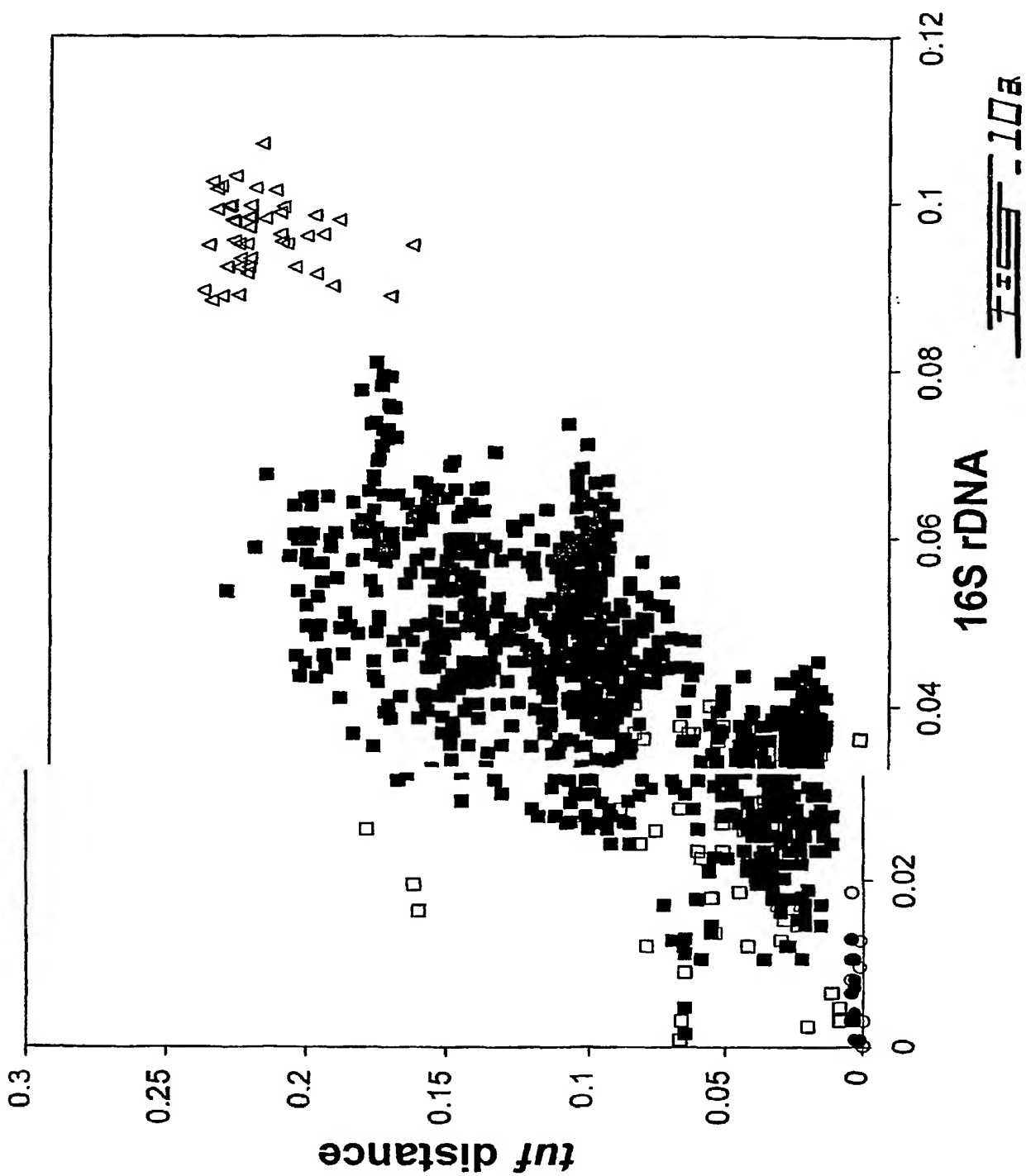
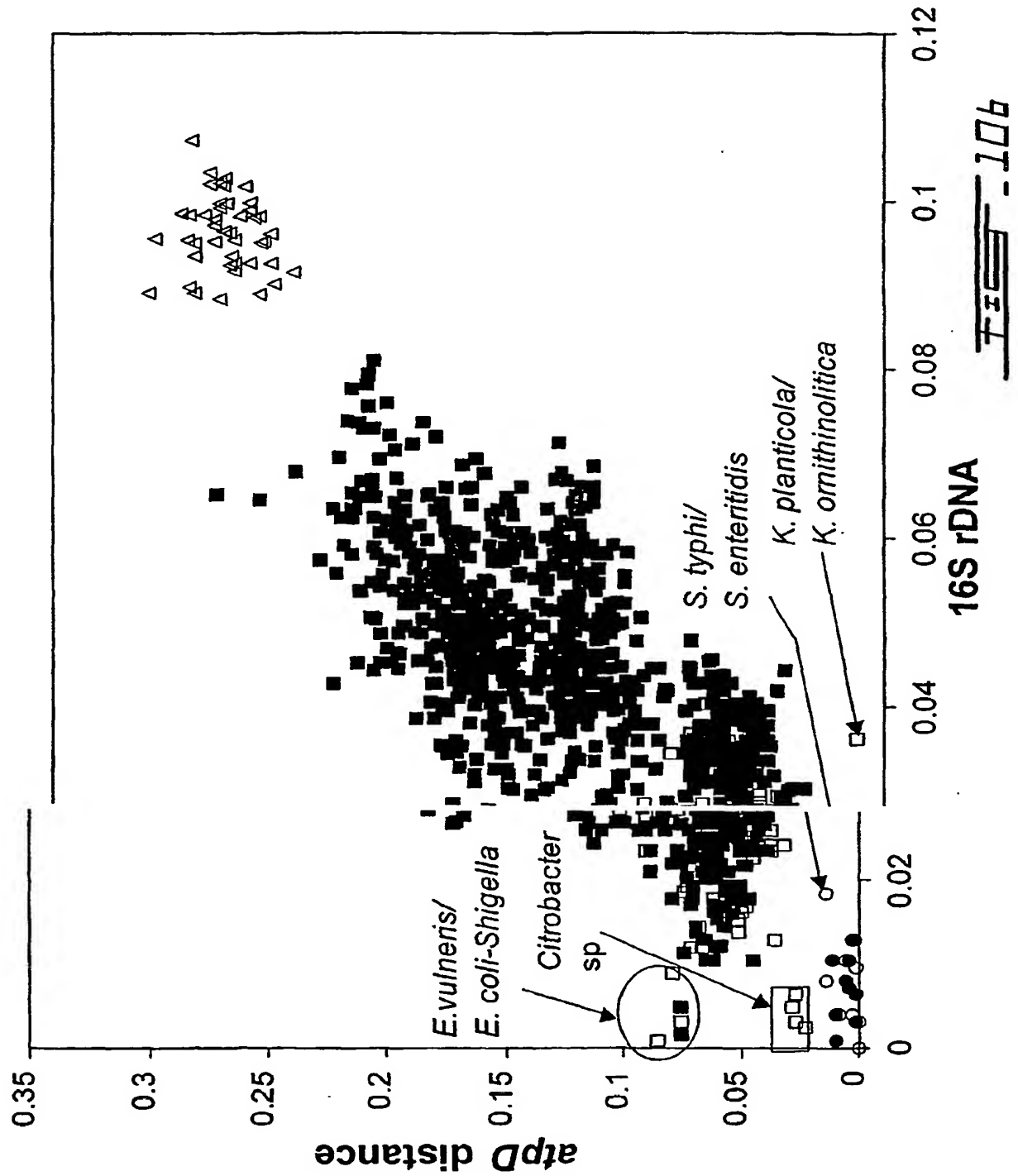


FIG. 9C

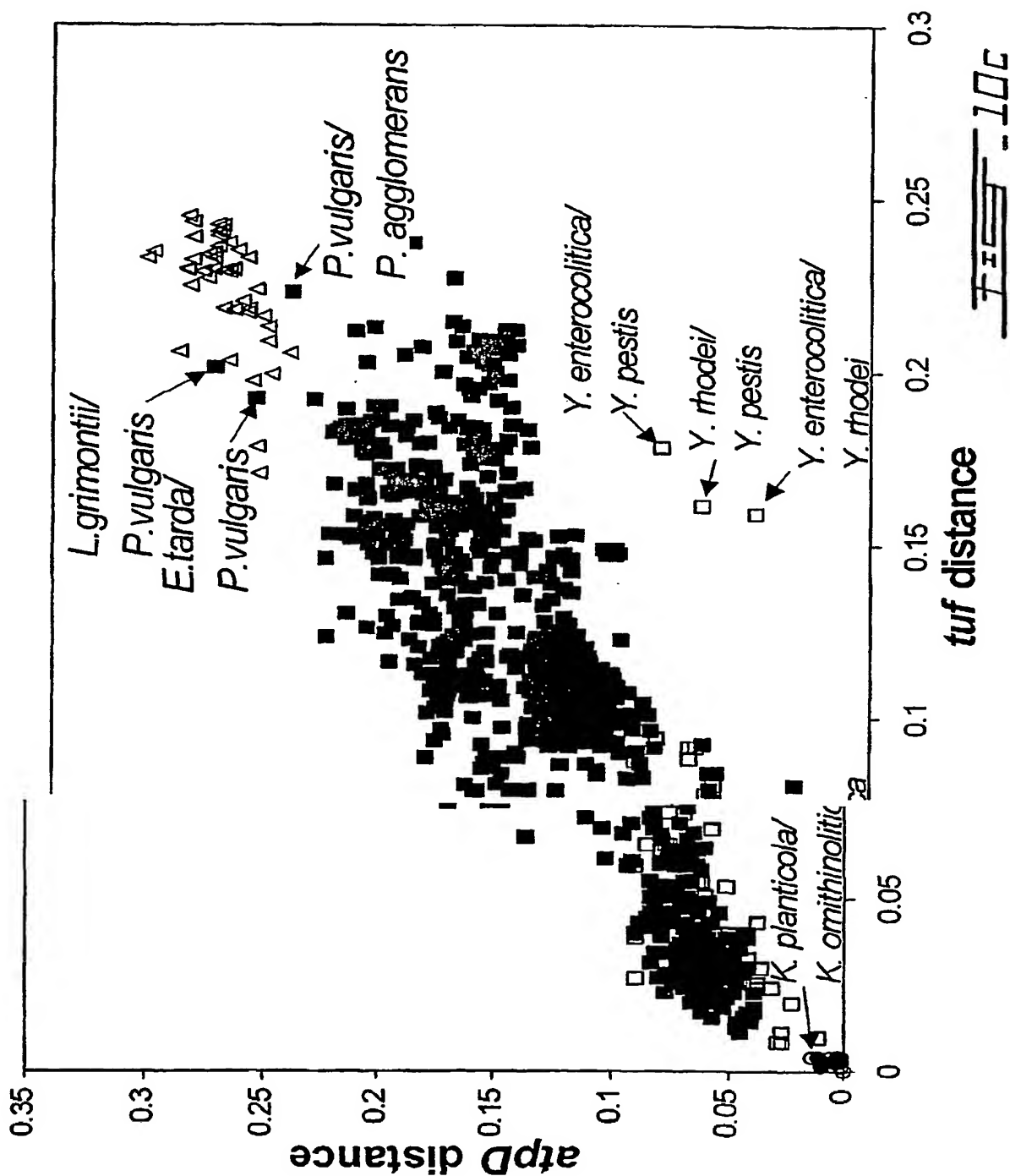
23/27



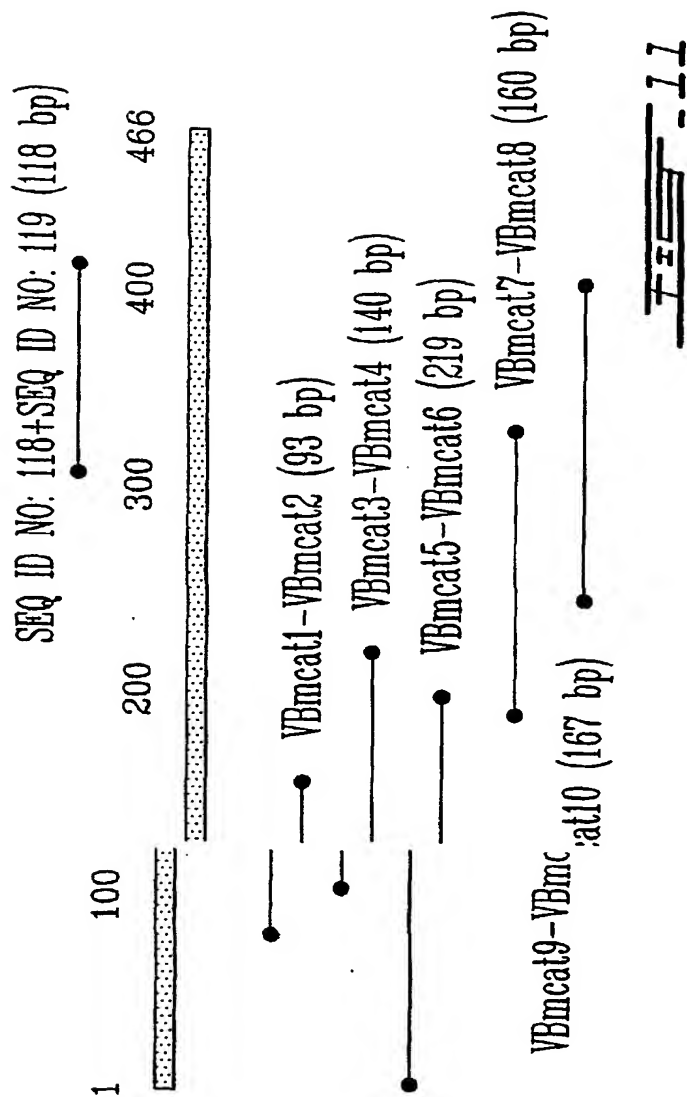
24/27



25 / 27



26/27





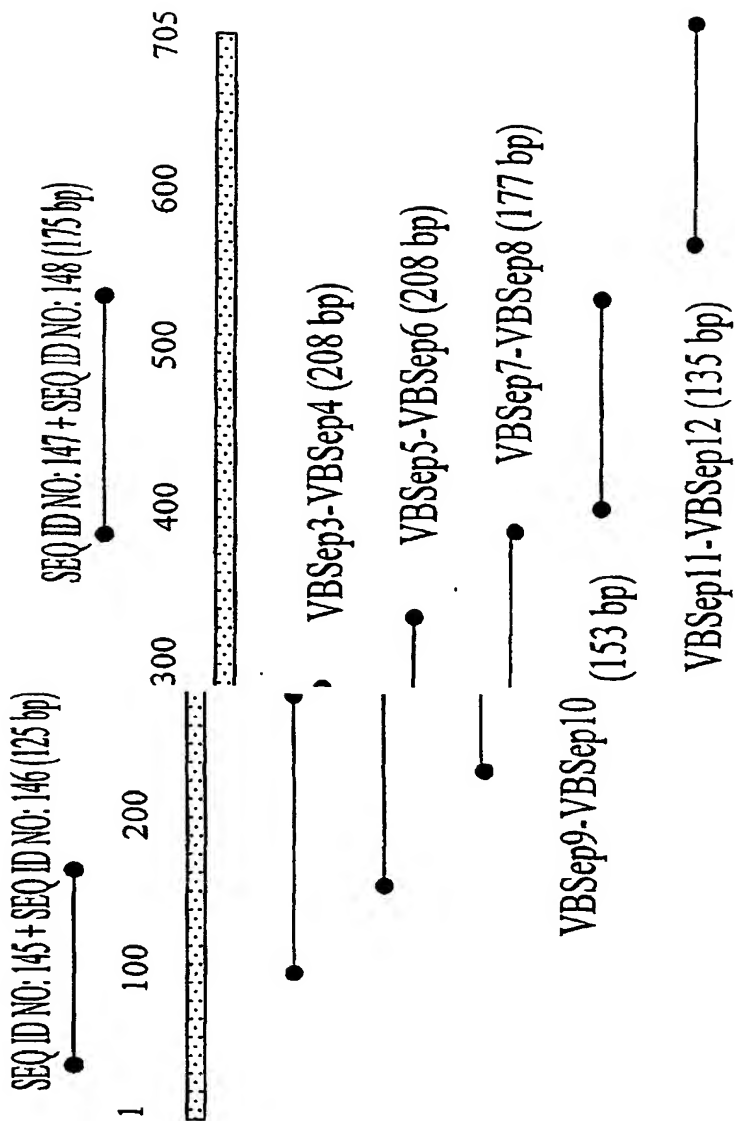


FIG. 12

## SEQUENCE LISTING

## (1) GENERAL INFORMATION:

## (i) APPLICANTS:

5 BERGERON, Michel G. <sup>1</sup>, 1145 des Érables, Québec City,  
 Québec, Canada, G2K 1T8  
 BOISSINOT, Maurice <sup>1</sup>, 109 Jean-Bruchési, St-Augustin-  
 de-Desmaures, Québec, Canada, G3A 2N2  
 10 HULETSKY, Ann <sup>1</sup>, 1231 Av des Pins, Sillery, Québec,  
 Canada, G1S 4J3  
 MÉNARD, Christian <sup>1</sup>, 1174 Rue du Pont, St-Lambert-de-  
 Lévis, Québec, Canada, G0S 2W0  
 OUELLETTE, Marc <sup>1</sup>, 1035 de Ploërmel, Sillery, Québec,  
 Canada, G1S 3S1  
 15 PICARD, François J. <sup>1</sup>, 1245 de la Sapinière, Cap-  
 Rouge, Québec, Canada, G1Y 1A1  
 ROY, Paul H. <sup>2</sup>, 28 Charles Garnier, Loretteville,  
 Québec, Canada, G2A 2X8

20 <sup>1</sup>:Canadian citizenship  
<sup>2</sup>:American citizenship

(ii) TITLE OF THE INVENTION: HIGHLY CONSERVED GENES AN THEIR  
 25 USE TO GENERATE SPECIES-SPECIFIC, GENUS-SPECIFIC AND  
 UNIVERSAL NUCLEIC ACID PROBES AND AMPLIFICATION PRIMERS TO  
 RAPIDLY DETECT AND IDENTIFY ALGAL, ARCHAEOAL, BACTERIAL,  
 FUNGAL AND PARASITICAL MICROORGANISMS FROM CLINICAL  
 SPECIMENS FOR DIAGNOSIS

30 (iii) NUMBER OF SEQUENCES: 2297

## (iv) CORRESPONDENCE ADDRESS:

35 (A) ADDRESSEE:  
 (B) STREET:  
 (C) CITY:  
 (D) STATE:  
 (E) COUNTRY:  
 40 (F) ZIP:

## (v) COMPUTER READABLE:

45 (A) MEDIUM TYPE:  
 (B) COMPUTER:  
 (C) OPERATING:  
 (D) SOFTWARE:

## (vi) CURRENT APPLICATION DATA:

50 (A) APPLICATION:  
 (B) FILING DATE:  
 (C) CLASSIFICATION:

## (vii) PRIOR APPLICATION DATA:

55 (A) APPLICATION:  
 (B) FILING DATE:

(viii) ATTORNEY/AGENT INFORMATION:

- (A) NAME:
- (B) REGISTRATION NUMBER:

5

(ix) TELECOMMUNICATION INFORMATION:

- (A) TELEPHONE:
- (B) TELEFAX:

## 2) INFORMATION FOR SEQ ID NO: 1

## (i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 750 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

## 10 (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Acinetobacter baumannii*  
 (B) STRAIN: ATCC 19606

## 15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1

	CAA	ACT	CGT	G	AGC	ACAT	CCT	TCT	TTCT	CTCGT	CAG	GTA	GGT	G	TAC	CTT	TAC	AT	50			
	CAT	CGT	AT	TC	TTA	AA	CAA	AT	GCG	AC	CTT	TGT	TG	AT	GAC	GAA	GA	ATT	ACT	TTG	100	
20	AAT	TAG	TAG	A	AAT	GGA	AGT	A	CGT	GA	ACT	TC	TTT	CT	ACT	TTA	TG	ACT	T	CCCA	150	
	GGT	GAT	GAC	A	CTC	CAG	TAA	T	CCG	TG	GTT	CA	GCT	CT	TG	CAG	CG	CTT	A	ACGG	200	
	TGA	AG	CT	GGT	CCT	TAC	GGT	G	AAG	AAT	CAG	T	TCT	TG	CT	CTT	GT	AG	CAG	CAC	250	
	TTG	ACT	CT	TA	CAT	CC	CAG	AG	CCG	AG	CGT	G	CA	AT	CG	ACAA	AG	CAT	T	CTTG	300	
	ATG	CCA	AT	CG	AAG	AC	GTA	T	CT	CA	AT	TTT	CT	GG	TC	GT	GTA	CAG	TAG	TA	AC	350
25	AGG	CCG	TG	TT	GA	AG	CT	GGT	TC	AT	CAA	AGT	TG	GT	GAA	GAA	GT	AG	AG	ATCG	400	
	TTG	GT	AT	TAA	AG	AT	CA	GTT	AAA	ACA	ACT	G	TA	ACT	GG	CGT	AG	AA	T	GTTC	450	
	CGT	AA	ACT	TC	TTG	AC	GA	AGG	CCG	TG	CAG	GT	GAG	AA	CT	GTG	GT	AT	CT	TACT	500	
	TCG	TG	GTA	CT	AAG	CGT	GA	AG	AAG	TAC	ACA	ACG	TG	GT	CA	AGT	CT	TG	CT	AAAC	550	
	CAG	GT	ACA	AT	CA	AG	CCG	CAC	ACT	AAA	TT	CG	AC	GC	AGA	AGT	AT	AC	GTA	CTT	600	
30	TCT	AA	AGA	AG	AAG	GT	GT	CG	TC	ACA	CT	CCA	TT	CT	TAA	ATG	GT	TAC	CG	TCC	650	
	AC	AG	TT	CTAC	TT	CCG	TAC	AA	CT	GAC	GTA	AC	TG	GT	G	CRATC	CAG	TT	GAA	AG	700	
	AAG	G	CGT	TGA	AAT	G	GTA	ATG	CC	AG	G	TGACA	AC	G	TT	GAAAT	G	T	CAG	TAGAA	750	

## 35 2) INFORMATION FOR SEQ ID NO: 2

## (i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 826 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

## 45 (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Actinomyces meyeri*  
 (B) STRAIN: ATCC 35568

## 50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2

	CGG	TG	CGATC	CTC	GT	GGT	CG	CCG	CG	ACC	G	CGG	CCCC	CATG	G	CCC	CAG	ACCC	50	
	GCG	AG	CACGT	CCT	GT	CTC	GCC	CGT	CAG	GTCG	G	CGT	TCCC	CAC	CAT	CCT	CATC	100		
	GCC	CT	CAACA	AGT	CC	GAC	AT	GGT	TG	ACG	AC	GAG	GAA	ATGA	TG	GAA	CTGGT	150		
55	CGA	GAG	GAG	TG	CCG	CG	ACC	TG	CT	G	GATC	CC	AGG	ACTTC	GAT	CG	CGATG	200		
	CCCC	GAT	CGT	CC	AGG	TTT	CC	GCT	CT	GA	AGG	CC	CT	CG	AGG	CG	AC	GCGG	250	
	TGG	GTT	GCCA	AG	AT	CG	AGGA	GCT	CAT	G	GAG	GCT	GT	G	AT	CCT	AC	ATCCC	300	
	CAC	CCCC	CGAG	CG	CG	ATAT	G	ACA	AG	CC	CCT	CCT	CAT	G	CCG	AT	CG	AGG	350	
	TCT	T	CACGAT	CAC	AGG	T	CGT	GG	CAC	G	GTCG	TC	AC	G	G	TG	TT	GAG	400	
60	GG	CAAG	CTGC	CG	AT	CA	ACTC	CG	AGG	T	CGAG	AT	CCT	CG	GTA	T	CCG	T	GATCC	450

```

      CCAGAAGACC ACGGTCACCG GCATCGAGAT GTTCCACAAG TCGATGGACG      500
      AGGCATGGGC CGGCGAGAAC TGTGGCCTGC TGCTGCGCGG TACCAAGCGC      550
      GATGAGGTTG AGCGCGGCCA GGTGTGGGCC ATTCCCGGCT CCATCACGCC      600
      TCACACCGAG TTCGAGGGCC AGGTTTACAT CCTCAAGAAG GAAGAGGGCG      650
5     GCCGTCAAA CCCGTTCTTC TCGAACTACC GTCCGCAGTT CTA CTTCCGT      700
      ACCACGGACG TGACCGGCGT CATCACCTC CCCGAGGGCA CCGACATGGT      750
      CATGCCTGGC GACACCACCG AGATCTCCGT TCAGCTGATC CAGCCCATCG      800
      CCATGGAGCC CGGCTGGGCT TCGCCA                                826

```

10

## 2) INFORMATION FOR SEQ ID NO: 3

```

      (i) SEQUENCE CHARACTERISTICS:
15     (A) LENGTH: 835 bases
      (B) TYPE: Nucleic acid
      (C) STRANDEDNESS: Double
      (D) TOPOLOGY: Linear

```

20 (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

```

      (A) ORGANISM: Aerococcus viridans
      (B) STRAIN: ATCC 11563

```

25

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3

```

      TGGTGC GATC TTAGTAGTAT CTGCTGCTGA TGGTCCAATG CCACAAACTC      50
      GTGAGCACAT CCTTTTAGCT GGCCAAATCG GTGTTCTGCTG ATTCGTTAGTA      100
30     TTCTTAAACA AAGTTGACCA AGTTGACGAT GAAGAATTAC TAGAATTAGT      150
      TGAAATGGAA GTTCGTGACT TATTATCTGA GTACAACTAC CCAGGTGACG      200
      ATCTACCTGT AATCGCTGGT TCTGCTTTAT TAGCATTACA AGGCGATGAA      250
      GCTCAAGAAG CTAAAATCAT GGAATTAATG GAAGCTGTAG ACTCTTACAT      300
      TCCAGAACCA GAACGTGACA ACGACAAACC ATTCATGATG CCAATTGAGG      350
35     ATGTATTCTC AATCACTGGT CGTGGTACTG TTGCTACAGG TCGTGTGAA      400
      CGTGGTGAAG TTCGTACAGG TGACGAAGTT GACATCGTTG GTATTGCTGA      450
      ACAATCGGT AAATCAGTTG TAACTGGTGT TGAAATGTTT CGTAAAAACT      500
      TAGACTACGC TCAAGCTGGT GACAACATCG GTGCATTATT ACGTGGTGT      550
      CAACGTGAAG ACATCCAACG TGGTCAAGTA TTGGCTGCTC CTGGTTCAAT      600
40     CACTCCACAT ACTAAATTTA AAGCGCAAGT TTACGTTTTA TCTAAAGAAG      650
      AAGGTGGACG TCATACACCA TTCTTAATA ACTACCGTCC ACAATTCTAC      700
      TTCCGTACTA CTGACATTAC TGGTGTATC ACTTTACCAAG AAGACGTAGC      750
      TATGGTTATG CCTGGTGACA ACGTTGATAT GGACGTTGAA TTGATTCACC      800
      CAGTTGCGAT CGAAGATGGT ACTAAATTCT CTATC                                835

```

45

## 2) INFORMATION FOR SEQ ID NO: 4

```

50     (i) SEQUENCE CHARACTERISTICS:
      (A) LENGTH: 827 bases
      (B) TYPE: Nucleic acid
      (C) STRANDEDNESS: Double
      (D) TOPOLOGY: Linear

```

55

(ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

```

      (A) ORGANISM: Achromobacter xylosoxidans subsp.
60     denitrificans

```

(B) STRAIN: ATCC 15173

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4

5	CCTGGTGGTG	TCGGCCGCTG	ACGGCCCAGT	GCCGCAAACG	CGCGAACACA	50
	TCCTGCTGAG	CCGCCAGGTT	GGCGTGCCGT	ACATCATCGT	CTTCCTGAAC	100
	AAGGCCGACA	TGGTTGACGA	CGCCGAGCTG	CTTGAGCTGG	TGGAAATGGA	150
	AGTTCGCGAR	CTGCTGAGCA	AGTACGACTT	CCCGGGCGAC	GACACCCCGA	200
	TCGTGAAGGG	TTCGGCCAAG	CTGGCGCTGG	AAGGCGACAA	GGGCGAACTG	250
10	GGCGAACAGG	CCATCATGGC	GCTGGCCGCT	GCGCTGGACT	CGTACATCCC	300
	GACGCCTGAG	CGTGCCGTTG	ACGGCGCGTT	CTGATGCCG	GTTGAAGACG	350
	TGTTCTCGAT	CTCGGCTCGC	GGCACCGTGG	TGACCGGCCG	TATCGAACGC	400
	GGCATCATCA	AGGTCGGCGA	GGAAATCGAA	ATCGTCGGTC	TGGTGCCGAC	450
	GGTGAAGACG	ACCTGCACGG	GCGTGGAAT	GTTCCGCAAG	CTGCTGGACC	500
15	AAGGTCAAGC	CGGCGACAAC	GTGGGCATCC	TRCTGCGCGG	CACCAAGCGT	550
	GAAGACGTCC	AGCGCGGCCA	GTTTCTGGCC	AAGCCGGGCT	CGATCACCCC	600
	GCACACGGAC	TTCACGTCCG	AGGTGTACAT	CCTGTCCAAG	GAAGAAGGCG	650
	GCCGTCACAC	TCCGTTCTTC	CAAGGCTATC	GTCCCCAGTT	CTACTTCCGC	700
	ACGACGGACG	TGACGGGCAC	GATCGAGCTG	CCGGCCGACA	AGGAAATGGT	750
20	CCTGCCGGGC	GACAACGTGG	CCATGACGGT	CAAGCTGCTG	GCTCCGATCG	800
	CCATGGAAGA	AGGCCTGCGT	TCGCCAC			827

25 2) INFORMATION FOR SEQ ID NO: 5

(i) SEQUENCE CHARACTERISTICS:

	(A)	LENGTH: 823 bases
	(B)	TYPE: Nucleic acid
30	(C)	STRANDEDNESS: Double
	(D)	TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

35 (vi) ORIGINAL SOURCE:

(A)	ORGANISM: <i>Anaerorhabdus furcosus</i>
(B)	STRAIN: ATCC 25662

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5

40	TGGATCAATC	CTAGTAGTTG	CTGCAACTGA	TGGACCAATG	CCTCAAATC	50
	GTGAACATAT	CTTACTTGCT	CGTCAAGTAG	GTGTTCCAAG	AATGGTTGTA	100
	TTCTTGAACA	AATGCGACAT	GGTTGAAGAT	GAAGAATTAA	TCGACCTTGT	150
	TGAAATGGAA	GTTTCGTGAAC	TTCTAAGTGC	TTACGGTTTC	GAAGGTGATG	200
45	ATACACCAGT	TATCCGTGGT	TCTGCATTAA	AATCTCTTGA	AGGAAATGCT	250
	GATTGGGAAG	CAAAAGTTGC	TGAATTAATG	GATGCAGTTG	ACTCTTGGAT	300
	TCCAACTCCA	ACTCATGAAA	CAGACAAACC	ATTCTTAATG	GCTGTTGAAG	350
	ATGTATTAC	AATTACAGGT	CGTGGTACAG	TTGCTACTGG	ACGTGTTGAA	400
	CGTGGACACT	TAAACCTTAA	CGAAGAAGTT	GAAATCGTTG	GTATTCATGA	450
50	TACTAAGAAA	TCAGTTGTTA	CTGGTATCGA	AATGTTCCGT	AAATTATTAG	500
	ACTATGCTGA	AGCAGGAGAC	AACATTGGTG	CATTATTACG	TGGTGTTTCT	550
	CGTGATGAAA	TCGAACGTGG	ACAATGTCTA	GCTAAACCTG	GATCAGTTAC	600
	TCCACATACA	GCTTTCAAAG	CTCAAGTATA	CGTATTAATC	AAAGAAGAAG	650
	GTGGACGTCA	TACACCATTC	GTAACATACT	ACCGTCCTCA	ATTCTATTTC	700
55	CGTACAACCTG	ACGTAAACAGG	AGTTGTTAAA	CTTCCTGAAG	GTAAGTAAAT	750
	GTTTATGCCT	GGAGACAACA	TCGAAATGAT	CGTTGAATTA	ATCGCTCCAA	800
	TCGCTGTTGA	ACAAGGAAC	AAG			823

60

## 2) INFORMATION FOR SEQ ID NO: 6

## (i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 825 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

10

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Bacillus anthracis*  
 (B) STRAIN: 4229

## 15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6

CGGCGGTATC TTAGTAGTAT CTGCTGCTGA TGGCCCAATG CCTCAAACCTC 50  
 GTGAGCACAT CCTTCTTTCT CGTCAAGTAG GTGTACCTTA CATCGTTGTA 100  
 TTCTTAAACA AATGCGACAT GGTAGACGAC GAAGAATTAT TAGAATTAGT 150  
 20 AGAAATGGAA GTTCGCGACC TATTATCTGA ATACGGATTC CCAGGCGACG 200  
 ACATTCCTGT AATCAAAGGT TCTGCTCTTA AAGCTCTTCA AGGAGAAGCT 250  
 GATTGGGAAG CAAAAATCAT TGAATTAATG GCTGAAGTTG ATGCTTACAT 300  
 CCCAACTCCA GAACGTGAAA CTGACAAACC ATTCTTAATG CCTGTAGAGG 350  
 ACGTATTCTC TATCACAGGT CGTGGTACAG TTGCTACTGG TCGTGTTGAG 400  
 25 CGCGGTATCG TTAAAGTTGG TGACGTAGTA GAAATCATCG GTCTTGCTGA 450  
 AGAAAATGCT TCTACAACTG TAACTGGTGT AGAGATGTTT CGTAAACTTC 500  
 TTGACCAAGC TCAAGCTGGA GACAACATCG GTGCTTTACT TCGTGGGGTT 550  
 GCTCGTGAAG ACATCCAACG TGGACAAGTA CTTGCAAAA GCGGTTCTGT 600  
 AAAAGCTCAC GCTAAATTCA AAGCTGAAGT TTTCGTATTA TCTAAAGAAG 650  
 30 AAGGTGGACG TCACACTCCA TTCTTCGCTA ACTACCGTCC TCAGTTCTAC 700  
 TTCCGTACAA CTGACGTAAC TGGTATCATC CAATTACCAG AAGGTACTGA 750  
 AATGGTAATG CCTGGTGACA ACATCGAAAT GACTATCGAA CTTATCGCTC 800  
 CAATCGCTAT CGAAGAGGGA ACTAA 825

35

## 2) INFORMATION FOR SEQ ID NO: 7

## (i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 829 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

45

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Bacillus cereus*  
 (B) STRAIN: ATCC 14579

50

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7

CGGCGGTATC TTAGTAGTAT CTGCTGCTGA TGGCCCAATG CCTCAAACAC 50  
 GTGAGCACAT CCTTCTTTCT CGTCAAGTAG GTGTTCTTA CATCGTTGTA 100  
 55 TTCTTAAACA AATGCGACAT GGTAGATGAC GAAGAATTAT TAGAATTAGT 150  
 AGAAATGGAA GTTCGCGACC TATTATCTGA ATACGGATTC CCAGGCGACG 200  
 ACATTCCTGT AATCAAAGGT TCTGCTCTTA AAGCTCTTCA AGGAGAAGCT 250  
 GATTGGGAAG CAAAAATCAT TGAATTAATG GCTGAAGTTG ATGCTTACAT 300  
 CCCAACTCCA GAACGTGAAA CTGACAAACC ATTCTTAATG CCTGTAGAGG 350  
 60 ACGTATTCTC TATCACAGGT CGTGGTACAG TTGCTACTGG TCGTGTTGAG 400

	CGCGGTATCG	TTAAAGTTGG	TGACGTAGTA	GAAATCATCG	GTCTTGCTGA	450
	AGAAAATGCT	TCTACAACTG	TAAC TGGTGT	AGAGATGTTT	CGTAAACTTC	500
	TTGACCAAGC	TCAAGCTGGA	GACAACATCG	GTGCTTTACT	TCGTGGGGTT	550
	GCTCGTGAAG	ACATCCAACG	TGGACAAGTA	CTTGCAAAAA	GCGGTTCTGT	600
5	AAAAGCTCAC	GCTAAATTCA	AAGCTGAAGT	TTTCGTATTA	TCTAAAGAAG	650
	AAGGTGGACG	TCACACTCCA	TTCTTCGCTA	ACTACCGTCC	TCAGTTCTAC	700
	TTCCGTACAA	CTGACGTAAC	TGGTATCATC	CAATTACCAG	AAGGTACTGA	750
	AATGGTAATG	CCTGGTGACA	ACATTGAAAT	GACTATCGAA	CTTATCGCTC	800
10	CAATCGCTAT	CGAAGAGGGA	ACTAAATTC			829

## 2) INFORMATION FOR SEQ ID NO: 8

## 15 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 818 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

## 20 (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Bacteroides distasonis*  
 25 (B) STRAIN: ATCC 8503

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8

	CGGTGCTATC	ATCGTAGTTG	CTGCTACTGA	TGGTCCTATG	CCTCAAACCTC	50
30	GCGAGCACAT	CCTTTTGGCT	CGTCAGGTAA	ACGTTCCGAG	ATTGGTTGTA	100
	TTCATGAACA	AGTGTGACAT	GGTTGACGAC	GAGGAAATGT	TGGAATTGGT	150
	TGAGATGGAG	ATGAGAGAGT	TGCTTTTCATT	CTATCAATTC	GACGGTGACA	200
	ACACTCCGAT	CATCCGTGGT	TCTGCTCTTG	GTGCATTGAA	CGGTGATGCT	250
	CAATGGGAAG	ATAAAGTAAT	GGAGTTGATG	GAAGCTTGTG	ATACTTGAT	300
35	TCCTCTGCCT	CCGCGCGAAA	TCGACAAGCC	GTTCTTGATG	CCGGTTGAGG	350
	ACGTATTCTC	AATCACGGGT	CGTGGTACTG	TTGCTACAGG	TCGTATCGAG	400
	ACAGGTATTG	TTAAGGTTGG	TGAGGAAGTT	CAGATCATCG	GTCTTGGCGC	450
	TGCTGGTAAG	AAATCTGTTG	TTACAGGTGT	TGAGATGTTT	CGTAAGTTAT	500
	TGGATCAAGG	TGAGGCTGGT	GATAACGTTG	GTTTGTTGCT	TCGCGGTATC	550
40	GATAAGAATG	AGATCAAGCG	TGGTATGGTA	ATCTGCCACC	CGGGTCAGGT	600
	TAAAGAGCAT	TCTAAGTTCA	AGGCTGAGGT	TTATATCTTG	AAGAAAGAGG	650
	AAGGTGGTTC	TCACACTCCG	TTCCACAACA	AATATCGTCC	TCAGTTCTAT	700
	ATCCGTACAT	TGGATGTAAC	TGGTGAGATC	ACTTTGCCCG	AAGGAACTGA	750
	AATGGTAATG	CCGGGTGATA	ACGTAACGAT	CGAGGTTGAG	TTGATCTATC	800
45	CGGTAGCATG	TAGCGTAG				818

## 2) INFORMATION FOR SEQ ID NO: 9

## 50 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 639 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 55 (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- 60 (A) ORGANISM: *Enterococcus casseliflavus*



(B) STRAIN: R763

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9

5	GGTCCTATGC	CTCAAACACG	TGAACACATC	TTGTTATCAC	GTAACGTTGG	50
	TGTACCATAC	ATCGTTGTTT	TCTTAAACAA	AATGGATATG	GTTGATGACG	100
	AAGAATTACT	AGAATTAGTT	GAAATGGAAG	TTCGTGACTT	ATTGTCAGAA	150
	TATGACTTCC	CAGGCGACGA	TGTTCTGTGA	ATCGCTGGTT	CTGCTTTGAA	200
	AGCTCTTGAA	GGCGATGCTT	CATACGAAGA	AAAAATCATG	GAATTAATGG	250
10	CTGCAGTTGA	CGAATACGTT	CCAACTCCAG	AACGTGACAC	TGACAAACCA	300
	TTCATGATGC	CAGTCGAAGA	CGTATTCTCA	ATCACTGGAC	GTGGTACTGT	350
	TGCTACAGGC	CGTGTGTAAC	GTGGACAAGT	TCGCGTTGGT	GACGAAGTTG	400
	AAATCGTTGG	TATTGCTGAA	GAAACTGCTA	AAACAACGTG	AACTGGTGTT	450
	GAAATGTTCC	GTAAATTGTT	AGACTATGCT	GAAGCAGGGG	ATAACATTGG	500
15	TGCATTGCTA	CGTGGTGTTG	CTCGTGAAGA	CATCCAACGT	GGACAAGTAT	550
	TGGCTAAAGC	TGGTACAATC	ACACCTCATA	CAAAATTTAA	AGCTGAAGTT	600
	TACGTTTTAA	CAAAGAAGA	AGGTGGACGT	CACACACCA		639

20

2) INFORMATION FOR SEQ ID NO: 10

(i) SEQUENCE CHARACTERISTICS:

	(A)	LENGTH: 692 bases
25	(B)	TYPE: Nucleic acid
	(C)	STRANDEDNESS: Double
	(D)	TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

30

(vi) ORIGINAL SOURCE:

	(A)	ORGANISM: <i>Staphylococcus saprophyticus</i>
	(B)	STRAIN: CSG 197

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10

	GAACACATTC	TTTTATCACG	TAACGTTGGT	GTTCCAGCAT	TAGTTGTATT	50
	CTTAAACAAA	GTTGACATGG	TTGACGATGA	AGAATTATTA	GAATTAGTAG	100
	AAATGGAAGT	TCGTGACTTA	TTAAGCGAAT	ATGACTTCCC	AGGTGACGAT	150
40	GTACCTGTAA	TCTCTGGTTC	TGCATTAAAA	GCTTTAGAAG	GCGACGCTGA	200
	CTATGAGCAA	AAAATCTTAG	ACTTAATGCA	AGCTGTTGAT	GACTTCATTC	250
	CAACACCAGA	ACGTGATTCT	GACAAACCAT	TCATGATGCC	AGTTGAGGAC	300
	GTATTCTCAA	TCACTGGTCG	TGGTACTGTT	GCTACAGGCC	GTGTTGAACG	350
	TGGTCAAATC	AAAGTCGGTG	AAGAAATCGA	AATCATCGGT	ATGCAAGAAG	400
45	AATCAAGCAA	AACAACGTGTT	ACTGGTGTAG	AAATGTTCCG	TAAATTATTA	450
	GACTACGCTG	AAGCTGGTGA	CAACATTGGT	GCATTATTAC	GTGGTGTTTC	500
	ACGTGATGAC	GTACAACGTG	GTCAAGTTTT	AGCTGCTCCT	GGTACTATTA	550
	CACCACATAC	AAAATTCAAA	GCGGATGTTT	ACGTTTTATC	TAAAGATGAA	600
	GGTGGTCGTC	ATACACCATT	CTTCACTAAC	TACCGCCAC	AATTCTATTT	650
50	CCGTACTACT	GACGTAACGTG	GTGTTGTAA	CTTACCAGAA	GG	692

2) INFORMATION FOR SEQ ID NO: 11

55

(i) SEQUENCE CHARACTERISTICS:

	(A)	LENGTH: 821 bases
	(B)	TYPE: Nucleic acid
	(C)	STRANDEDNESS: Double
60	(D)	TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 5 (A) ORGANISM: *Bacteroides ovatus*  
(B) STRAIN: ATCC 8483

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11

10	CGGTGCTATC ATCGTTTGTG CTGCAACTGA TGGTCCGATG CCTCAAACCTC	50
	GCGAACACAT TCTGTTAGCT CGTCAGGTAA ACGTACCTCG TCTGGTTGTA	100
	TTCTTGAACA AATGCGATAT GGTAGACGAC GAAGAAATGT TGGAATCGT	150
	TGAAATGGAA ATGAGAGAAC TCCTTTTCATT CTATGATTTC GATGGTGACA	200
	ATACTCCTAT CATCCGTGGT TCTGCTCTTG GCGCATTGAA CGGTGTTGAA	250
15	AAATGGGAAG ACAAAGTTAT GGAAGTATG GATGCAGTTG ATAAGTGGAT	300
	TCCACTGCCT CCGCGCGATG TTGATAAACC ATTCTTGATG CCGGTTGAAG	350
	ACGTGTTCTC TATCACAGGT CGTGGTACTG TAGCAACAGG TCGTATCGAA	400
	ACAGGTGTCA TCCACGTTGG TGATGAAGTC GAAATTCTTG GTTTAGGTGA	450
	AGATAAGAAA TCAGTTGTAA CTGGTGTGTA AATGTTCCGT AAAGTGTGG	500
20	ATCAAGGTGA AGCTGGTGAC AACGTAGGTC TTTTGCTTCG TGGTATTGAC	550
	AAGAACGAAA TCAAACGTGG TATGGTTCTT TGTAACCAGG GTCAGATTAA	600
	ACCGCACTCT AAATTCAAAG CTGAGGTTTA TATCTTGAAG AAAGAAGAAG	650
	GTGGTCGTCA CACTCCGTTT CACAACAAAT ACCGTCCTCA GTTCTACTTG	700
	CGTACTATGG ACTGTACAGG TGAAATCACT TTGCCGGAAG GAACAGAAAT	750
25	GGTAATGCCG GGTGATAACG TAACTATTAC AGTTGAGTTG ATTTACCCAG	800
	TAGCATTGAA CCCGGGCTTC G	821

30 2) INFORMATION FOR SEQ ID NO: 12

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 838 bases  
(B) TYPE: Nucleic acid  
35 (C) STRANDEDNESS: Double  
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

40 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Bartonella henselae*  
(B) STRAIN: ATCC 49882

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12

45	TGGTGCGATT TTGGTTGTTT CAGCTGCTGA TGGTCCGATG CCTCAAACAC	50
	GTGAGCATAT TCTTCTTGCC CGTCAGGTTG GTGTTCCAGC GATTGTTGTT	100
	TTTCTTAATA AGGTTGATCA GGTGATGAT GCTGAGCTTT TGGAGCTTGT	150
	TGAGCTTGAA GTTCGGGAGT TATGTGCGAA ATATGATTTT CCAGGAGACG	200
50	ATATTCCGAT CGTTAAAGGT TCTGCTTTGG CAGCGCTTGA AGATAAAGAT	250
	AAAAGCATTG GTGAAGATGC GGTTCGTCTT TTGATGAGTG AAGTTGATAA	300
	TTATATAACG ACGCCTGAAC GTCCTGTTGA TCAGCCGTTT TTGATGCCAA	350
	TTGAAGATGT TTTTTCGATT TCGGGTCGTG GAACTGTTGT GACGGGTCGT	400
	GTTGAGCGTG GTGTTATTAA GGTGGTGAA GAAGTTGAGA TTATCGGCAT	450
55	TCGTCCAAC TCTAAGACAA CAGTTACAGG GGTGAAATG TTCCGCAAGC	500
	TTTTAGATCA GGGGCAAGCG GGTGATAATA TTGGAGCGCT GCTTCGTGGT	550
	ATTGATCGTG AAGGGATTGA GCGTGGACAA GTTTTGCGA AGCCTGCTTC	600
	GGTTACACCT CATACGAGAT TTAAAGCAGA GGTTCACATT TTGACGAAAG	650
	ATGAAGGTGG TCGTCATACT CCATTTTTCG CGAATTATCG TCCTCAGTTT	700
60	TATTTCCGTA CTACGGATGT AACGGGAATT GTTACGCTTC CAGAAGGTAC	750

AGAGATGGTT ATGCCTGGTG ATAATGTTGC TATGGATGTC TCTCTGATTG 800  
 TTCCAATTGC CATGGAAGAA AACTTTCGTT TTGCTATC 838

5

## 2) INFORMATION FOR SEQ ID NO: 13

## (i) SEQUENCE CHARACTERISTICS:

10

- (A) LENGTH: 839 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

15

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Bifidobacterium adolescentis*  
 (B) STRAIN: ATCC 15703

20

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13

	TGGCGCCATC	CTTGTTGTGG	CCGCCACCGA	CGGCCCGATG	GCTCAGACCC	50
	GCGAGCACGT	GCTGCTCGCT	CGTCAGGTGG	GCGTCCCGAA	GATCCTCGTC	100
	GCTCTGAACA	AGTGCGATAT	GGTCGACGAC	GACGAGCTCA	TCGAGCTCGT	150
25	TGAGGAAGAG	GTCCGTGACC	TCCTCGACGA	AAATGGCTTC	GATCGCGATT	200
	GCCCGGTCAT	CCACGTGTCC	GCTTACGGCG	CACTGCACGA	TGACGCTCCG	250
	GACCACGAGA	AGTGGGTTGA	GCAGATCAAG	AAGCTCATGG	ACGCCGTCGA	300
	TGACTACATC	CCGACCCCGG	TCCACGATCT	GGACAAGCCG	TTCTTGATGC	350
	CGATCGAAGA	TGTCTTCACC	ATCTCCGGCC	GTGGCACCGT	GGTGACCGGC	400
30	CGTGTCGAGC	GTGGTAAGCT	CCCAGTCAAC	TCCAACGTCG	AGATCGTCGG	450
	CATCCGTCCG	ACCCAGACCA	CCACCGTCAC	CTCCATCGAG	ACCTTCCACA	500
	AGCAGATGGA	CGAGTGCGAG	GCTGGCGACA	ACACCGGTCT	GCTGCTCCGC	550
	GGCATCAACC	GTGACCAGGT	CGAGCGTGGC	CAGGTTCTGG	CTGCTCCGGG	600
	CTCCGTGACC	CCGCACACCA	AGTTCGAGGG	CGAAGTCTAC	GTGCTGACCA	650
35	AGGACGAAGG	CGGCCGTCAC	TCGCCGTTCT	TCTCCAACCTA	CCGTCCGCAG	700
	TTCTACTTCC	GTACCACCGA	CGTCACCGGC	GTCATCACCC	TGCCGGAAGG	750
	CGTTGAGATG	GTGCAGCCGG	GCGATCACGC	TACCTTCGGC	GTTGAGCTGA	800
	TCCAGCCGAT	CGCTATGGAA	GAGGGCCTGA	CCTTCGCAG		839

40

## 2) INFORMATION FOR SEQ ID NO: 14

## (i) SEQUENCE CHARACTERISTICS:

45

- (A) LENGTH: 839 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

50

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Bifidobacterium dentium*  
 (B) STRAIN: ATCC 27534

55

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 14

	TGGCGCTATC	CTCGTTGTGG	CCGCCACCGA	CGGCCCGATG	GCTCAGACCC	50
	GCGAGCACGT	GCTGCTCGCT	CGTCAGGTGG	GCGTGCCGCG	TATCCTCGTC	100
60	GCCCTGAACA	AGTGCGATAT	GGTCGACGAC	GAAGAGCTCA	TCGAGCTCGT	150

	TGAGGAAGAG	GTCCGTGACC	TCCTCGACGA	AAACGGCTTC	GATCGCGATT	200
	GCCCCGTGTCAT	CCACACCTCC	GCCTACGGCG	CGCTGCACGA	TGACGCTCCG	250
	GACCACGACA	AGTGGGTTGA	GTCCGTCAAG	GAATCATGA	AGGCCGTCGA	300
	CGAGTACATC	CCGACCCCGA	CCCACGATCT	GGACAAGCCG	TTCCTGATGC	350
5	CGATCGAAGA	TGTGTTTACC	ATCTCCGGCC	GTGGCACCCT	GGTTACCGGC	400
	CGTGTCGAGC	GTGGTAAGCT	CCCAGTCAAC	TCCAACGTTG	AGATCGTCGG	450
	CATCCGTCCG	ACCCAGACCA	CCACCGTCAC	CTCCATCGAG	ACCTTCCACA	500
	AGCAGATGGA	CGAGTGCGAG	GCTGGCGACA	ACACCGGTCT	GCTGCTCCGC	550
	GGCATCAACC	GTGACCAGGT	CGAGCGTGGC	CAGGTTCTGG	CTGCTCCGGG	600
10	CTCCGTGACC	CCGCACACCA	AGTTCGAGGG	CGAAGTCTAC	GTGCTGACCA	650
	AGGACGAAGG	CGGCCGTCAC	TCGCCGTTCT	TCTCCAACCTA	CCGTCCGCAG	700
	TTCTACTTCC	GTACCACCGA	CGTCACCGGC	GTCATCACCC	TGCCGGAAGG	750
	CGTTGAGATG	GTGCAGCCGG	GCGATCACGC	TACCTTCGGC	GTTGAGCTGA	800
15	TCCAGCCGAT	CGCTATGGAA	GAGGGCCTGA	CCTTCGCAG		839

## 2) INFORMATION FOR SEQ ID NO: 15

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 838 bases
  - (B) TYPE: Nucleic acid
  - (C) STRANDEDNESS: Double
  - (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

- (vi) ORIGINAL SOURCE:
- (A) ORGANISM: *Brucella abortus*
  - (B) STRAIN: S2308

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 15

	TGGCGCGATC	CTGGTGGTTT	CGGCTGCTGA	CGGCCCGATG	CCGCAGACCC	50
35	GCGAGCACAT	CCTGCTTGCC	CGTCAGGTTG	GCGTTCCGGC	GATCGTCGTG	100
	TTCCTCAACA	AGTGCGACCA	GGTTGACGAT	GCAGAACTGC	TCGAACTGGT	150
	TGAACTGGAA	GTGCGCGAAC	TTCTGTCGAA	GTACGAATTC	CCCGGCGACG	200
	AAATCCCGAT	CATCAAGGGC	TCGGCTCTTG	CTGCTCTGGA	AGATTCTTCC	250
	AAGGAACTGG	GCGAAGATGC	CATCCGCAAC	CTGATGGACG	CGGTTGACAG	300
40	CTACATTCCG	ACCCCGGAAC	GCCCAGTCGA	CCAGCCGTTT	CTGATGCCGA	350
	TCGAAGACGT	GTTCTCGATC	TCCGGCCGTG	GTACGGTTGT	GACGGGTCCG	400
	GTGAGCGCG	GTATCGTTAA	GTTGGTGA	GAAGTTGAAA	TGTTGGGCAI	450
	CAAGGCGACG	ACGAAGACCA	CGGTTACCGG	CGTTGAAATG	TTCCGCAAGC	500
	TGCTCGACCA	GGGCCAGGCT	GGCGACAACA	TTGGCGCGCT	GATCCGCGGC	550
45	GTTGGCCGTG	AAGACGTTGA	ACGCGGCCAG	GTTCTCTGCA	AGCCGGGGTTC	600
	TGTGAAGCCG	CACACCAAGT	TTAAGGCAGA	AGCCTATATT	CTGACCAAGG	650
	ACGAAGGTGG	CCGTCATACG	CCGTTCTTCA	CCAACCTACC	TCCGCAGTTC	700
	TACTTCCGTA	CGACGGACGT	GACGGGTGTT	GTGACGCTTC	CGGCTGGCAC	750
	GGAAATGGTC	ATGCCTGGCG	ATAACGTCGC	CATGGACGTT	ACCCTGATCG	800
50	TGCCGATCGC	CATGGAAGAG	AAGCTTCGCT	TCGCTATC		838

## 2) INFORMATION FOR SEQ ID NO: 16

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 771 bases
  - (B) TYPE: Nucleic acid
  - (C) STRANDEDNESS: Double
  - (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 5 (A) ORGANISM: *Burkholderia cepacia*  
(B) STRAIN: LSPQ 2217

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 16

10	GGCAGCAGAC	GGCCCGATGC	CGCAAACGCG	TGAGCACATC	CTGCTGGCGC	50
	GTCAGGTTGG	CGTTCCGTAC	ATCATCGTGT	TCCTGAACAA	GTGCGACATG	100
	GTGGACGACG	CCGAAGTGCT	CGAGCTGGTC	GAGATGGAAG	TTCGCGAACT	150
	CCTGTCTGAAG	TACGACTTCC	CGGGCGACGA	CACGCCGATC	GTGAAGGGTT	200
	CGGCGAAGCT	GGCGCTGGAA	GGCGACACGG	GCGAGCTGGG	CGAAGTGGCG	250
15	ATCATGAGCC	TGGCCGACGC	GCTGGACACG	TACATCCCGA	CGCCGGAGCG	300
	TGCAGTTGAC	GGCGCGTTCC	TGATGCCCGT	GGAAGACGTG	TTCTCGATCT	350
	CGGGCCGCGG	TACGGTGGTG	ACGGGTCGTG	TCGAGCGCGG	CATCGTGAAG	400
	GTCGGCGAAG	AAATCGAAAT	CGTCGGTATC	AAGCCGACGG	TGAAGACGAC	450
	CTGCACGGGC	GTTGAAATGT	TCCGCAAGCT	GCTGGACCAA	GGTCAAGCAG	500
20	GCGACAACGT	TGGTATCCTG	CTGCGCGGCA	CGAAGCGTGA	AGACGTGGAG	550
	CGTGGCCAGG	TTCTGGCGAA	GCCGGGTTCG	ATCACGCCGC	ACACGCACTT	600
	CACGGCTGAA	GTGTACGTGC	TGAGCAAGGA	CGAAGGCGGC	CGTCACACGC	650
	CGTTCTTCAA	CAACTACCGT	CCGCAGTTCT	ACTTCCGTAC	GACGGACGTG	700
	ACGGGCTCGA	TCGAGCTGCC	GAAGGACAAG	GAAATGGTGA	TGCCGGGCGA	750
25	CAACGTGTCT	ATCACGGTGA	A			771

2) INFORMATION FOR SEQ ID NO: 17

30

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 829 bases  
(B) TYPE: Nucleic acid  
(C) STRANDEDNESS: Double  
35 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 40 (A) ORGANISM: *Cedecea davisae*  
(B) STRAIN: ATCC 33431

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 17

45	GGCGCTATCC	TGGTTGTTGC	TGCGACTGAT	GGCCCAATGC	CACAGACCCG	50
	TGAGCACATC	CTGCTGGGTC	GTCAGGTTGG	CGTTCCGTAC	ATCATCGTGT	100
	TCCTGAACAA	ATGCGACATG	GTTGATGACG	AAGAGCTGCT	GGAAGTGGTA	150
	GAAATGGAAG	TTCGTGAACT	TCTGTCCCAG	TACGACTTCC	CGGGCGACGA	200
	TACTCCAATC	GTTCGTGGTT	CTGCTCTGAA	AGCGCTGGAA	GGCGAAGCAG	250
50	AGTGGGAAGC	TAAATATCGTT	GAGCTGGCTG	GCTACCTGGA	TTCTTACATC	300
	CCTGAGCCAG	AGCGTGCTAT	CGATAAGCCG	TTCCTGCTGC	CAATCGAAGA	350
	CGTATTCTCC	ATCTCCGGCC	GTGGTACCGT	TGTTACCGGT	CGTGTAGAGC	400
	GCGGTATCAT	CAAAGTTGGT	GAAGAAGTTG	AAATCGTTGG	TATCAAAGAT	450
	ACTGCGAAAT	CTACCTGTAC	CGGCGTTGAA	ATGTTCCGCA	AACTGCTGGA	500
55	CGAAGGCCGT	GCTGGTGAGA	ACGTTGGTGT	TCTGCTGCGT	GGTATCAAAC	550
	GTGAAGAAAT	CGAACGTGGT	CAGGTACTGG	CTAAGCCAGG	CTCTATCAAG	600
	CCACACACCA	AGTTCGAATC	TGAAGTGTAC	ATCCTGTCCA	AAGACGAAGG	650
	CGGCCGTCAT	ACTCCGTTCT	TCAAAGGCTA	CCGTCCACAG	TTCTACTTCC	700
	GTACAACCTGA	CGTGACCGGC	ACCATCGAAC	TGCCAGAAGG	CGTTGAGATG	750
60	GTAATGCCTG	GCGACAACAT	CAAAATGGTT	GTTACCCTGA	TCCACCCAAT	800

CGCGATGGAT GACGGTCTGC GTTTCGCAA

## 5 2) INFORMATION FOR SEQ ID NO: 18

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 824 bases  
 (B) TYPE: Nucleic acid  
 10 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

## 15 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Cedecea neteri*  
 (B) STRAIN: ATCC 33855

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 18

20 CGCTATCCTG GTTGTGCTG C GACTGACGG CCCTATGCCT CAGACCCGTG 50  
 AGCACATCCT GCTGGGTCGT CAGGTTGGCG TTCCTTACAT CATCGTGTTT 100  
 CTGAACAAAT GTGACATGGT TGATGACGAA GAGCTGCTGG AGCTGGTTGA 150  
 AATGGAAGTT CGTGAAC TTC TGTCTCAGTA CGACTTCCCG GCGATGACA 200  
 25 CTCCAATCAT CCGTGGTTCT GCTCTGAAAG CGCTGGAAGG CGAAGCAGAG 250  
 TGGGAAGCTA AAATYGTGA GCTGGCTGGC TTCCTGGATT CCTACATCCC 300  
 AGAACCACTA CGTGCAATCG AYCTGCCGTT CCTGCTGCCA ATCGAAGACG 350  
 TATTCTCCAT CTCGGGCCGT GGTACCGTTG TTACCGGTCG TGTAAGAGCG 400  
 GGTATCGTTA AAGTGGGCGA AGAAGTAGAA ATCGTTGGTA TCAAAGATAC 450  
 30 TGCAGAAATCT ACCTGTACCG GCGTTGAAAT GTTCCGCAAA CTGCTGGACG 500  
 AAGGCCGTGC TGGTGAGAAC GTTGGTGTTT TGCTGCGTGG TATCAAACGT 550  
 GAAGAAATCG AACGTGGTCA GGTTCCTGGCT AAGCCAGGCT CTATCAAGCC 600  
 GCACACCAAG TTCGAATCTG AAGTGTACAT CCTGTCCAAA GACGAAGGCG 650  
 GCCGTCATAC TCCGTTCTTC AAAGGCTACC GTCCACAGTT CTACTTCCGT 700  
 35 ACAACTGACG TGACCGGTAC CATCGAACTG CCAGAAGGCG TAGAGATGGT 750  
 AATGCCAGGC GACAACATCA AAATGGTTGT TACCCTGATC CACCCAATCG 800  
 CGATGGACGA CGGTCTGCGT TTCG 824

## 40 2) INFORMATION FOR SEQ ID NO: 19

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 827 bases  
 45 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

## 50 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Cedecea lapagei*  
 (B) STRAIN: ATCC 33432

## 55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 19

CGCTATTCCTG GTTGTGCTG CAACTGACGG CCCTATGCCT CAGACCCGTG 50  
 AGCACATCCT GCTGGGTCGC CAGGTTGGCG TTCCTTACAT CATCGTGTTT 100  
 CTGAACAAAT GTGACATGGT TGATGACGAA GAGCTGCTGG AGCTGGTAGA 150  
 60 AATGGAAGTT CGTGAAC TTC TGTCTCAGTA CGACTTCCCA GCGATGATA 200

	CCCCAATCAT	CCGTGGTTCT	GCTCTGAAAG	CGCTGGAAGG	CGAAGCAGAG	250
	TGGGAAGCTA	AAATCGTTGA	GCTGGCTGGC	TTCCTGGATT	CCTACATCCC	300
	AGAACCAGTA	CGTGCAATCG	ACCTGCCGTT	CCTGCTGCCA	ATCGAAGACG	350
	TATTCTCCAT	CTCCGGCCGT	GGTACCGTTG	TKACCGGTCG	TGTAGAGCGC	400
5	GGTATCGTTA	AAGTGGGCGA	AGAAGTAGAA	ATCGTTGGTA	TCAAAGATAC	450
	TGCGAAATCT	ACCTGTACTG	GCGTTGAAAT	GTTCCGCAA	CTGCTGGACG	500
	AAGGCCGTGC	TGGTGAGAAC	GTTGGTGTTT	TGCTGCGTGG	TATCAAACGT	550
	GAAGAAATCG	AACGTGGTCA	GGTTCTGGCT	AAGCCAGGCT	CTATCAAGCC	600
	GCACACCAAG	TTCGAATCTG	AAGTGTACAT	CCTGTCCAAA	GACGAAGGCG	650
10	GCCGTCATAC	TCCGTTCTTC	AARGGCTACC	GTCCACAGTT	CTACTTCCGT	700
	ACCACTGACG	TGACCGGTAC	CATCGAACTG	CCAGAAGGCG	TAGAGATGGT	750
	AATGCCAGGT	GACAACATCA	AAATGGTTGT	TACCCTGATC	CACCCAATCG	800
	CGATGGACGA	CGGTCTGCGT	TTCGCAA			827

15

## 2) INFORMATION FOR SEQ ID NO: 20

(i) SEQUENCE CHARACTERISTICS:

20 (A) LENGTH: 831 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

25 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Chlamydia pneumoniae*

(B) STRAIN: CWL 029

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 20

	GCGGAGCTAT	CCTAGTCGTT	TCAGCTACAG	ACGGAGCTAT	GCCACAAACT	50
	AAAGAACATA	TCTTGCTAGC	TCGCCAGGTT	GGAGTTCCTT	ATATCGTTGT	100
35	TTTCTTGAAT	AAAGTAGATA	TGATCTCTCA	AGAAGATGCT	GAACTTATTG	150
	ACCTTGTTGA	GATGGAACCT	AGTGAGCTTC	TTGAAGAAAA	AGGCTACAAA	200
	GGATGCCCTA	TTATCCGTGG	TTCTGCTTTG	AAAGCTCTTG	AAGGTGATGC	250
	AAATTATATC	GAAAAAGTTC	GAGAACTTAT	GCAAGCTGTG	GATGACAACA	300
	TCCCTACACC	AGAAAGAGAA	ATTGATAAGC	CTTTCTTAAT	GCCTATCGAA	350
40	GACGTATTCT	CAATCTCTGG	TCGTGGTACT	GTGGTTACAG	GAAGAATCGA	400
	GCGTGGAATC	GTTAAAGTTT	CTGATAAAGT	TCAGCTCGTG	GGATTAGGAG	450
	AGACTAAAGA	AACAATCGTT	ACTGGAGTCG	AAATGTTTCA	GAAAGAACTT	500
	CCTGAAGGTC	GTGCAGGAGA	AAACGTTGGT	TTACTCCTCA	GAGGTATTGG	550
	AAAGAACGAT	GTTGAAAGAG	GTATGGTGGT	TTGTCAGCCT	AACAGCGTGA	600
45	AGCCTCATAC	GAAATTTAAG	TCAGCTGTTT	ACGTTCTTCA	GAAAGAAGAA	650
	GGCGGACGTC	ATAAGCCTTT	CTTCAGCGGA	TACAGACCTC	AGTTCTTCTT	700
	CCGTACTACA	GACGTGACAG	GAGTCGTAAC	TCTTCCTGAA	GGAAGTGAAG	750
	TGGTAATGCC	TGGAGATAAC	GTTGAGCTTG	ATGTTGAGCT	CATTGGAACA	800
50	GTTGCTCTTG	AAGAAGGAAT	GAGATTTGCA	A		831

## 2) INFORMATION FOR SEQ ID NO: 21

55 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 826 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

60 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Chlamydia psittaci*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 21

```

5      TGGAGCGATT CTCGTTGTTT CCGCTACTGA CGGTGCGATG CCTCAGACCA      50
      AAGAACATAT TCTTTTGGCG AGACAGGTTG GTGTTCCCTTA CATCGTTGTT      100
10     TTCCTTAACA AAATCGATAT GATTTCCTCA GAAGATGCTG AGCTCGTAGA      150
      CTTAGTTGAA ATGGAATTGT CCGAACTTCT AGAAGAAAAA GGTATAAAAG      200
      GTTGCCCAAT TATCCGTGGT TCTGCTTTGA AAGCCTTAGA AGGTGATGCA      250
      AGCTACGTTG AAAAAATTCT CGAGTTAATG CAAGCAGTGG ATGATAACAT      300
      CCCTACTCCA GAGCGTGAAG TTGATAAGCC TTTCTTAATG CCTATCGAAG      350
15     ACGTATTCTC TATTTCTGGT CGTGGTACTG TGGTCACAGG ACGTATCGAG      400
      CGTGGAATCG TTAAAGTGGG TGATAAAGTA CAGATTGTTG GTTTAAGAGA      450
      TACTAGAGAG ACAATTGTTA CCGGTGTGGA AATGTTTCTA AAAGAACTTC      500
      CAGAAGGTCA AGCAGGGGAA AACGTTGGTT TGCTCCTCAG AGGTATCGGT      550
      AAGAATGACG TTGAACGTGG TATGGTTATC TGCCAACCTA ATAGCGTGAA      600
20     ATCTCACACA CAATTTAAAG GTGCTGTCTA CATTCTACAA AAAGAAGAGG      650
      GTGGACGTCA TAAACCTTTC TTTACCGGAT ACAGACCTCA GTTCTTCTTC      700
      CGTACAACAG ATGTTACAGG TGTGTAACT CTCCCAGAAG GTACAGAGAT      750
      GGTATGCCA GGCATAACG TTGAATTCGA AGTTCAATTA ATTAGCCCAG      800
25     TAGCTCTAGA AGAAGGTATG AGATTT      826

```

2) INFORMATION FOR SEQ ID NO: 22

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 822 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Chlamydia trachomatis*

(B) STRAIN: LGV 12

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 22

```

45     GGGGCTATTC TAGTAGTTTC TGCAACAGAC GGAGCTATGC CTCAAACTAA      50
      AGAGCATATT CTTTGGCAA GACAAGTTGG GGTTCCTTAC ATCGTTGTTT      100
      TTCTCAATAA AATTGACATG ATTTCCGAAG AAGACGCTGA ATTGGTCGAC      150
      TTGGTTGAGA TGGAGTTGGC TGAGCTTCTT GAAGAGAAAG GATACAAAGG      200
      GTGTCCAATC ATCAGAGGTT CTGCTCTGAA AGCTTTGGAA GGGGATGCTG      250
      CATACATAGA GAAAGTTCGA GAGCTAATGC AAGCCGTCGA TGATAATATC      300
50     CCTACTCCAG AAAGAGAAAT TGACAAGCCT TTCTTAATGC CCATTGAGGA      350
      CGTGTCTCT ATCTCCGGAC GAGGAACTGT AGTAACTGGA CGTATTGAGC      400
      GTGGAATTGT TAAAGTTTCC GATAAAGTTC AGTTGGTCGG TCTTAGAGAT      450
      ACTAAAGAAA CGATTGTTAC TGGGGTTGAA ATGTTTCAGAA AAGAACTCCC      500
      AGAAGGTCGT GCAGGAGAGA ATGTTGGATT GCTCCTCAGA GGTATTGGTA      550
      AGAACGATGT GGAAAGAGGA ATGGTTGTTT GCTTGCCAAA CAGTGTTAAA      600
      CCTCATACAC GGTTTAAGTG TGCTGTTTAC GTTCTGCAA AAGAAGAAGG      650
      TGGACGACAT AAGCCTTCT TCACAGGATA TAGACCTCAA TTCTTCTTCC      700
      GTACAACAGA CGTTACAGGT GTGGTAACTC TGCCTGAGGG AGTTGAGATG      750
      GTCATGCCTG GGGATAACGT TGAGTTTGAA GTGCAGTTGA TTAGCCCTGT      800
60     GGCTTTAGAA GAAGGTATGA GA      822

```



## 2) INFORMATION FOR SEQ ID NO: 23

5

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 835 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

10

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Chryseobacterium meningosepticum*  
 (B) STRAIN: CDC B7681

15

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 23

20	CGGAGCTATC TTAGTATGTG CTGCTACAGA TGGTCCAATG CCTCAAACCTA	50
	GAGAACACAT CCTACTTTGC CGTCAGGTAA ACGTACCTAG AATTGTTGTG	100
	TTCATGAACA AAGTTGACAT GGTAGATGAT CCAGAATTGT TAGAGCTTGT	150
	TGAGCTTGAA CTTAGAGATC TATTATCTAC TTACGAATAT GATGGTGATA	200
	ACTCTCCAGT AATTCAAGGT TCTGCTCTTG GTGCTCTTAA CGGTGATGCT	250
25	AAGTGGGTAG CTAAGGTAGA AGCTCTAATG GATGCTGTTG ATACTTGGAT	300
	CGAGCAACCA GTAAGAGATT CTGATAAGCC ATTCTTATG CCAATCGAAG	350
	ACGTATTCTC TATTACAGGT AGAGGTACTG TAGCAACTGG TAGAATCGAG	400
	GCTGGTGTA TCAACACAGG TGATCCTGTT GACATCGTAG GTATGGGTGA	450
	CGAGAAGTTA ACTTCTACTA TTACAGGTGT TGAGATGTTT AGAAAAATCC	500
30	TAGACAGAGG TGAAGCTGGT GATAACGTAG GTCTATTGTT GAGAGGTATT	550
	GAAAAGACTG ACATCAAGAG AGGTATGGTT ATCGCTAAGA AAGATTCAGT	600
	TAAGCCACAC AAGAAATTCA AAGCTGAGGT TTATATCCTT TCTAAAGAAG	650
	AAGGTGGACG TCACACTCCA TTCCACAACA AATACCGTCC TCAGTTCTAT	700
	GTAAGAACTA CTGACGTTAC AGGTGAAATC TTCTTACCAG AAGGTGTAGA	750
35	AATGGTAATG CCTGGTGATA ACTTAACTAT CACTGTAGAA TTGTTACAAC	800
	CAATCGCTCT TAACGAGGGT CTTAGATTCTG CGATC	835

## 40 2) INFORMATION FOR SEQ ID NO: 24

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 816 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

45

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Citrobacter amalonaticus*  
 (B) STRAIN: ATCC 25405

50

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 24

55

	CGGCGCGATC CTGTTGTTG CTGCGACTGA CGGCCCGATG CCGCAGACTC	50
	GTGAGCACAT CCTGCTGGGT CGTCAGGTAG GCGTTCCGTA CATCATCGTG	100
	TTCCTGAACA AATGCGACAT GGTGATGAC GAAGAGCTGC TGGAAGTGGT	150
	AGAAATGGAA GTTCGTGAAC TTCTGTCTCA GTACGATTTC CCGGGCGACG	200
60	ACACCCCGAT CGTTCGTGGT TCTGCTCTGA AAGCGCTGGA AGGCGACGCA	250

	GAGTGGGAAG	CGAAAATCAT	CGAACTGGCC	GGCTTCCTGG	ATTCTTACAT	300
	CCCGGAACCA	GAGCGTGCGA	TTGACAAGCC	GTTCCCTGCTG	CCGATCGAAG	350
	ACGTATTCTC	CATCTCCGGT	CGTGGTACCG	TTGTTACCGG	TCGTGTAGAA	400
	CGCGGTATCA	TCAAAGTGGG	CGAAGAAGTT	GAAATCGTTG	GTATCAAAGA	450
5	GACTGCCAAG	TCTACCTGTA	CTGGCGTTGA	AATGTTCCGC	AAACTGCTGG	500
	ACGAAGGCCG	TGCGGGTGAG	AACGTTGGTG	TTCTGCTGCG	TGGTATCAAA	550
	CGTGAAGAAA	TCGAACGTGG	TCAGGTAAGT	GCTAAGCCGG	GCWCCATCAA	600
	GCCGCACACC	ATGTTTCAAT	CYGAAGTGTA	CATCCTGTCC	AAAGACGAAG	650
	GCGGCCGTCA	TACTCCGTTT	TTCAAAGGCT	ACCGTCCGCA	GTTCTACTTC	700
10	CGTACAACCTG	ACGTGACTGG	CACCATCGAA	CTGCCGGAAG	GCGTTGAGAT	750
	GGTAATGCCG	GGCGACAACA	TCAAATGGT	TGTTACCCTG	ATCCACCCGA	800
	TCGCGATGGA	CGACGG				816

15

## 2) INFORMATION FOR SEQ ID NO: 25

## (i) SEQUENCE CHARACTERISTICS:

- 20 (A) LENGTH: 825 bases  
(B) TYPE: Nucleic acid  
(C) STRANDEDNESS: Double  
(D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

25

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Citrobacter braakii*  
(B) STRAIN: ATCC 43162

30

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 25

	CGCGATCCTG	GTTGTTGCTG	CAACTGACGG	CCCGATGCCG	CAGACTCGTG	50
	AGCACATCCT	GCTGGGTTCG	CAGGTAGGCG	TTCCGTACAT	CATCGTGTTC	100
	CTGAACAAAT	GCGACATGGT	TGATGACGAA	GAGCTGCTGG	AACTGGTAGA	150
35	AATGGAAGTT	CGTGAAC TTC	TGTCTCAGTA	CGATTTCCTG	GGCGACGACA	200
	CGCCGATCGT	TCGTGGTTCT	GCTCTGAAAG	CGCTGGAAGG	CGAWGCAGAG	250
	TGGGAAGCGA	AAATCATCGA	ACTGGCTGGC	TTCTTGGATT	CTTACATCCC	300
	GGAACCAGAG	CGTGCGATTG	ACAAGCCGTT	CCTGCTGCCT	ATCGAAGACG	350
	TATTCTCCAT	CTCTGGTCGT	GGTACCGTTG	TTACCGGTCG	TGTAGAGCGC	400
40	GGTATCATCA	AAGTTGGTGA	AGAAGTTGAA	ATCGTTGGTA	TCAARGACAC	450
	TGCTAAGTCT	ACCTGTACTG	GCGTTGAAAT	GTTCCGCAAA	CTGCTGGACG	500
	AAGGCCGTGC	TGGTGAGAAC	GTTGGTGTTC	TGCTGCGTGG	TATCAAGCGT	550
	GAAGAAATCG	AACGTGGTCA	GGTACTGGCT	AAGCCGGGCT	CTATCAAGCC	600
	GCACACCAAG	TTCGAATCTG	AAGTGACAT	TCTGTCCAAA	GACGAAGGCG	650
45	GCCGTCATAC	TCCGTTCTTC	AARGGCTACC	GTCCGCAGTT	CTACTTCCGT	700
	ACTACTGACG	TGACTGGTAC	CATCGAAGTG	CCGGAAGGCG	TTGAGATGGT	750
	AATGCCGGGC	GACAACATCA	AAATGGTTGT	TACCCTGATC	CACCCAATCG	800
	CGATGGACGA	CGGTCTGCGT	TTCGC			825

50

## 2) INFORMATION FOR SEQ ID NO: 26

## (i) SEQUENCE CHARACTERISTICS:

- 55 (A) LENGTH: 830 bases  
(B) TYPE: Nucleic acid  
(C) STRANDEDNESS: Double  
(D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Citrobacter koseri*  
 (B) STRAIN: ATCC 27156

5

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 26

	CGGCGCGATC	CTGGTTGTTG	CTGCGACTGA	CGGCCCCGATG	CCGCAGACCC	50
	GTGAGCACAT	CCTGCTGGGT	CGTCAGGTAG	GCGTTCCGTA	CATCATCGTG	100
10	TTCCTGAACA	AATGCGACAT	GGTTGATGAC	GAAGAGCTGC	TGGAAGTGGT	150
	TGAGATGGAA	GTGCGTGAAC	TGCTGTCTCA	GTACGATTTC	CCGGGCGACG	200
	ACACGCCGAT	CGTTCGTGGT	TCTGCTCTGA	AAGCGCTGGA	AGGCGAMGCT	250
	GAGTGGGAAG	CGAAAATCAT	CGAACTGGCT	GGCTACCTGG	ATTCTTACAT	300
	CCCGGAACCA	GAGCGTGCGA	TTGACAAGCC	GTTCTTGCTG	CCGATCGAAG	350
15	ACGTATTCTC	CATCTCCGGT	CGTGGTACCG	TTGTTACCGG	TCGTGTAGAG	400
	CGCGGTATCA	TCAAAGTGGG	CGAAGAAGTT	GAAATYGTTG	GTATCAAAGA	450
	GACTGCGAAG	TCTACCTGTA	CTGGCGTTGA	AATGTTCCGC	AAACTGCTGG	500
	ACGAAGGCCG	TGCTGGTGAG	AACGTAGGTG	TTCTGCTGCG	TGGTATCAAA	550
	CGTGAAGAAA	TCGAACGTGG	TCAGGTACTG	GCTAAGCCGG	GYTCCATCAA	600
20	GCCGCACACC	AAGTTCGAAT	CTGAAGTGTA	CATYCTGTCY	AAAGATGAAG	650
	GCGGCCGTCA	TACTCCGTTT	TTCAAAGGCT	ACCGTCCGCA	GTTCTACTTC	700
	CGTACAACCTG	ACGTGACTGG	CACCATCGAA	CTGCCGGAAG	GCGTAGAGAT	750
	GGTAATGCCG	GGCGACAACA	TCAAATGGT	TGTTACCCTG	ATCCACCCGA	800
25	TCGCGATGGA	CGACGGTCTG	CGTTTCGCAA			830

## 2) INFORMATION FOR SEQ ID NO: 27

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 827 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

35

(ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Citrobacter farmeri*  
 (B) STRAIN: ATCC 51112

40

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 27

	CGCGATCCTG	GTTGTTGCTG	CGACTGACGG	CCCGATGCCG	CAGACTCGTG	50
45	AGCACATCCT	GCTGGGTCGT	CAGGTAGGCG	TTCCGTACAT	CATCGTGTTC	100
	CTGAACAAAT	GCGACATGGT	TGATGACGAA	GAGCTGCTGG	AACTGGTAGA	150
	GATGGAAGTT	CGTGAAGTGC	TGTCTCAGTA	CGATTTCCCC	GGCGACGACA	200
	CGCCGATCGT	TCGTGGTTCT	GCTCTGAAAG	CGCTGGAAGG	CGACGCAGAG	250
	TGGGAAGCGA	AAATCATCGA	ACTGGCAGGC	TTCTTGATTT	CTTACATCCC	300
50	GGAACCAGAG	CGTGCGATTG	ACAAGCCGTT	CCTGCTGCCG	ATCGAAGACG	350
	TATTCTCCAT	CTCTGGTCGT	GGTACCGTTG	TTACCGGTCG	TGTAGAGCGC	400
	GGTATCATCA	AAGTGGGTGA	AGAAGTTGAA	ATCGTTGGTA	TCAAAGAGAC	450
	TGCCAAGTCT	ACCTGTACTG	GCGTTGAAAT	GTTCCGCAAA	CTGCTGGACG	500
	AAGGCCGTGC	TGGTGAGAAC	GTAGGTGTTT	TGCTGCGTGG	TATCAAACGT	550
55	GAAGAAATCG	AACGTGGTCA	GGTACTGGCT	AAGCCGGGCW	CCATCAAGCC	600
	RCACACTATG	TTTGAATCTG	AAGTGTACAT	TCTGTCCAAA	GACGAAGCCG	650
	GCCGTCATAC	TCCGTTCTTC	AAAGGCTACC	GTCCGCAGTT	CTACTTCCGT	700
	ACGACTGACG	TGACTGGCAC	CATCGAACTG	CCGGAAGGTG	TTGAGATGGT	750
	TATGCCGGGC	GACAACATCA	AAATGGTTGT	TACCCTGATC	CACCCGATCG	800
60	CGATGGACGA	CGGTCTGCGT	TTCGCAA			827

## 2) INFORMATION FOR SEQ ID NO: 28

5

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 797 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

10

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Citrobacter freundii*  
 (B) STRAIN: ATCC 8090

15

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 28

20	CCTGGTTGTT	GCTGCGACTG	ACGGCCCGAT	GCCGCAGACT	CGTGAGCACA	50
	TCCTGCTGGG	TCGTCAGGTA	GGCGTTCCGT	ACATCATCGT	GTCCTGAAC	100
	AAATGCGACA	TGGTTGATGA	CGAAGAGCTG	CTGGAAGTGG	TAGAAATGGA	150
	AGTTCGTGAA	CTTCTGTCTC	AGTACGATTT	CCCGGGCGAC	GACACTCCGA	200
	TCGTTTCGTGG	TTCTGCTCTG	AAAGCGCTGG	AAGGCGAAGC	AGAGTGGGAA	250
25	GCGAAAATCA	TCGAACTGGC	TGGCTTCCTG	GATTCTTACA	TCCCAGAACC	300
	AGAGCGTGCG	ATTGACAAGC	CGTTCCTGCT	GCCTATCGAA	GACGTATTCT	350
	CCATCTCCGG	TCGTGGTACC	GTTGTTACCG	GTCGTGTAGA	GCGCGGTATC	400
	ATCAAAGTTG	GTGAAGAAGT	TGAAATCGTT	GGTATCAAAG	AGACTGCTAA	450
	GTCTACCTGT	ACTGGCGTTG	AAATGTTCCG	CAAAGTCTG	GACGAAGGCC	500
30	GTGCTGGTGA	GAACGTTGGT	GTTCTGCTGC	GTGGTATCAA	ACGTGAAGAA	550
	ATCGAACGTG	GTCAGGTACT	GGCTAAGCCG	GGCTCTATCA	AGCCGCACAC	600
	CAAGTTCGAA	TCTGAAGTGT	ACATTCTGTC	CAAAGACGAA	GGCGGCCGTC	650
	ATACTCCGTT	CTTCAAAGGC	TACCGTCCGC	AGTTCTACTT	CCGTACTACT	700
	GACGTGACTG	GTACCATCGA	ACTGCCCGAA	GGCGTAGAGA	TGGTAATGCC	750
35	GGGCGACAAC	ATCAAAATGG	TTGTTACCCT	GATCCACCCA	ATCGCGA	797

## 2) INFORMATION FOR SEQ ID NO: 29

40

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 826 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

45

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Citrobacter sedlakii*  
 (B) STRAIN: ATCC 51115

50

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 29

55	CGGCGCGATC	CTGGTTGTTG	CCGCGACTGA	CGGCCCGATG	CCGCAGACCC	50
	GTGAGCACAT	CCTGCTGGGT	CGTCAGGTAG	GCGTTCGGTA	CATCATCGTG	100
	TTCCTGAACA	AATGCGACAT	GTTGATGAC	GAAGAGCTGC	TGGAAGTGGT	150
	AGAGATGGAA	GTTCTGTGAAC	TGCTGTCTCA	GTACGATTTC	CCGGGCGACG	200
	ACACGCCGAT	CGTTCGTGGT	TCAGCTCTGA	AAGCGCTGGA	AGGCGACGCA	250
60	GAGTGGGAAG	CGAAAATCAT	CGAACTGGCT	GGCTTCCTGG	ATTCTTACAT	300

	TCCGGAACCA	GAGCGTGCGA	TTGACAAGCC	GTTCTGCTG	CCGATCGAAG	350
	ACGTATTCTC	CATCTCCGGT	CGTGGTACCG	TTGTTACCGG	TCGTGTAGAG	400
	CGCGGTATCA	TCAAAGTGGG	CGAAGAAGTT	GAAATCGTTG	GTATCAAAGA	450
	GACTGCGAAG	TCTACCTGTA	CTGGCGTTGA	AATGTTCCGC	AAACTGCTGG	500
5	ACGAAGGCCG	TGCGGGTGAG	AACGTAGGTG	TTCTGCTGCG	TGGTATCAAA	550
	CGTGAAGAAA	TCGAACGTGG	TCAGGTACTG	GCGAAGCCGG	GCACCATCAA	600
	GCCGCACACC	AAGTTTCAAT	CTGAAGTGTA	TATTCTGTCC	AAAGATGAAG	650
	GCGGCCGTCA	TACTCCGTTC	TTCAAAGGCT	ACCGTCCGCA	GTTCTACTTC	700
	CGTACAAC TG	ACGTGACTGG	CACCATCGAA	CTGCCGGAAG	GCGTAGAGAT	750
10	GGTAATGCCG	GGCGACAACA	TCAAAATGGT	TGTTACCCTG	ATCCACCCGA	800
	TCGCGATGGA	CGACGGTCTG	CGTTTC			826

15 2) INFORMATION FOR SEQ ID NO: 30

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 823 bases  
 (B) TYPE: Nucleic acid  
 20 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

25 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Citrobacter werkmanii*  
 (B) STRAIN: ATCC 51114

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 30

30	GCGATCCTGG	TTGTTGCTGC	GACTGACGGC	CCGATGCCGC	AGACTCGTGA	50
	GCACATCCTG	CTGGGTCGTC	AGGTAGGCGT	TCCGTACATC	ATCGTGTTCC	100
	TGAACAAATG	CGACATGGTT	GATGACGAAG	AGCTGCTGGA	ACTGGTAGAA	150
	ATGGAAGTTC	GTGAACTTCT	GTCTCAGTAC	GATTTCCCGG	GCGACGACAC	200
35	TCCGATCGTT	CGTGGTTCTG	CTCTGAAAGC	GCTGGAAGGC	GAAGCAGAGT	250
	GGGAAGCGAA	AATCATCGAA	CTGGCTGGCT	TTCTGGATTC	TTACATCCCG	300
	GAACCAAGAG	GTGCGATTGA	CAAGCCGTTT	CTGCTRCCTA	TCGAAGACGT	350
	ATTCTCCATC	TCCGGTCGTG	GTACCGTTGT	TACCGGTCGT	GTAGAGCGCG	400
	GTATCATCAA	AGTTGGTGAA	GAAGTTGAAA	TCGTTGGTAT	CAAAGACACC	450
40	GCTAAGTCTA	CCTGTACCGG	CGTTGAAATG	TTCCGCAAAC	TGCTGGACGA	500
	AGGCCGTGCT	GGTGAGAACG	TTGGTGTTCT	GCTGCGTGGT	ATCAAACGTG	550
	AAGAAATCGA	ACGTGGTCAG	GTACTGGCTA	AGCCGGGCTC	TATCAAGCCG	600
	CACACCAAGT	TCGAATCTGA	AGTGATACATC	CTGTCCAAAG	ACGAAGGCGG	650
	CCGTCATACT	CCGTTCTTCA	AAGGCTACCG	TCCGCAGTTC	TACTTCCGTA	700
45	CTACTGACGT	GACTGGTACC	ATCGAACTGC	CGGAAGGCGT	AGAGATGGTA	750
	ATGCCGGGCG	ACAACATYAA	AATGGTTGTT	ACYCTGATCC	ACCCGATCGC	800
	GATGGACGAC	GGTCTGCGTT	TCG			823

50

2) INFORMATION FOR SEQ ID NO: 31

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 826 bases  
 55 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

60

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Citrobacter youngae*  
 (B) STRAIN: ATCC 29935

## 5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 31

	GGCGCGATCC	TGGTTGTTGC	TGCGACTGAC	GGCCCGATGC	CGCAGACTCG	50
	TGAGCACATC	CTGCTGGGTC	GTCAGGTAGG	CGTTCCGTAC	ATCATCGTGT	100
	TCCTGAACAA	ATGCGACATG	GTTGATGACG	AAGAGCTGCT	GGAAGTGGTA	150
10	GAAATGGAAG	TTCGTGAACT	TCTGTCTCAG	TACGATTTCC	CGGGCGACGA	200
	TACGCCGATC	GTTCTGTGGT	CTGCTCTGAA	AGCGCTGGAA	GGCGAAGCAG	250
	AGTGGGAAGC	GAAAATCATC	GAAGTGGCTG	GCTTCCTGGA	TTCTTACATC	300
	CCGGAACCAG	AACGTGCTAT	CGATAAGCCG	TTCTGCTGCT	CAATCGAAGA	350
	CGTATTCTCC	ATCTCCGGTC	GTGGTACCGT	TGTTACTGGT	CGTGTAGAAC	400
15	GCGGTATCAT	CAAAGTTGGT	GAAGAAGTTG	AAATCGTTGG	TATCAAAGAG	450
	ACTGCCAAGT	CTACCTGTAC	TGGCGTTGAA	ATGTTCCGCA	AACTGCTGGA	500
	CGAAGGCCGT	GCTGGTGAGA	ACGTTGGTGT	TCTGCTGCGT	GGTATCAAAC	550
	GTGAAGAAAT	CGAACGTGGT	CAGGTACTGG	CTAAGCCGGG	CTCTATCAAG	600
	CCGCACACCA	AGTTCGAATC	TGAAGTGTAC	ATTCTGTCCA	AAGACGAAGG	650
20	CGGCCGTCAT	ACTCCGTTCT	TCAAAGGCTA	CCGTCCGCAG	TTCTACTTCC	700
	GTACTACTGA	CGTGACGGGT	ACCATCGAAC	TGCCGGAAGG	CGTAGAGATG	750
	GTAATGCCGG	GCGACAACAT	CAAAATGGTT	GTTACCCTGA	TCCACCCAAT	800
	CGCGATGGAT	GACGGTCTGC	GTTTCG			826

25

## 2) INFORMATION FOR SEQ ID NO: 32

## (i) SEQUENCE CHARACTERISTICS:

- 30 (A) LENGTH: 841 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

## 35 (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Clostridium perfringens*  
 (B) STRAIN: ATCC 13124

40

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 32

	CGGAGCTATA	TTAGTTTGTT	CAGCAGCTGA	TGGTCCAATG	CCTCAAACAA	50
	GAGAGCACAT	CTTATTATCA	TCAAGAGTTG	GAGTTGACCA	CATCGTAGTA	100
45	TTCTTAAACA	AAGCAGATAT	GGTTGACGAC	GAAGAATTAT	TAGAATTAGT	150
	TGAAATGGAA	GTTAGAGAGT	TATTAAGCGA	GTACAAC TTC	CCAGGAGACG	200
	AYATTCCAGT	AATCAARGGA	TCAGCTTTAG	TAGCATTAGA	AAACCCAACT	250
	GACGAAGCTG	CAACAGCTTG	TATCAGAGAG	TTAATGGATG	CTGTAGATAG	300
	CTACATCCCA	ACACCAGAAA	GAGCAACAGA	TAAGCCATTC	TTAATGCCAG	350
50	TAGAGGACGT	ATTCACAATC	ACTGGTAGAG	GAACAGTTGC	AACAGGAAGA	400
	GTTGAAAGAG	GAGTTCCTACA	TGTAGGAGAC	GAAGTAGAAG	TAATCGGATT	450
	AACTGAAGAA	AGAAGAAAAA	CTGTTGTAAC	AGGAATCGAA	ATGTTTCAGAA	500
	AGTTATTAGA	TGAAGCACAA	GCTGGAGATA	ACATCGGAGC	ATTATTAAGA	550
	GGTATCCAAA	GAAGTAYAT	CGAAAGAGGT	CAAGTTT TAG	CTCAAGTTGG	600
55	AACAATCAAC	CCACACAAAA	AATTCGTAGG	TCAAGTATAC	GTACTTAAAA	650
	AAGAAGAAGG	TGGAAGACAT	ACTCCATTCT	TGCATGGATA	CAGACCACAA	700
	TTCTACTTCA	GAACAACAGA	CGTTACAGGA	TCAATCAAAT	TACCGAAGG	750
	AATGGAAATG	GTTATGCCTG	GAGACCACAT	CGACATGGAA	GTTGAATTAA	800
60	TCACAGAAAT	CGCTATGGAY	GAAGGATTAA	GATTTCGCTAT	C	841

## 2) INFORMATION FOR SEQ ID NO: 33

## 5 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 822 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

10

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Comamonas acidovorans*  
 (B) STRAIN: ATCC 15668

15

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 33

	CGGCGCCATC	CTGGTGTGCT	CGGCCGCTGA	CGGCCCCATG	CCCCAGACCC	50
20	GCGAGCACAT	CCTGCTGGCC	CGTCAGGTGG	GCGTGCCCTA	CATCATCGTG	100
	TTCCTGAACA	AGTGCGACAT	GGTGGACGAC	GAAGAGCTGC	TGGAAGTGGT	150
	CGAAATGGAA	GTGCGCGAGC	TGCTTGCCAA	GTACGACTTC	CCCGGCGACG	200
	ACACCCCAT	CATCCGCGGC	TCGGCCAAGC	TGGCCCTGGA	AGGCGACCAG	250
	TCCGACAAGG	GCGAACCTGC	CATCCTGCGC	CTGGCTGAAG	CACTGGACTC	300
25	CTACATCCCC	ACGCCCAGAGC	GCGCTGTGGA	CGGCGCCTTT	GCAATGCCCG	350
	TGGAAGACGT	GTTCTCGATC	TCTGGCCGTG	GCACCGTGGT	GA CTGGCCGT	400
	ATCGAGCGCG	GCATCATCAA	GGTCGGCGAA	GAAATCGAAA	TCGTCGGTAT	450
	CCGCGACACC	CAGAAGACCA	TCGTCACCGG	CGTGGAATG	TTCCGCAAGC	500
	TGCTGGACCA	AGGTCAAGCT	GGCGACAACG	TGGGTCTGCT	GCTGCGCGGC	550
30	ACCAAGCGTG	AAGACGTGGA	ACGCGGCCAA	GTGCTGTGCA	AGCCCGGCTC	600
	CATCAAGCCC	CACACCCACT	TCACGGCTGA	GGTGTACGTG	CTGTCCAAGG	650
	ACGAAGGTGG	TCGCCACACT	CCGTTCTTCA	ACA ACTACCG	TCCCCAGTTC	700
	TATTTCCGTA	CGACCGACGT	GACCGGCTCC	ATCGAGCTGC	CCGCCGACAA	750
	GGAAATGGTG	ATGCCTGGCG	ACAACGTGTC	GATCACCGTC	AAGCTGATCG	800
35	CCCCCATCGC	CATGGAAGAA	GG			822

## 2) INFORMATION FOR SEQ ID NO: 34

40

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 702 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

45

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Corynebacterium bovis*  
 (B) STRAIN: ATCC 7715

50

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 34

55	GCCGCAGACC	CGTGAGCAGC	TCCTCCTGGC	CCGTCAGGTC	GGTGTGCCCT	50
	ACATCCTCGT	CGCCCTCAAC	AAGTGCGACA	TGGTCGACGA	CGAGGACCTC	100
	ATCGAGCTCG	TCGAGATGGA	GGTCCGTGAG	CTCCTCGCCG	AGCAGGACTA	150
	CGACGAGGAC	GCCCCGATCA	TCCACATCTC	CGCCCTCAAG	GCCCTCGAGG	200
	GTGACCCGGA	GTGGACGCAG	CGCATCGTCG	ACCTCATGAA	GGCCTGCGAC	250
60	GACGCCATCC	CGGATCCGGA	GCGCGAGACG	GACAAGCCGT	TCCTCATGCC	300

```

      GATCGAGGAC ATCTTCACGA TCACCGGCCG CGGCACCGTC GTCACGGGCC      350
      GTGTCGAGCG TGGCATCCTC AACGTCAACG AGGAGGTCGA GATCCTGGGT      400
      ATCTGCGAGA ACTCCCAGAA GACGACCGTC ACCTCCATCG AGATGTTCAA      450
      CAAGTTCCTC GACACGGCCG AGGCCGGCGA CAACGCCGCC CTGCTGCTCC      500
5     GTGGCCTGAA GCGCGAGGAC GTCGAGCGTG GCCAGATCGT GGCCAAGCCG      550
      GGCGCCTACA CGCCGCACAC CGAGTTCGAG GGCTCCGTGT ACATCCTCTC      600
      CAAGGACGAG GGTGGCCGCC ACACGCCGTT CTTCGACAAC TACCGTCCGC      650
      AGTTCTACTT CCGGACGACC GACGTCACCG GCGTCGTCAA GCTGCCGGAG      700
      GG
10

```

## 2) INFORMATION FOR SEQ ID NO: 35

## 15 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 689 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

## 20 (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Corynebacterium cervicis*  
 25 (B) STRAIN: NCTC 10604

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 35

```

      GGCTCAGACC CGCGAGCACG TTCTGCTTGC TCGCCAGGTT GCGGTTCCGA      50
30     CGATCCTGGT TGCCCTCAAC AAGGCCGATA TGGTCGACGA TGAGGAAATG      100
      CTGGAGCTCG TTGAGGAAGA GTGCCGCGAC CTGCTCGAGT CCCAGGACTT      150
      CGATCGTGAC GCCCCGATCA TCCAGGTTTC CGCGCTGAAG GCTCTCGAAG      200
      GTGATCCGCA GTGGGTTGCT AAGGTCGAGG AGCTCATGGA GGCAGTCGAC      250
      ACCTTCGTGC CGACTCCTGA GCGCGACATG GACAAGCCGT TCCTCATGCC      300
35     GATCGAAGAC GTCTTCACCA TCACCGGCCG TGGCACCGTT GTTACCGGTC      350
      GTGTTGAGCG TGGCAAGCTC CCGATCAACT CTGAGGTTGA AATCCTCGGT      400
      ATCCGCGAAC CGCAGAAGAC CACCGTTACC GGTATCGAGA TGTTCCACAA      450
      GTCCATGGAT GAAGCATGGG CAGGCGAGAA CTGTGGTCTC CTCCTGCGTG      500
      GCACCAAGCG CGATGAGGTT GAGCGCGGTC AGGTCGTTGC CGTTCCCGGT      550
40     TCGATACCC CGCACACCAA CTTACCGGA CAGGTCTACA TCCTCAAGAA      600
      GGAAGAAGGC GGTCGTCACA ACCCGTTCTT CTCGAACTAC CGTCCGCAGT      650
      TCTACTTCCG CACCACGGAC GTGACCGGCG TCATCACCC

```

689

45

## 2) INFORMATION FOR SEQ ID NO: 36

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 804 bases  
 50 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

55

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Corynebacterium flavescens*  
 (B) STRAIN: ATCC 10340

## 60 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 36



```

GGTTGTTGCT GCAACCGATG GTCCTATGCC GCAGACCCGC GAGCACGTTG      50
TTCTGGCTCG CCAGGTTGGC GTTCCTTACA TCCTCGTTGC TCTTAACAAG      100
TGCGACATGG TTGATGATGA GGAAATCATC GAGCTCGTTG AGATGGAAAT      150
5 CCGCGAACTG CTCGCTGAGC AGGACTACGA CGAGGATGCC CCCATCATCC      200
ACATCTCCGC TCTCAAGGCT CTTGAGGGTG ACGAGAAGTG GGTACAGGCC      250
ATCGTCGACC TCATGCAGGC CTGCGATGAC TCCATTCCGG ATCCGGAGCG      300
CGAGACCGAC AAGCCCTTCC TCATGCCTAT CGAGGACATC TTCACCATCA      350
CCGGCCGCGG TACCGTTGTT ACCGGCCGTG TTGAGCGTGG CGTTTTGAAG      400
10 GTCAACGAGG ATGTTGAGAT CATCGGCATC AAGGAGAAGT CCATCTCCAC      450
CACCGTTACC GGTATCGAAA TGTTCGCAA GATGATGGAC TACACCGAGG      500
CTGGCGACAA CTGTGGTCTG CTTCTGCGTG GTACCAAGCG TGAAGAGGTC      550
GAGCGCGGCC AGGTTGTTAT CAAGCCGGGC GCCTACACCC CCCACACCAA      600
GTTTCGAGGGT TCCGTCTACG TCCTCAAGAA GGAAGAGGGC GGCCGCCACA      650
15 CCCCCTTCAT GGACAACCTAC CGTCCGCAGT TCTACTTCCG TACCACTGAC      700
GTGACCGGCG TTGTTACCT GCCTGAGGGC ACCGAGATGG TCATGCCTGG      750
CGACAACGTT GATATGACCG TTGAGCTCAT CCAGCCCGTC GCTAGGATGA      800
GGGC                                                                804

```

20

## 2) INFORMATION FOR SEQ ID NO: 37

```

25 (i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 692 bases
    (B) TYPE: Nucleic acid
    (C) STRANDEDNESS: Double
    (D) TOPOLOGY: Linear

```

30 (ii) MOLECULE TYPE: Genomic DNA

```

(vi) ORIGINAL SOURCE:
    (A) ORGANISM: Corynebacterium kutscheri
    (B) STRAIN: ATCC 15677

```

35

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 37

```

TGCCTCAGAC CCGTGAGCAC GTTCTTCTTG CTCGCCAGGT TGGCGTTCCT      50
TACATCCTCG TTGCTCTTAA CAAGTGCGAC ATGGTTGACG ATGAGGAAAT      100
40 CATCGAGCTC GTTGAGATGG AAGTTCGCGA GCTTCTTGCT GAGCAGGAGT      150
ACGATGAAGA GGCTCCAATC ATCCACATCT CTGCTTTGAA GGCTCTTGAG      200
GGCGACGAGA AGTGGACTCA GGCCATCATC GACCTCATGC AGGCTTGTGA      250
TGACTCCATC CCAGATCCAG AGCGTGAGAC CGACAAGCCA TTCCTCATGC      300
CTATCGAGGA TATCTTCACC ATCACC GGTC GTGGCACC GTTACCGGT      350
45 CGTGTGAGC GCGGTTCTT GAAGGTGAAT GAGGACGTCG AGATCATCGG      400
CATCAAGGAG AAGTCCACCA CTACTACCGT TACCGGTATC GAAATGTTCC      450
GTAAGCTTCT TGATTACACC GAAGCTGGCG ATAAGTGTGG TCTGCTTCTT      500
CGTGGTATCA AGCGCGAAGA CGTTGAGCGT GGTGAGGTTG TTGTTAAGCC      550
AGGCGCTTAC ACACCTCACA CCGAGTTCGA GGGCTCTGTT TACGTTCTTT      600
50 CCAAGGACGA GGGCGGCCGC CACACCCCAT TCTTCGACAA CTACCGTCCA      650
CAGTTCTACT TCCGCACCAC TGACGTTACC GGTGTTGTGA AG              692

```

## 55 2) INFORMATION FOR SEQ ID NO: 38

```

    (i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 797 bases
    (B) TYPE: Nucleic acid
    (C) STRANDEDNESS: Double

```

60

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

5 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Corynebacterium minutissimum*

(B) STRAIN: ATCC 23348

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 38

```

10 CCTGGTTGTT GCTGCAACCG ATGGCCCGAT GCCGCAGACC CGCGAGCACG      50
   TTCTTCTGGC CCGCCAGGTT GGCGTTCCGT ACATCCTCGT TGCACTGAAC      100
   AAGTGTGACA TGGTTGACGA TGAGGAAATC ATCGAGCTCG TTGAGATGGA      150
   GATCCGTGAG CTGCTCGCTG AGCAGGACTA CGACGAGGAA GCTCCGATCG      200
15  TTCACATCTC CGCTCTGAAG GCTCTTGAGG GCGACGAGAA GTGGGCACAG      250
   TCCATCGTTG ACCTGATGCA GGCTTGCGAT GACTCCATCC CGGATCCGGA      300
   GCGCGAGCTG GACAAGCCGT TCCTGATGCC GATCGAGGAC ATCTTCACCA      350
   TTACCGGCCG CCGTACCGTT GTTACCGGCC GTGTTGAGCG TGGCTCCCTG      400
   AACGTTAACG AGGACATCGA GATCATCCGT ATCAAGGACA AGTCCATGTC      450
20  CACCACCGTT ACCGGTATCG AGATGTTCCG CAAGATGATG GACTACACCG      500
   AGGCTGGCGA CAACTGTGGT CTGCTTCTGC GTGGTACCAA GCGTGAAGAG      550
   GTTGAGCGTG GCCAGGTTTG CATCAAGCCG GGCGCTTACA CCGCGCACAC      600
   CAAGTTCGAG GGTTCGTCT ACGTCCTGAA GAAGGAAGAG GGCGGCCGCC      650
   ACACCCCGTT CATGGACAAC TACCGTCCGC AGTTCTACTT CCGCACCACC      700
25  GACGTCACCG GTGTCATCAA GCTGCCGGAG GGCACCGAGA TGGTCATGCC      750
   GGGCGACAAC GTTGAGATGT CCGTAGAGCT GATCCAGCCG GTCGCTA        797

```

30 2) INFORMATION FOR SEQ ID NO: 39

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 702 bases

(B) TYPE: Nucleic acid

35 (C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

40 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Corynebacterium mycetoides*

(B) STRAIN: ATCC 21134

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 39

```

45 GCCGCAGACC CGCGAGCACG TTCTTCTGGC CCGCCAGGTC GGCGTCCCCT      50
   ACATCCTCGT TGCGCTGAAC AAGTGCAGCA TGGTTGATGA TGAGGAGATC      100
   ATCGAGCTCG TGGAGATGGA GGTCCTGAG CTGCTCGGCG AGCAGGACTA      150
   CGACGAGGAC GCCCCATCA TCCACATCTC CGCTCTGAAG GCTCTGAGG      200
50  GCGACGAGAA GTGGGTTTCA TCCGTGCTCG ACCTCATGCA GGCGTGCGAC      250
   GACTCCATCC CGGATCCGGT CCGCGAGACC GACCGCGACT TCCTGATGCC      300
   GATCGAGGAC ATCTTCACCA TCTCCGGCCG CGGCACCGTG GTTACCGGTC      350
   GTGTGGAGCG CGGCGTGCTC AACCTCAACG ACGAGGTCGA GATCATCGGC      400
   ATCCGCGACA AGTCCCAGAA GACCACCGTC ACCTCCATCG AGATGTTCAA      450
55  CAAGCTGCTC GATACCGCTG AGGCAGGCGA CAACGCGGCT CTGCTGCTCC      500
   GCGGTCTGAA GCGCGAGGAC GTCGAGCGTG GCCAGGTTGT CATCAAGCCG      550
   GGCGCCTACA CCGCGCACAC CAAGTTCGAG GGTTCGTCT ACGTCTGTC      600
   CAAGGACGAG GGCGGCCGCC ACACCCCGTT CTTGACAAAC TACCGTCCGC      650
   AGTTCTACTT CCGCACCACC GACGTGACCG GTGTTGTGAA GCTGCCGGAG      700
60  GG                                                    702

```

## 2) INFORMATION FOR SEQ ID NO: 40

- 5 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 674 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 10 (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:  
 15 (A) ORGANISM: *Corynebacterium pseudogenitalium*  
 (B) STRAIN: ATCC 33038

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 40

20	GCTCGCCAGG TTGGCGTTCC TTACATCCTC GTTGCGCTGA ACAAGTGCGA	50
	CATGGTTGAT GATGAGGAAA TCATCGAGCT CGTTGAGATG GAGATCCGTG	100
	AGCTGCTCGC AGAGCAGGAT TACGATGAGG AAGCTCCTAT CGTTCACATC	150
	TCCGCTCTGA AGGCCCTCGA GGGCGATGAC AAGTGGGTAC AGTCCGTCGT	200
	TGATCTGATG GAAGCCTGCG ACAACTCCAT CCCGGATCCG GAGCGCGCTA	250
25	CCGACCAGCC GTTCCTGATG CCTATCGAGG ACATCTTCAC CATTACCGGC	300
	CGCGGTACCG TTGTTACCGG CCGTGTTGAG CGTGGCCGTC TGAACGTCAA	350
	CGAGGACGTT GAGATCATCG GTATCCAGGA GAAGTCCAG ACCACCACCG	400
	TTACCGGTAT CGAGATGTTT CGCAAGATGA TGGACTACAC CGAGGCTGGC	450
	GACAACTGTG GTCTGCTTCT GCGTGGTACC AAGCGTGAGG ACGTTGAGCG	500
30	TGGCCAGGTT GTTATCAAGC CGGGCGCTTA CACCCCGCAC ACCAAGTTCG	550
	AGGGCTCCGT CTACGTCCTG AAGAAGGAAG AGGGCGGCCG CCACACCCCG	600
	TTCATGAACA ACTACCGTCC GCAGTTCTAC TTCCGTACCA CGGACGTTAC	650
	CGGTGTTGTT CACCTGCCAG AGGG	674

35

## 2) INFORMATION FOR SEQ ID NO: 41

- 40 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 694 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear
- 45 (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: *Corynebacterium renale*  
 (B) STRAIN: ATCC 19412

50

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 41

	TGCCTCAGAC CCGTGAGCAC GTTCTGCTTG CTCGTCAGGT CGGCGTTCCT	50
	TACATCCTCG TTGCACTGAA CAAGTGCGAC ATGGTCGACG ACGAAGAAAT	100
55	CATCGAGCTC GTCGAGATGG AAATCCGTGA ACTGCTCGCA GAGCAGGACT	150
	ACGATGAGGA AGTCCCTATC GTTCACATCT CCGCTCTGGG CGCCCTGAAC	200
	GGCGAGCAGA AGTGGGTGTA CTCCATCGTC GAAGTGATGG AAGCTTGCGA	250
	CAACTCCATC CCAGACCCAG TTCGCGACAT CGACCACCCA TTCCTGATGC	300
	CTATCGAGGA CATCTTCACC ATTACCGGTC GCGGTACCGT TGTTACCGGC	350
60	CGTGTCGAGC GTGGCCGTCT CAACGTCAAC GAAGAAGTTG AGATCATCGG	400

	TATCAAGGAC	AAGTCCCAGA	AGACCACCGT	CACCGGTATC	GAGATGTTCC	450
	GCAAGATGCT	GGACTACACC	GAAGCTGGCG	ACAACTGTGG	TCTGCTGCTC	500
	CGCGGCATCG	GCCGTGAGGA	TGTCGAGCGT	GGCCAGGTTA	TCATCAAGCC	550
	AGGCGCTTAC	ACCCCTCACT	CTGAGTTCGA	GGGCTCTGTC	TACGTCCTGT	600
5	CCAAGGACGA	GGGTGGCCGC	CACACCCCAT	TCTTCGACAA	CTACCGTCCA	650
	CAGTTCTACT	TCCGCACCAC	CGACGTGACC	GGCGTTGTGC	ACCT	694

## 10 2) INFORMATION FOR SEQ ID NO: 42

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 687 bases  
 (B) TYPE: Nucleic acid  
 15 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

## 20 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Corynebacterium ulcerans*  
 (B) STRAIN: NCTC 8665

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 42

25	GCCGCAGACC	CGCGAGCACG	TTCTGCTGGC	TCGCCAGGTT	GGCGTTCCKT	50
	ACATCCTSGT	TGCACTGAAC	AAGTGCGACA	TGGTTGACGA	TGAGGARCTC	100
	CTSGAGCTCG	TCGAGATGGA	GGTCCGCGAG	CTGCTGGCTG	AGCAGGACTA	150
	CGACGAGGAA	GCTCCGRTCG	TTCACATCTC	CGCWCTGAAC	GCCCTGGACG	200
30	GCGACSAGAA	GTGGGCTVAC	TCCATCCTCG	AGCTGATGCA	GGCTTGCGAC	250
	GAGTCCATCC	CGGATCCGGA	GCGCGAGACC	GACAAGCCGT	TCCTGATGCC	300
	GATTGAGGAC	ATCTTCACCA	TTACCGGTCG	CGGYACCGTT	GTTACCGGCC	350
	GTGTTGAGCG	TGGCDTCCTG	AACGTSAAAC	ACGASGTTGA	GATCATGGGY	400
	ATCCGGGAGA	AGTCCCAGAA	GACCACCGTY	ACCKSCATCG	AGATGTTCAA	450
35	CAAGMTGMTG	GACWCCGCAG	AGGCTGGCGA	CAACGCTGSW	CTGCTGCTGC	500
	GTGGTMTSAA	GCGTGAGGAC	GTTGAGCGTG	GCCAGATCAT	CGYTAAGCCG	550
	GGCGCKTACA	CCCCGCACAC	CGAGTTCGAG	GGCTCCGTCT	ACGTCCTGTC	600
	CAAGGACGAG	GGCGGCCGCC	ACACCCCGTT	CTTCGACAAC	TACCGTCCGC	650
40	AGTTCTACTT	CCGCACCACC	GACGTSACCG	GTGTTTGT		687

## 2) INFORMATION FOR SEQ ID NO: 43

## 45 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 778 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 50 (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Corynebacterium urealyticum*  
 55 (B) STRAIN: ATCC 43042

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 43

	CTGGTTGTTG	CTGCAACCGA	TGGCCCGATG	CCGCAGACCC	GTGAGCACGT	50
60	TCTGCTGGCT	CGCCAGGTTG	GCGTTCCGTA	CATCCTCGTT	GCACTGAACA	100

	AGTGCGACAT	GGTTGACGAT	GAGGAGCTCC	TCGAGCTCGT	CGAGATGGAG	150
	GTCCGCGAGC	TTCTGGCTGA	GCAGGACTAC	GACGAGGAGG	CTCCGGTCGT	200
	CCCGATCTCC	GCACTGGGCG	CCCTGGACGG	CGATCAGAAG	TGGGTCGACT	250
	CCATCCTCGA	GCTCATGAAG	GCTTGCGACG	AGTCCATCCC	GGACCCGGAG	300
5	CGCGAGACCG	ACAAGCCGTT	CCTGATGCCG	GTTGAGGACA	TCTTCACCAT	350
	TACCGGTCGC	GGCACCGTCG	TTACCGGCCG	TGTTGAGCGT	GGCGTCCTGA	400
	ACCTGAACGA	CGAGGTCGAG	ATCCTGGGCA	TCCGCGAGAA	GTCCACCAAG	450
	ACCACCGTCA	CCTCCATCGA	GATGTTCAAC	AAGCTGCTGG	ACACCGCAGA	500
	GGCTGGCGAC	AACGCTGCAC	TGCTGCTGCG	TGGTCTGAAG	CGTGAGGACG	550
10	TCGAGCGAGG	CCAGATCATC	GCTAAGCCGG	GCGCTTACAC	CCCGCACACC	600
	GAGTTCGAGG	GCTCCGTCTA	CGTCCTGTCC	AAGGACGAGG	GCGGCCGTCA	650
	CACCCCGTTC	TTCGACAAC	ACCGTCCGCA	GTTCTACTTC	CGTACCACCG	700
	ACGTCACCGG	TGTCGTTACC	CTGCCAGAGG	GCACCGACAT	GGTCATGCCG	750
15	GGCGACAACG	TTGAGATGAG	CGTCAAGC			778

## 2) INFORMATION FOR SEQ ID NO: 44

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 703 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Corynebacterium xerosis*

(B) STRAIN: ATCC 373

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 44

	CGCAGACCCG	TGAGCACGTC	CTCCTGGCCC	GCCAGGTCGG	CGTCCCCTAC	50
35	ATCCTCGTCG	CCCTGAACAA	GTGCGACATG	GTCGACGATG	AGGAGATCAT	100
	CGAGCTCGTG	GAGATGGAGG	TGCGTGAGCT	TCTCGCCGAG	CAGGACTACG	150
	ACGAGGAGGC	CCCGATCGTG	CACATCTCCG	CCCTGGGCGC	CCTCAATGGC	200
	GAAGAGAAGT	GGGTGCACTC	CATCGTCGAG	CTCATGAACG	CCGTGCGACG	250
	GAACGTTCCG	GACCCGGTCC	GCGAGACCGA	CAAGCCGTTT	CTGATGCCCG	300
40	TCGAGGACAT	CTTCACCATC	ACCGGCCGCG	GCACCGTCGC	CACCGGTCGC	350
	GTGGAGCGCG	GCACCCTGAA	GGTCAACGAC	GAGGTCGAGA	TCCTGGGCAT	400
	CCAGGAGAAG	TCCCAGACCA	CCACCGTCAC	CGGCATCGAG	ATGTTCCGCA	450
	AGCTGCTGGA	CTCCGCCGAG	GCCGGCGACA	ACTGTGGCCT	GCTGCTCCGC	500
	GGCATCAAGC	GCGAGGACAT	CGAGCGCGGC	CAGATCATCG	CGAAGCCGGG	550
45	CGCCTACACC	CCGCACACCG	AGTTCGAGGG	CTCCGTCTAC	ATCCTGGCCA	600
	AGGACGAGGG	CGGCCGCCAC	ACCCCGTTCT	TCGACAAC	CCGTCCGCAG	650
	TTCTACTTCC	GCACCACCGA	CGTCACCGGC	GTCGTGAAGC	TGCCGGAGGG	700
	CAC					703

## 2) INFORMATION FOR SEQ ID NO: 45

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 832 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Coxiella burnetii*

(B) STRAIN: Nine Mile phase II

5

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 45

	GGAGCGATAT	TGGTGGTGAG	CGCAGCGGAC	GGCCCGATGC	CGCAAACGCG	50
	GGAACACATT	GTATTGGCGA	AGCAAGTGGG	TGTTCCGAAC	ATAGTGGTTT	100
10	ACTTGAACAA	AGCGGACATG	GTGGATGACA	AAGAGCTGTT	GGAATTAGTG	150
	GAAATGGAAG	TGAGGGATTT	ATTGAACAGT	TATGATTTCC	CTGGGGATGA	200
	GACGCCGATA	ATAGTGGGGT	CAGCGTTAAA	GGCGTTAGAA	GGTGACAAGA	250
	GTGAGGTTGG	GGAGCCATCG	ATAATCAAAT	TAGTGGAAAC	GATGGACACG	300
	TACTTCCCGC	AGCCGGAGCG	AGCGATAGAC	AAACCGTTTT	TAATGCCGAT	350
15	CGAAGATGTG	TTTTTCGATAT	CGGGCCGAGG	GACGGTGGTG	ACGGGACGCG	400
	TAGAGCGAGG	GATCATCAAA	GTGGGCGACG	AGATAGAGAT	TGTGGGGATC	450
	AAGGACACGA	CGAAGACGAC	GTGCACGGGC	GTTGAGATGT	TTCGCAAATT	500
	ATTGGATGAA	GGTCAAGCGG	GTGACAACGT	AGGAATTTTA	TTGAGAGGGA	550
	CGAAACGCGA	AGAAGTGGAG	CGTGGTCAAG	TATTGGCGAA	ACCGGGATCG	600
20	ATCACGCCAC	ACAAGAAATT	TGAGGCGGAG	ATTTATGTGT	TGTCGAAGGA	650
	AGAAGGGGGA	CGCCACACAC	CGTTTTTACA	AGGCTATCGA	CCGCAATTTT	700
	ATTTCCGCAC	GACGGACGTG	ACGGGCCAGT	TATTGAGTTT	ACCGGAGGGG	750
	ATAGAGATGG	TGATGCCGGG	AGATAACGTG	AAAGTGACGG	TTGAATTGAT	800
25	TGCGCCGGTA	GCGATGGATG	AAGGGCTACG	AT		832

## 2) INFORMATION FOR SEQ ID NO: 46

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 816 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

35

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Edwardsiella hoshinae*

(B) STRAIN: ATCC 33379

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 46

	GGCGCTATCC	TGGTTGTTGC	TGCGACTGAC	GGCCCGATGC	CGCAGACCCG	50
45	TGAGCACATC	CTGCTGGGTC	GCCAGGTAGG	CGTTCCGTAC	ATCATCGTGT	100
	TCCTGAACAA	GTGCGACATG	GTTGATGACG	AAGAGCTGCT	GGAAC TGGTT	150
	GAGATGGAAG	TTCGCGAACT	GCTGTCTCAG	TACGATTTCC	CGGGCGACGA	200
	TACGCCGGTA	ATCCGCGGTT	CTGCGCTGAA	AGCGCTGGAA	GGCGAAGCCG	250
	AGTGGGAAGC	GAAGATCATC	GAAC TGGCTG	AAACGCTGGA	CTCCTACATT	300
50	CCGGAACCTG	AGCGTGACAT	CGACAAGCCG	TTCCTGCTGC	CGATCGAAGA	350
	CGTATTCTCA	ATCTCTGGTC	GTGGTACCGT	TGTTACCGGT	CGTGTAGAGC	400
	GCGGTATCAT	CAAGGTAGGC	GACGAAGTTG	AAATCGTAGG	TATCAAGCCG	450
	ACCACCAAGA	CTACCTGTAC	TGGCGTTGAA	ATGTTCCGCA	AACTGCTGGA	500
	CGAAGGCCGT	GCTGGTGAGA	ACGTAGGTGT	TCTGCTGCGT	GGTACCAAGC	550
55	GTGACGAAAT	CGAACGTGGT	CAGGTACTGG	CTAAGCCGGG	CACCATCACT	600
	CCGCACACCA	AGTTCTGAATC	AGAAGTGTAC	ATCCTGAGCA	AGGATGAAGG	650
	CGGCCGTCAT	ACTCCGTTCT	TCAAAGGTTA	CCGTCCGCAG	TTCTACTTCC	700
	GTACCACTGA	CGTGACTGGC	ACCATCGAAC	TGCCGGAAGG	CGTAGAGATG	750
	GTAATGCCCG	GCGACAACAT	CAAGATGGTT	GTTACCCTGA	TCCACCCGAT	800
60	CGCCATGGAC	GATGGT				816

## 2) INFORMATION FOR SEQ ID NO: 47

5

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 821 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

10

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Edwardsiella tarda*  
 (B) STRAIN: ATCC 15947

15

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 47

20 GGCGCGATCC TGGTTGTTGC TCGACTGAC GGCCCGATGC CGCAGACCCG 50  
 TGAGCACATC CTGTTGGGTC GCCAGGTAGG CGTTCCGTAC ATCATCGTGT 100  
 TCCTGAACAA GTGCGACATG GTTGATGACG AAGAGCTGCT GGAAGCTGGT 150  
 GAGATGGAAG TTCGCGAACT GCTGTCTCAG TACGACTTCC CGGGCGACGA 200  
 CACGCCGGTA ATCCGCGGTT CTGCGCTGAA AGCGCTGGAA GGCGAAGCCG 250  
 25 AGTGGGAAGC GAAGATCATC GAACTGGCTG AAATCTTGGA CTCCTACATC 300  
 CCGGAACCTG AGCGTGACAT CGACAAGCCG TTCCTGCTGC CGATCGAAGA 350  
 CGTATTCTCT ATCTCTGGCC GTGGTACCGT TGTACCGGT CGTGTAGAGC 400  
 GCGGTATCAT CAAGGTAGGC GACGAAGTTG AAATCGTTGG TATCAAGCCG 450  
 ACCACCAAGA CCACCTGTAC TGGCGTTGAA ATGTTCCGCA AACTGCTGGA 500  
 30 CGAAGGCCGT GCTGGTGAGA ACGTTGGTGT TCTGCTGCGT GGTACTAAGC 550  
 GTGACGAAAT CGAACGTGGT CAGGTACTGG CTAAGCCGGG CACCATCACT 600  
 CCGCACACCA AGTTCGAATC TGAAGTGATC ATCCTGAGCA AGGATGAAGG 650  
 CGGCCGTCAT ACTCCGTTCT TCAAAGGCTA CCGTCCGCAG TTCTACTTCC 700  
 GTACTACTGA CGTGACTGGT ACCATCGAAC TGCCGGAAGG CGTAGAGATG 750  
 35 GTAATGCCGG GCGACAACAT CAAGATGGTT GTTACCCTGA TCCACCCGAT 800  
 CGCCATGGAC GATGGTCTGC G 821

## 40 2) INFORMATION FOR SEQ ID NO: 48

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 830 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

45

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Eikenella corrodens*  
 (B) STRAIN: ATCC 23834

50

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 48

55

CGGTGCCATC CTGGTGGTAT CCGCTGCTGA CGGCCCATG CCTCAGACTC 50  
 GCGAACACAT CCTGTTGGCT CGTCAGGTAG GTGTACCCTA CATCCTCGTA 100  
 TTCATGAACA AATGCGACAT GGTAGATGAT GCCGAGCTGC TTGAGTTGGT 150  
 TGAGATGGAA ATCCGCGACC TGCTCTCCAG CTATGACTTC CCTGGTGACG 200  
 60 ACTGCCCGAT CGTACAAGGT TCCGCTCTCA AAGCCCTCGA AGGCGATGCC 250

	GGTTACAAAG	AAAAAATCTT	CGAACTAGCT	GCTGCTTTGG	ATAGCTACAT	300
	CCCCACTCCT	CAACGTGCTG	TAGACAAACC	CTTCCTGTTG	CCGATCGAAG	350
	ACGTATTCTC	TATCTCCGGC	CGTGGTACCG	TAGTAACCGG	TCGTGTAGAG	400
	CGCGGCATCA	TCAAAGTAGG	TGAAGAGATC	GAAATCGTTG	GTCTGAAGCC	450
5	CACTCAGAAA	ACTACCTGTA	CTGGCGTGGA	AATGTTCCGC	AAACTGCTGG	500
	ACGAAGGTCA	GGCCGGTGAC	AACGTAGGCG	TACTGCTGCG	CGGTACCAAA	550
	CGTGAAGAAG	TTGAGCGTGG	TCAAGTATTG	GCTAAACCCG	GCACCATCAC	600
	TCCGCACACC	AAGTTCAAAG	CCGAAGTATA	CGTATTGAGC	AAAGAAGAAG	650
	GTGGTCGTCA	CACCCCGTTC	TTTGCCAACT	ACCGTCCACA	GTTCTACTTC	700
10	CGTACTACTG	ACGTAACCGG	TGCTGTAGAG	CTGGAGCCTG	GTGTAGAAAT	750
	GGTTATGCCT	GGTGAGAACG	TAACCATCAC	CGTAGAACTG	ATTGCTCCGA	800
	TTGCTATGGA	AGAAGGTCTG	CGCTTTGCGA			830

15

## 2) INFORMATION FOR SEQ ID NO: 49

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 808 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

25

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterobacter aerogenes*  
 (B) STRAIN: ATCC 13048

## 30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 49

	GGCGCGATCC	TGGTTGTTGC	TGCGACTGAC	GGCCCGATGC	CGCAGACTCG	50
	TGAGCACATC	CTGCTGGGTC	GTCAGGTAGG	CGTTCCGTAC	ATCATCGTGT	100
	TCCTGAACAA	ATGCGACATG	GTTGATGACG	AAGAGCTGCT	GGAAGTGGTT	150
35	GAGATGGAAG	TTCGTGAACT	GCTGTCTCAG	TACGATTTCC	CGGGCGACGA	200
	CACTCCGATC	GTTCGTGGTT	CTGCTCTGAA	AGCGCTGGAA	GGCGACGCAG	250
	AGTGGAAGC	GAAAATCATC	GAAGTGGCTG	GCTTCCTGGA	TTCTTACATC	300
	CCRGAAACCAG	AGCGTGCGAT	TGACAAGCCG	TTCTTGCTGC	CGATCGAAGA	350
	CGTATTCTCC	ATCTCCGGTC	GTGGTACCGT	TGTTACCGGT	CGTGTAGAGC	400
40	GCGGTATCAT	CAAAGTTGGT	GAAGAAGTTG	AAATCGTTGG	TATCAAAGAC	450
	ACCGCGAAAA	CCACCTGTAC	TGGCGTTGAA	ATGTTCCGCA	AACTGCTGGA	500
	CGAAGGCCGT	GCTGGTGAGA	ACGTAGGYGT	TCTGCTGCGT	GGTATCAAAC	550
	GTGAAGAAAT	CGAACGTGGT	CAGGTACTGG	CTAAGCCGGG	CAGCATCAAG	600
	CCGCACACCA	AGTTCGAATC	TGAAGTGATC	ATCCTGTCCA	AAGACGAAGG	650
45	CGGCCGTCAT	ACTCCGTTCT	TCAAAGGCTA	CCGTCCGCAG	TTCTACTTCC	700
	GTACTACTGA	CGTGACTGGT	ACCATCGAAC	TGCCGGAAGG	CGTAGAGRTG	750
	GTAATGCCCG	GCGACAACAT	CAAAATGGTT	GTTACCCTGA	TCCACCCGAT	800
	CGCGATGG					808

50

## 2) INFORMATION FOR SEQ ID NO: 50

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 828 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

## 60 (ii) MOLECULE TYPE: Genomic DNA



## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterobacter agglomerans*  
 (B) STRAIN: ATCC 27989

5

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 50

	CGGCGCGATC	CTGGTTGTTG	CTGCGACTGA	CGGCCCGATG	CCGCAGACTC	50
	GTGAGCACAT	CCTGCTGGGT	CGTCAGGTAG	GCGTTCCGTA	CATCATCGTG	100
10	TTCTTGAACA	AATGTGACAT	GGTTGATGAC	GAAGAGCTGC	TGGAAGTGGT	150
	TGAAATGGAA	GTTTCGTGAAC	TTCTGTCTCA	GTACGATTTC	CCGGGCGACG	200
	ATACTCCGAT	CGTTCGTGGT	TCTGCTCTGA	AAGCGCTGGA	AGGCGAMGCW	250
	GAGTGGGAAG	CGAAAATCAT	CGARCTGGCT	GGCCACCTGG	ATACCTATAT	300
	CCCGGAACCA	GAGCGTGCGA	TTGACAAGCC	GTTCTGCTG	CCGATCGAAG	350
15	ACGTATTCTC	CATCTCCGGT	CGCGGTACCG	TTGTTACCGG	TCGTGTAGAG	400
	CGCGGTATCA	TYAAAGTGGG	CGAAGAAGTT	GAAATCGTTG	GTATCAAAGA	450
	TACYGCGAAA	TCAACCTGTA	CCGCGCTTGA	AATGTTCCGC	AAACTGCTGG	500
	ACGAAGGCCG	TGCTGGTGAG	AACGTTGGTG	TTCTGCTGCG	TGGTATCAAA	550
	CGTGAAGAAA	TCGAACGTGG	TCAGGTACTG	GCTAAGCCGG	GCACCATCAA	600
20	GCCGCACACC	AAGTTCGAAT	CTGAAGTGTA	CATTCTGTCC	AAAGATGAAG	650
	GCGGTCGTCA	CACTCCGTTC	TTCAAAGGCT	ACCGTCCSCA	GTTCTACTTC	700
	CGTACAACCTG	ACGTGACTGG	CACCATCGAA	CTGCCGGAAG	GCGTAGAGAT	750
	GGTAATGCCG	GGCGACAACA	TCAAATGGT	TGTTACCCTG	ATCCACCCGA	800
25	TCGCGATGGA	CGACGGTCTG	CGTTCGCA			828

## 2) INFORMATION FOR SEQ ID NO: 51

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 825 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

35

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterobacter amnigenus*  
 (B) STRAIN: ATCC 33072

40

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 51

	TGGCGCGATC	CTGGTTGTTG	CTGCAACTGA	TGGCCCTATG	CCACAGACGC	50
45	GTGAGCACAT	CCTGCTGGGT	CGTCAGGTAG	GCGTTCCTTA	CATCATCGTG	100
	TTCTTGAACA	AATGCGACAT	GGTTGATGAC	GAAGAGCTGC	TGGAAGTGGT	150
	AGAAATGGAA	GTTTCGTGAAC	TTCTGTCTCA	GTACGATTTC	CCAGGTGATG	200
	ACACTCCAAT	CATCCGTGGT	TCTGCTCTGA	AAGCGCTGGA	AGGCGAAGCA	250
	GAGTGGGAAG	CTAAAATCGT	TGAGCTGGCT	GGCTACCTGG	ATTCTTACAT	300
50	CCCGGAACCA	GAACGTGCTA	TCGATAAGCC	ATTCTGCTG	CCAATCGAAG	350
	ACGTATTCTC	TATCTCCGGC	CGTGGTACTG	TTGTAACCGG	TCGTGTAGAG	400
	CGCGGTATCG	TTAAAGTTGG	CGAAGAAGTT	GAAATCGTTG	GTATCAAAGA	450
	GACTGCTAAG	TCTACCTGTA	CTGGCGTTGA	AATGTTCCGC	AAACTGCTGG	500
	ACGAAGGCCG	TGCTGGTGAG	AACGTTGGTG	TTCTGCTGCG	TGGTATCAAA	550
55	CGTGAAGAAA	TCGAACGTGG	TCAGGTACTG	GCTAAGCCAG	GCTCAATCAA	600
	GCCGCACACC	AAATTCGAAT	CTGAAGTTTA	TATTCTGTCC	AAAGATGAAG	650
	GCGGCCGTCA	TACTCCGTTC	TTCAAAGGCT	ACCGTCCACA	GTTCTACTTC	700
	CGTACAACCTG	ACGTGACCGG	CACCATCGAA	CTGCCAGAAG	GCGTAGAGAT	750
	GGTAATGCCA	GGCGACAACA	TTCAGATGGT	TGTTACCCTG	ATCCACCCAA	800
60	TCGCGATGGA	TGACGGTCTG	CGTTT			825

## 2) INFORMATION FOR SEQ ID NO: 52

5

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 822 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

10

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterobacter asburiae*  
 (B) STRAIN: ATCC 35953

15

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 52

20	CGGCGCGATC	CTGGTTGTTG	CTGCGACTGA	CGGCCCAATG	CCTCAGACTC	50
	GTGAGCACAT	CCTGCTGGGT	CGTCAGGTAG	GCGTTCCTTT	CATCATCGTG	100
	TTCCTGAACA	AATGCGACAT	GGTTGATGAC	GAAGAGCTGC	TGGAAGTGGT	150
	AGAGATGGAA	GTTCGTGAAC	TGCTGTCTCA	GTACGATTTT	CCGGGCGACG	200
	ATACTCCAAT	CGTTCGTGGT	TCTGCTCTGA	AAGCGCTGGA	AGGCGACGCA	250
25	GAGTGGGAAG	CGAAAATCAT	CGAACTGGCT	GGCTTCCTGG	ATTCTTACAT	300
	CCCAGAACCA	GAGCGTGCGA	TTGACAAGCC	ATTCCTGCTG	CCAATCGAAG	350
	ACGTATTCTC	CATCTCCGGT	CGTGGTACCG	TTGTTACCGG	TCGTGTAGAG	400
	CGCGGTATCA	TCAAAGTTGG	CGAAGAAGTT	GAAATCGTTG	GTATCAAAGA	450
	GACTGCTAAG	TCTACCTGTA	CTGGCGTTGA	AATGTTCCGC	AAACTGCTGG	500
30	ACGAAGGCCG	TGCTGGTGAG	AACGTTGGTG	TTCTGCTGCG	TGGTATCAAA	550
	CGTGAAGAAA	TCGAACGTGG	TCAGGTTCTG	GCGAAGCCAG	GCTCAATCAA	600
	GCCACACACC	AAGTTCGAAT	CTGAAGTGTA	CATCCTGTCC	AAAGACGAAG	650
	GCGGCCGTCA	TACTCCGTTC	TTCAAAGGCT	ACCGTCCACA	GTTCTACTTC	700
	CGTACAACCTG	ACGTGACCGG	TACCATCGAA	CTGCCAGAAG	GCGTTGAGAT	750
35	GGTAATGCCA	GGCGACAACA	TCAAGATGGT	TGTGACTCTG	ATCCACCCAA	800
	TCGCGATGGA	CGACGGTCTG	CG			822

## 40 2) INFORMATION FOR SEQ ID NO: 53

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 826 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

45

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterobacter cancerogenus*  
 (B) STRAIN: ATCC 35317

50

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 53

55

	CGGCGCGATC	CTGGTTGTTG	CTGCGACTGA	CGGCCCAATG	CCTCAGACTC	50
	GTGAGCACAT	CCTGCTGGGT	CGTCAGGTAG	GCGTTCCTTA	CATCATCGTG	100
	TTCCTGAACA	AGTGCACAT	GGTTGATGAC	GAAGAGCTGC	TGGAAGTGGT	150
	AGAAATGGAA	GTTCGTGAAC	TGCTGTCTCA	GTACGATTTT	CCAGGCGACG	200
60	ACACTCCAAT	CGTTCGTGGT	TCCGCGCTGA	AAGCGCTGGA	AGGCGAAGCT	250

	GAGTGGGAAG	CAAAAATCAT	CGAACTGGCT	GGCTTCCTGG	ATTCTTACAT	300
	CCCAGAACCA	GAGCGTGCGA	TTGACAAGCC	ATTCCTGCTG	CCAATCGAAG	350
	ACGTATTCTC	CATCTCCGGT	CGTGGTACCG	TTGTTACCGG	TCGTGTAGAG	400
	CGCGGTATCA	TCAAAGTTGG	TGAAGAAGTT	GAAATCGTTG	GTATCAAAGA	450
5	TACTGCKAAA	TCTACCTGTA	CTGGCGTTGA	AATGTTCCGC	AAACTGCTGG	500
	ACGAAGGCCG	TGCTGGTGAG	AACGTTGGTG	TTCTGCTGCG	TGGTATCAAA	550
	CGCGAAGAAA	TCGAACGTGG	TCAGGTTCTG	GCGAAGCCAG	GCTCAATCAA	600
	GCCACACACC	AAGTTCGAAT	CTGAAGTGTA	CATCCTGTCC	AAAGACGAAG	650
	GCGGCCGTCA	TACTCCGTTT	TTCAAAGGCT	ACCGTCCACA	GTTCTACTTC	700
10	CGTACAACTG	ACGTGACCGG	TACCATCGAA	CTGCCAGAAG	GCGTAGAGAT	750
	GGTAATGCCA	GGCGACAACA	TCAAGATGGT	TGTGACGCTG	ATCCACCCAA	800
	TCGCGATGGA	CGACGGTCTG	CGTTTC			826

15

## 2) INFORMATION FOR SEQ ID NO: 54

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 806 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

25

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterobacter cloacae*  
 (B) STRAIN: ATCC 13047

## 30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 54

	GATCCTGGTA	GTAGCTGCGA	CTGACGGCCC	AATGCCTCAG	ACTCGTGAGC	50
	ACATCCTGCT	GGGTCGTCAG	GTAGGCGTTC	CTTACATCAT	CGTGTTCCCTG	100
	AACAAATGCG	ACATGGTTGA	TGACGAAGAG	CTGCTGGAAC	TGGTAGAGAT	150
35	GGAAGTTCGT	GAAGTGTCTG	CTCAGTACGA	TTTCCCAGGC	GACGATACCC	200
	CAATCGTTTCG	TGGTTCTGCT	CTGAAAGCGC	TGGAAGGCCA	CGCAGAGTGG	250
	GAAGMGAAAA	TCATCGAACT	GGCTGGCTAC	CTGGATTCTT	ACATCCCAGA	300
	ACCAGAGCGT	GCGATTGAYA	AGCCATTCTT	GCTGCCAATC	GAAGACGTAT	350
	TCTCCATCTC	CGGTCGTGGT	ACCGTTGTTA	CCGGTCGTGT	AGAGCGCGGT	400
40	ATCATCAAAG	TGGGTGAAGA	AGTTGAAATC	GTTGGTATCA	AAGAGACTGC	450
	GAAGTCTACC	TGTACTGGCG	TTGAAATGTT	CCGCAAACTG	CTGGACGAAG	500
	GCCGTGCTGG	TGAGAACGTT	GGTGTCTGTC	TGCGTGGTAT	CAAACGTGAA	550
	GAAATCGAAC	GTGGTCAGGT	TCTGGCGAAG	CCAGGCTCAA	TCAAGCCACA	600
	CACCAAGTTC	GAATCTGAAG	TGTACATCCT	GTCCAAAGAC	GAAGGCGGCC	650
45	GTCATACTCC	GTTCTTCAAA	GGCTACCGTC	CACAGTTCTA	CTTCCGTACA	700
	ACTGACGTGA	CCGGTACCAT	CGAACTGCCA	GAAGGCGTAG	AGGTGGTAAT	750
	GCCAGGCGAC	AACATCAAGA	TGGTTGTGAC	TCTGATCCAC	CCAATCGCGA	800
	TGGACG					806

50

## 2) INFORMATION FOR SEQ ID NO: 55

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 826 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

## 60 (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterobacter gergoviae*  
 (B) STRAIN: ATCC 33028

5

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 55

```

CGGCGCGATC CTGGTTGTTG CTGCGACTGA CGGCCCGATG CCGCAGACCC      50
GTGAGCACAT CCTGCTGGGT CGTCAGGTAG GCGTTCCGTA CATCATCGTG      100
10  TTCCTGAACA AGTGCACAT GGTGATGAC GAAGAGCTGC TGGAACTGGT      150
AGAGATGGAA GTTCGTGAAC TGCTGTCTCA GTACGATTTC CCGGCGACG      200
ACACCCCGAT CGTTCGCGGT TCTGCGCTGA AAGCGCTGGA AGGCGACGCA      250
GAGTGGGAAG CGAAAATCAT CGAACTGGCT GGCCACCTGG ATACCTAYAT      300
CCCGGAACCA GAGCGTGCGA TTGACAAGCC GTTCCTGCTG CCGATCGAAG      350
15  ACGTATTCTC CATTTCCGGT CGTGGTACCG TTGTTACCGG TCGTGTAGAG      400
CGCGGTATCA TCAAGGTTGG TGAAGAAGTT GAAATCGTTG GTATCAAAGA      450
CACCGCGAAA ACCACCTGTA CTGGCGTTGA AATGTTCCGC AAAGTGTCTG      500
ACGAAGGCCG TGCTGGTGAG AACGTCGGCG TTCTGCTGCG TGGTATCAAG      550
CGTGAAGAAA TCGAACGTGG TCAGGTACTG GCTAAGCCGG GCTCCATCAA      600
20  GCCGCACACC AAGTTCGAAT CTGAAGTGTA CATCCTGTCC AAAGACGAAG      650
GCGGCCGTCA CACTCCGTTT TCAAAGGCT ACCGTCCGCA GTTCTACTTC      700
CGTACAACCTG ACGTGACTGG CACCATCGAA CTGCCGGAAG GCGTAGAGAT      750
GGTAATGCCG GCGACAACA TCAAGATGGT TGTTACCCTG ATCCACCCGA      800
25  TCGCGATGGA CGACGGTCTG CGTTTC      826

```

## 2) INFORMATION FOR SEQ ID NO: 56

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 829 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

35

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterobacter hormaechei*  
 (B) STRAIN: ATCC 49162

40

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 56

```

GGCGCGATCC TGGTTGTTGC TGCGACTGAC GGCCCTATGC CTCAGACCCG      50
45  TGAGCACATC CTGCTGGGTC GTCAGGTAGG CGTTCCTTAC ATCATCGTGT      100
TCCTGAACAA ATGCGACATG GTTGATGACG AAGAGCTGCT GGAAGTGGTA      150
GAGATGGAAG TTCGTGAAC TCTGTCTCAG TACGATTTC CAGGCGACGA      200
CACCCCAATC GTTCGTGGTT CCGCGCTGAA AGCGCTGGAA GGCGAMGCAG      250
AGTGGGAAGM GAAAATCATC GARCTGGCTG GCTTCCTGGA TTCTTACATC      300
50  CCAGAACCAG AGCGTGCGAT TGACAAGCCA TTCCTGCTGC CAATCGAAGA      350
CGTATTCTCC ATCTCCGGTC GTGGTACCGT TGTTACCGGT CGTGTWGAGC      400
GCGGTATCAT CAAAGTAGGT GAAGAAGTTG AAATCGTTGG TATCAAAGAG      450
ACTGCGAAGT CTACCTGTAC TGGCGTTGAA ATGTTCCGCA AACTGCTGGA      500
CGAAGGCCGT GCTGGTGAGA ACGTTGGTGT TCTGCTGCGT GGTATCAAAC      550
55  GTGAAGAAAT CGAACGTGGT CAGGTTCTGG CGAAGCCAGG CTCAATCAAG      600
CTACACACCA AGTTCGAATC TGAAGTGTAC ATTCTGTCCA AAGACGAAGG      650
CGGCCGTCAT ACTCCGTTCT TCAAAGGCTA CCGTCCACAG TTCTACTTCC      700
GTACAACCTGA CGTGACCGGT ACCATCGAAC TGCCAGAAGG CGTAGAGATG      750
GTAATGCCAG GCGACAACAT CAAGATGGTT GTGACGCTGA TCCACCCAAT      800
60  CGCGATGGAC GACGGTCTGC GTTTCGCAA      829

```

35

## 2) INFORMATION FOR SEQ ID NO: 57

5

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 831 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

10

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterobacter sakazakii*  
 (B) STRAIN: ATCC 29544

15

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 57

20	GGCGCTATCC	TGGTTGTTGC	TGCGACTGAC	GGCCCGATGC	CGCAGACCCG	50
	TGAGCACATC	CTGCTGGGTC	GTCAGGTAGG	CGTTCCGTAC	ATCATCGTGT	100
	TCCTGAACAA	ATGCGACATG	GTTGATGACG	AAGAGCTGCT	GGAAGTGGTT	150
	GAGATGGAAG	TGCGCGAGCT	GCTGTCTCAG	TACGACTTCC	CGGGCGACGA	200
	CACCCCGATC	GTTTCGTGGTT	CTGCTCTGAA	AGCGCTGGAA	GGCGACGCTG	250
25	AGTGGGAAGC	GAAAATCATC	GAGCTGGCAG	GTCACCTGGA	TTCCTACATC	300
	CCGGAACCGG	AGCGTGCGAT	TGACAAGCCG	TTCCTGCTGC	CGATCGAAGA	350
	CGTATTCTCC	ATCTCYGGTC	GTGGTACCGT	TGTTACCGGT	CGTGTAGAGC	400
	GCGGTATCAT	CAAGGTTGGT	GAAGAAGTTG	AAATCGTGCG	CATCAAAGAC	450
	ACCGCGAAAT	CCACCTGTAC	CGGCGTTGAA	ATGTTCCGCA	AACTGCTGGA	500
30	CGAAGGCCGT	GCGGGCGAGA	ACGTAGGTGT	TCTGCTGCGT	GGTATCAAAC	550
	GTGAAGAAAT	CGAACGTGGT	CAGGTACTGG	CTAAGCCGGG	CTCCATCAAG	600
	CCGCACACCA	AGTTCGAATC	TGAAGTGTAC	ATTCTGTCCA	AAGATGAAGG	650
	CGGCCGTCAC	ACTCCGTTCT	TCAAAGGCTA	CCGTCCGCAG	TTCTACTTCC	700
	GTACRACTGA	CGTGAAGTGC	ACCATCGAAC	TGCCGGAAGG	CGTTGAGATG	750
35	GTAATGCCGG	GCGACAACAT	CAAAATGGTT	GTTACCCTGA	TCCACCCGAT	800
	CGCGATGGAC	GACGGTCTGC	GTTTCGCAAT	C		831

## 40 2) INFORMATION FOR SEQ ID NO: 58

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 835 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

45

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus casseliflavus*  
 (B) STRAIN: ATCC 25788

50

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 58

55

	CGGCGCGATC	TTAGTAGTAT	CTGCTGCTGA	TGGTCCTATG	CCTCAAACAC	50
	GTGAACACAT	CTTGTTATCA	CGTAACGTTG	GTGTACCATA	CATCGTTGTT	100
	TTCTTAAACA	AAATGGATAT	GGTTGATGAC	GAAGAATTAC	TAGAATTAGT	150
	TGAAATGGAA	GTTTCGTGACT	TATTGTCAGA	ATATGACTTC	CCAGGCGACG	200
60	ATGTTCCCTGT	AATCGCTGGT	TCTGCTTTGA	AAGCTCYTGA	AGGCGATGCT	250

	TCATACGAAG	AAAAAATCAT	GGAATTAATG	GCTGCAGTTG	ACGAATACGT	300
	TCCAACCTCCA	GAACGTGACA	CTGACAAACC	ATTCATGATG	CCAGTCGAAG	350
	ACGTATTCTC	AATCACTGGA	CGTGGTACTG	TTGCTACAGG	CCGTGTTGAA	400
	CGTGGACAAG	TTCGCGTTGG	TGACGAAGTT	GAAATCGTTG	GTATTGCTGA	450
5	AGAAACTGCT	AAAACAACCTG	TAACCTGGTGT	TGAAATGTTC	CGTAAATTGT	500
	TAGACTATGC	TGAAGCAGGG	GATAACATTG	GTGCATTGCT	ACGTGGTGT	550
	GCTCGTGAAG	ACATCCAACG	TGGACAAGTA	TTGGCTAAAG	CTGGTACAAT	600
	CACACCTCAT	ACAAAATTTA	AAGCTGAAGT	TTACGTTTTA	ACAAAAGAAG	650
	AAGGTGGACG	TCACACACCA	TTCTTCACTA	ACTACCGTCC	TCAGTTCTAC	700
10	TTCCGTACAA	CTGACGTAAAC	TGGTGTGTT	GAATTACCAG	AAGGAACTGA	750
	AATGGTTATG	CCTGGTGATA	ACGTAAACAAT	CGACGTTGAA	TTGATCCACC	800
	CAATCGCTAT	CGAAGACGGA	ACTCGTTTCT	CAATT		835

15

## 2) INFORMATION FOR SEQ ID NO: 59

## (i) SEQUENCE CHARACTERISTICS:

- 20 (A) LENGTH: 826 bases  
(B) TYPE: Nucleic acid  
(C) STRANDEDNESS: Double  
(D) TOPOLOGY: Linear

## 25 (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus cecorum*  
(B) STRAIN: ATCC 43198

## 30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 59

	GGTGCTATCT	TAGTAGTATC	TGCTGCTGAT	GGTCCTATGC	CACAAACTCG	50
	TGAACACATT	CTTTTATCAC	GTAACGTTGG	TGTTCCATAC	ATCGTTGTTT	100
	TCTTAAACAA	AGTTGATATG	GTTGACGACG	AAGAATTATT	AGAATTAGTT	150
35	GAAATGGAAG	TACGTGACTT	ATTAAC TGAA	TACGACTTCC	CAGGAGACGA	200
	TGTTCTGTGA	ATCGCTGGTT	CTGCATTAAA	AGCTTTAGAA	GGCGACCCAT	250
	CTTACGAAGA	AAAAATCTTA	GAATTAATGG	CTGCAGTTGA	CGAATACATC	300
	CCAACCTCCAG	AACGTGACAA	CGATAAACCA	TTTATGATGC	CAGTCGAAGA	350
	CGTATTTTCA	ATCACTGGTC	GTGGTACTGT	TGCTACAGGT	CGTGTGGAAC	400
40	GTGGACAAGT	ACGTGTTGGT	GACGAAGTTG	AAATAGTTGG	TATCCATGAT	450
	GAAATTTCTA	AAACAACAGT	TACTGGTGTT	GAAATGTTCC	GTAAATTATT	500
	AGATTACGCT	GAAGCTGGAG	ACAACATCGG	TGCATTATTA	CGTGGTGTGG	550
	CTCGTGAAGA	TATCCAACGT	GGTCAAGTAT	TAGCTAAACC	AGGTTCAATC	600
	ACTCCACATA	CAAAATTCAC	TGCTGAAGTG	TACGTTTTAA	CTAAAGAAGA	650
45	AGGTGGACGT	CATACTCCAT	TCTTCACTAA	CTACCGTCCA	CAATTCTACT	700
	TCCGTACAAC	TGACGTTACA	GGTGTAGTTA	ACTTACCAGA	AGGTACTGAA	750
	ATGGTTATGC	CTGGTGATAA	CGTAACTATG	GAAGTTGAAT	TAATCCACCC	800
	AATCGCTATC	GAAGACGGAA	CTCGTT			826

50

## 2) INFORMATION FOR SEQ ID NO: 60

## (i) SEQUENCE CHARACTERISTICS:

- 55 (A) LENGTH: 835 bases  
(B) TYPE: Nucleic acid  
(C) STRANDEDNESS: Double  
(D) TOPOLOGY: Linear

## 60 (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus dispar*  
 (B) STRAIN: ATCC 51266

5

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 60

```

CGGCGCGATC TTGGTAGTAT CTGCTGCTGA TGGTCCTATG CCTCAAACCTC      50
GTGAACACAT CCTATTGTCA CGTAACGTTG GTGTTCCCTTA CATCGTCGTT      100
10 TTCTTGAACA AAATGGACAT GGTTCGATGAC GAAGAATTAT TAGAATTAGT      150
TGAAATGGAA GTTCGTGACT TATTGTCAGA ATACGACTTC CCAGGCGACG      200
ACACTCCAGT TATCGCAGGT TCAGCTTTGA AAGCCTTAGA AGGCGACGCT      250
TCATATGAAG AAAAAATCTT AGAATTAATG GCTGCAGTTG ACGAATATAT      300
CCCAACTCCA GTTCGTGATA CTGACAAACC ATTCATGATG CCAGTCGAAG      350
15 ATGTATTCTC AATCACTGGT CGTGGTACTG TTGCAACTGG TCGTGTGAA      400
CGTGGACAAG TTCGCGTTGG TGACGAAGTT GAAATCGTAG GTATCGCTGA      450
AGAAACTGCT AAAACTACTG TAACAGGTGT TGAAATGTTT CGTAAATTGT      500
TGGATTACGC TGAAGCTGGC GACAACATTG GTGCATTATT ACGTGGTGTG      550
GCTCGTGAAG ATATCCAACG TGGTCAAGTA TTATCAAAAC CAGGTTCAAT      600
20 CACTCCACAT ACAAATTTG CGGCAGAAGT TTACGTTTTA ACTAAAGAAG      650
AAGGTGGACG TCATACTCCA TTCTTCACTA ACTACCGCCC ACAATTCTAC      700
TTCCGTACAA CTGACGTAAC AGGTGTTGTT GAATTACCAG AAGGTACTGA      750
AATGGTTATG CCTGGCGATA ACGTTACTAT GGACGTTGAA TTAATCCACC      800
CAATCGCGAT CGAAGACGGT ACTCGTTTCT CAATC      835
25

```

## 2) INFORMATION FOR SEQ ID NO: 61

## 30 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 835 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

35

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus durans*  
 40 (B) STRAIN: ATCC 19432

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 61

```

CGGAGCTATC TTAGTAGTTT CTGCTGCTGA TGGCCCTATG CCTCAAACCTC      50
45 GTGAACATAT CCTATTATCT CGTCAAGTTG GTGTTCCCTTA CATCGTYGTA      100
TTCTTGAACA AAGTAGATAT GGTTCGATGAC GAAGAATTAC TAGAATTAGT      150
TGAAATGGAA GTTCGTGACT TATTAACAGA ATACGAATTC CCTGGTGACG      200
ATGTTCTGT AATCGCTGGT TCAGCTTTGA AAGCTTTAGA AGGCGACGCT      250
TCATACGAAG AAAAAATCCT TGAATTAATG GTCGCAGTTG ACGAATATAT      300
50 CCCAACTCCA GAACGTGACA ACGACAAACC ATTCATGATG CCAGTTGAAG      350
ATGTATTCTC RATCACTGGT CGTGGTACTG TTGCTACAGG TCGTGTGAA      400
CGTGGACAAG TTCGCGTTGG TGACGTTGTA GATATCGTTG GTATCGCAGA      450
AGAAACAGCT CAAACAACAG TTAAGTGGTGT TGAAATGTTT CGTAAATTAT      500
TAGRCTACGC TGAAGCTGGA GACAACATTG GTGCTTTACT ACGTGGTGT      550
GCACGTGAAG ACATCCAACG TGGACAAGTT TTAGCTAAAC CAGGTACAAT      600
CAKCKCTCAT ACAAATTTCT CTGCAGAAGT ATACGTGTTG ACTAAAGAAG      650
55 AAGGTGGACG TCATACTCCA TTCTTCACTA ACTACCGTCC ACAATTCTAC      700
TTCCGTACAA CTGACGTAAC AGGTGTTGTT GAATTACCAG AAGGTACTGA      750
AATGGTTATG CCTGGCGACA ACGTAACAAT GGAAGTTGAA TTAATCCACC      800
60 CAATCGCTAT CGAAAATGGT ACTAAATTCT CAATC      835

```

## 2) INFORMATION FOR SEQ ID NO: 62

5

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 680 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

10

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus faecalis*  
 (B) STRAIN: R610

15

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 62

20	AGTAGTTTCT	GCTGCTGATG	GTCCTATGCC	TCAAACACGT	GAACATATCT	50
	TATTATCACG	TAACGTTGGT	GTACCATACA	TCGTTGTATT	CTTAAACAAA	100
	ATGGATATGG	TTGATGACGA	AGAATTATTA	GAATTAGTAG	AAATGGAAGT	150
	TCGTGACTTA	TTATCAGAAT	ACGATTTCCC	AGGCGATGAT	GTTCCAGTTA	200
	TCGCAGGTTT	TGCTTTGAAA	GCTTTAGAAG	GCGACGAGTC	TTATGAAGAA	250
25	AAAATCTTAG	AATTAATGGC	TGCAGTTGAC	GAATATATCC	CAACTCCAGA	300
	ACGTGATACT	GACAAACCAT	TCATGATGCC	AGTCGAAGAC	GTATTCTCAA	350
	TCACTGGACG	TGGTACTGTT	GCTACAGGCC	GTGTTGAACG	TGGTGAAGTT	400
	CGCGTTGGTG	ACGAAGTTGA	AATCGTTGGT	ATTAAAGACG	AAACATCTAA	450
	AACAACGTGT	ACAGGTGTTG	AAATGTTCCG	TAAATTATTA	GACTACGCTG	500
30	AAGCAGGCGA	CAACATCGGT	GCTTTATTAC	GTGGTGTAGC	ACGTGAAGAT	550
	ATCGAACGTG	GACAAGTATT	AGCTAAACCA	GCTACAATCA	CTCCACACAC	600
	AAAATTCAAA	GCTGAAGTAT	ACGTATTATC	AAAAGAAGAA	GGCGGACGTC	650
	AACTCCATT	CTTCACTAAC	TACCGTCCTC			680

35

## 2) INFORMATION FOR SEQ ID NO: 63

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 680 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

40

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus faecalis*  
 (B) STRAIN: R487

45

50

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 63

	AGTAGTTTCT	GCTGCTGATG	GTCCTATGCC	TCAAACACGT	GAACATATCT	50
	TATTATCACG	TAACGTTGGT	GTACCATACA	TCGTTGTATT	CTTAAACAAA	100
55	ATGGATATGG	TTGATGACGA	AGAATTATTA	GAATTAGTAG	AAATGGAAGT	150
	TCGTGACTTA	TTATCAGAAT	ACGATTTCCC	AGGCGATGAT	GTTCCAGTTA	200
	TCGCAGGTTT	TGCTTTGAAA	GCTTTAGAAG	GCGACGAGTC	TTATGAAGAA	250
	AAAATCTTAG	AATTAATGGC	TGCAGTTGAC	GAATATATCC	CAACTCCAGA	300
	ACGTGATACT	GACAAACCAT	TCATGATGCC	AGTCGAAGAC	GTATTCTCAA	350
60	TCACTGGACG	TGGTACTGTT	GCTACAGGCC	GTGTTGAACG	TGGTGAAGTT	400



	CGCGTTGGTG	ACGAAGTTGA	AATCGTTGGT	ATTAAAGACG	AAACATCTAA	450
	AACAACGTGT	ACAGGTGTTG	AAATGTTCCG	TAAATTATTA	GACTACGCTG	500
	AAGCAGGCGA	CAACATCGGT	GCTTTATTAC	GTGGTGTAGC	ACGTGAAGAT	550
	ATCGAACGTG	GACAAGTATT	AGCTAAACCA	GCTACAATCA	CTCCACACAC	600
5	AAAATTCAAA	GCTGAAGTAT	ACGTATTATC	AAAAGAAGAA	GGCGGACGTC	650
	ACACTCCATT	CTTCACTAAC	TACCGTCCTC			680

## 10 2) INFORMATION FOR SEQ ID NO: 64

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 685 bases  
 (B) TYPE: Nucleic acid  
 15 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

## 20 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus faecium*  
 (B) STRAIN: R482

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 64

25	AGTAGTTTCT	GCTGCTGACG	GCCCAATGCC	TCAAACCTCGT	GAACACATCC	50
	TATTGTCTCG	TCAAGTTGGT	GTTCCCTTACA	TCGTTGTATT	CTTGAACAAA	100
	GTAGACATGG	TTGATGACGA	AGAATTACTA	GAATTAGTTG	AAATGGAAGT	150
	TCGTGACCTA	TTAACAGAAT	ACGAATTCCC	TGGTGACGAT	GTTCTGTAG	200
30	TTGCTGGATC	AGCTTTGAAA	GCTCTAGAAG	GCGACGCTTC	ATACGAAGAA	250
	AAAATTCTTG	AATTAATGGC	TGCAGTTGAC	GAATACATCC	CAACTCCAGA	300
	ACGTGACAAC	GACAAACCAT	TCATGATGCC	AGTTGAAGAC	GTGTTCTCAA	350
	TTACTGGACG	TGGTACTGTT	GCTACAGGTC	GTGTTGAACG	TGGACAAGTT	400
	CGCGTTGGTG	ACGAAGTTGA	AGTTGTTGGT	ATTGCTGAAG	AAACTTCAAA	450
35	AACAACAGTT	ACTGGTGTTG	AAATGTTCCG	TAAATTGTTA	GACTACGCTG	500
	AAGCTGGAGA	CAACATTGGT	GCTTTACTAC	GTGGTGTTGC	ACGTGAAGAC	550
	ATCCAACGTG	GACAAGTTT	AGCTAAACCA	GGTACAATCA	CACCTCATAC	600
	AAAATTCTCT	GCAGAAGTAT	ACGTGTTGAC	AAAAGAAGAA	GGTGGACGTC	650
40	ATACTCCATT	CTTCACTAAC	TACCGTCCTC	AATTT		685

## 2) INFORMATION FOR SEQ ID NO: 65

## 45 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 825 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 50 (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus flavescens*  
 55 (B) STRAIN: ATCC 49996

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 65

60	CGGCGCGATC	TTAGTAGTAT	CTGCTGCTGA	TGGTCCTAYG	CCTCAAACAC	50
	GTGAACACAT	CTTGTTATCA	CGTAACGTTG	GTGTACCATA	CATCGTTGTT	100

	TTCTTAAACA	AAATGGATAT	GGTTGATGAC	GAAGAATTAC	TAGAATTAGT	150
	TGAAATGGAA	GTTCTGACT	TATTGTCAGA	ATATGACTTC	CCAGGCGACG	200
	ATGTTCTGT	AATCGCTGGT	TCTGCTTTGA	AAGCTCTTGA	AGGCGATGCT	250
	TCATACGAAG	AAAAAATCAT	GGAATTAATG	GCTGCAGTTG	ACGAATACGT	300
5	TCCAACCTCCA	GAACGTGACA	CTGACAAACC	ATTCATGATG	CCAGTCGAAG	350
	ACGTATTCTC	AATCACTGGA	CGTGGTACTG	TTGCTACAGG	CCGTGTTGAA	400
	CGTGGACAAG	TTCGCGTTGG	TGACGAAGTT	GAAATCGTTG	GTATTGCTGA	450
	AGAAACTGCT	AAAACAACTG	TAACGGTGT	TGAAATGTTT	CGTAAATTGT	500
	TAGACTATGC	TGAAGCAGGG	GATAACATTG	GTGCATTGCT	ACGTGGGGTT	550
10	GCTCGTGAAG	ACATCCAACG	TGGACAAGTA	TTAGCTAAAG	CTGGTACAAT	600
	CACACCTCAT	ACAAAATTTA	AAGCTGAAGT	TTACGTTTTA	ACAAAAGAAG	650
	AAGGTGGACG	TCACACTCCA	TTCTTCACTA	ACTACCGTCC	TCAGTTCTAC	700
	TTCCGTACAA	CTGACGTAA	TGGTGTGTT	GAATTACCAG	AAGGAACTGA	750
	AATGGTTATG	CCTGGTGATA	AMGTAACAAT	CGACGTTGAA	TTGATCCACC	800
15	CAATCGCTAT	CGAAGACGGA	ACTCG			825

## 2) INFORMATION FOR SEQ ID NO: 66

20

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 636 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

25

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus gallinarum*  
 (B) STRAIN: R420

30

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 66

35	TCCTATGCCT	CAAACCTCGTG	AACACATCTT	GTTATCACGT	AACGTTGGCG	50
	TACCATACAT	CGTTGTTTTT	TTGAACAAAA	TGGATATGGT	TGATGACGAA	100
	GAATTGCTAG	AATTAGTTGA	AATGGAAGTT	CGTGACCTAT	TGTCTGAGTA	150
	TGACTTCCCA	GGCGACGATG	TTCCTGTAAT	CGCCGGTTCT	GCTTTGAAAG	200
	CTCTTGAAGG	AGATCCTTCA	TACGAAGAAA	AAATCATGGA	ATTGATGGCT	250
40	GCAGTTGACG	AATACGTTCC	AACTCCAGAA	CGTGATACTG	ACAAACCATT	300
	CATGATGCCA	GTCGAAGACG	TATTCTCAAT	CACTGGACGT	GGTACTGTTG	350
	CTACAGGCCG	TGTTGAACGT	GGACAAGTTC	GCGTTGGTGA	TGAAGTAGAA	400
	ATCGTTGGTA	TTGCTGACGA	AACTGCTAAA	ACAACTGTAA	CAGGTGTTGA	450
	AATGTTCCGT	AAATTGTTAG	ACTATGCTGA	AGCAGGGGAT	AACATTGGTG	500
45	CATTGCTACG	TGGGGTTGCT	CGTGAAGACA	TCCAACGTGG	ACAAGTATTG	550
	GCTAAAGCTG	GTACAATCAC	ACCTCATACA	AAATTCAAAG	CTGAAGTTTA	600
	TGTTTTGACA	AAAGAAGAAG	GTGGACGTCA	CACTCC		636

50

## 2) INFORMATION FOR SEQ ID NO: 67

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 835 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

55

## (ii) MOLECULE TYPE: Genomic DNA

60

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus hirae*  
 (B) STRAIN: ATCC 8043

## 5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 67

	CGGAGCTATC	TTAGTAGTTT	CTGCTGCTGA	TGGTCCTATG	CCTCAAACCTC	50
	GTGAACATAT	CCTAYTATCT	CGTCAAGTTG	GTGTTCCATA	CATCGTTGTA	100
	TTCTTGAACA	AAGTAGATAT	GGTTGACGAC	GAAGAATTAC	TAGAATTAGT	150
10	TGAAATGGAA	GTTTCGTGACT	TATTAACAGA	ATACGAATTC	CCTGGTGACG	200
	ATGTTCTCTG	AGTTGCTGGT	YCAGCTTTGA	AAGCTTTAGA	AGGCGACGCT	250
	TCATACGAAG	AAAAAATCCT	TGAATTGATG	GCTGCAGTTG	ACGAATATAT	300
	CCCAACTCCA	GAACGTGACA	ACGACAAACC	ATTCATGATG	CCAGTCGAAG	350
	ACGTATTCTC	AATCACTGGT	CGTGGTACTG	TTGCTACAGG	TCGTGTTGAA	400
15	CGTGGACAAG	TTCGCGTTGG	TGACGTTGTA	GATATCGTTG	GTATCGCAGA	450
	AGAAACAGCT	CAAACAACAG	TTACTGGTGT	TGAAATGTTT	CGTAAATTAT	500
	TAGACTACGC	TGAAGCTGGA	GACAACATTG	GTGCTTTACT	ACGTGGTGTT	550
	GCACGTGAAG	ACATCCAACG	TGGACAAGTT	TTAGCTAAAC	CAGGTACAAT	600
	CACACCTCAT	ACAAAATTCT	CTGCAGAAGT	ATACGTGTTG	ACAAAAGAAG	650
20	AAGGTGGACG	TCATACTCCA	TTCTTCACTA	ACTACCGTCC	ACAATTCTAC	700
	TTCCGTACRA	CTGACGTAAC	AGGTGTTGTT	GAATTACCAG	AAGGAACTGA	750
	AATGGTTATG	CCTGGCGACA	ACGTAACAAT	GGAAGTTGAA	TTAATCCACC	800
	CAATCGCTAT	CGAAAACGGT	ACTAAATTCT	CAATC		835

25

## 2) INFORMATION FOR SEQ ID NO: 68

## (i) SEQUENCE CHARACTERISTICS:

- 30 (A) LENGTH: 835 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

## 35 (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus mundtii*  
 (B) STRAIN: ATCC 43186

40

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 68

	CGGAGCAATC	TTAGTTGTTT	CTGCTGCTGA	CGGCCCTATG	CCTCAAACCTC	50
	GTGAACACAT	CCTATTATCT	CGTCAAGTTG	GTGTACCATA	CATCGTTGTA	100
45	TTCTTGAACA	AAGTAGATAT	GGTTGATGAC	GAAGAATTAC	TTGAATTAGT	150
	TGAAATGGAA	GTTTCGTGACC	TATTAACAGA	ATACGAATTC	CCTGGTGACG	200
	ATGTTCTCTG	AATCGCTGGT	TCAGCTTTAA	GAGCTTTAGA	AGGCGACGCT	250
	KCATACGAAG	AAAAAATTCT	TGAATTGATG	GCTGCAGTTG	ACGAATATAT	300
	CCCAACTCCA	GAACGTGATA	ACGACAAACC	ATTCATGATG	CCAGTTGAGG	350
50	ACGTATTCTC	AATCACTGGT	CGTGGTACTG	TTGCTACAGG	ACGTGTTGAA	400
	CGTGGACAAG	YTCGTGTTGG	TGACGTTATC	GATATCGTTG	GTATCGCAGA	450
	AGAAACAGCT	CAAACAACCTG	TAAGTGGTGT	TGAAATGTTT	CGTAAATTAT	500
	TAGACTACGC	TGAAGCAGGC	GATAACATTG	GTGCGTTACT	ACGTGGTGTT	550
	TCACGTGAAG	ACATCCAACG	TGGTCAAGTT	TTAGCTAAAC	CAGGTACAAT	600
55	CACACCTCAT	ACAAAATTCT	CTGCAGAAGT	ATACGTGTTG	ACTAAAGAAG	650
	AAGGTGGACG	TCATACTCCA	TTCTTCACTA	ACTACCGTCC	ACAATTCTAC	700
	TTCYGTACGA	CTGACGTAAC	TRGTGTTGTY	GAATTACCAG	AAGGAACTGA	750
	AATGGTTATG	CCTGGCGACA	ACGTAACAAT	GGAAGTTGAA	TTAATCCACC	800
60	CAATCGCTAT	CGAAAATGGT	ACTAAATTCT	CAATC		835

## 2) INFORMATION FOR SEQ ID NO: 69

- 5 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 836 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear
- 10 (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: *Enterococcus pseudoavium*  
 15 (B) STRAIN: ATCC 49372

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 69

	CGGAGCTATC	TTAGTAGTAT	CTGCTGCTGA	TGGCCCTATG	CCTCAAACAC	50
20	GTGAACACAT	CTTGTTATCT	CGTAACGTTG	GTGTTCTTA	CATCGYTGTA	100
	TTCTTAAACA	AAATGGATAT	GGTTGATGAC	GAAGAATTAC	TAGAATTAGT	150
	TGAAATGGAA	GTTTCGTGACT	TATTGTCAGA	ATACGATTTT	CCAGGCGACG	200
	ACACTCYAGT	TATCGCTGGT	TCAGCYTTGA	AAGCTTTAGA	AGGCGACCCT	250
	TCATACRAAG	AAAAAATCTT	AGAATTAATG	SCTGCTGTTG	ACGAATACAT	300
25	CCCAACACCA	GTTCGTGATA	CTGACAAACC	ATTCATGATG	CCAGTCGAAG	350
	ACGTATTCTC	AATCACTGGT	CGTGGTACTG	TTGCAACTGG	TCGTGTTGAA	400
	CGTGGACAAG	TTCGCGTTGG	TGACGAAGTT	GAAATCGTAG	GTATCGCTGA	450
	AGAAACTGCT	AAAACAACCTG	TTACAGGTGT	TGAAATGTTT	CGTAAATTGT	500
	TAGACTACGC	TGAAGCAGGC	GATAACATCG	GTGCATTATT	ACGTGGTGTT	550
30	GCACGTGAAG	ACATCCAACG	TGGACAAAGTA	TTGGCTAAAC	CAGCTTCAAT	600
	CACTCCACAT	ACAAAATTCT	CTGCAGAAGT	TTACGTTTTA	ACTAAAGAAG	650
	AAGGCGGGCG	TCACACTCCG	TTCTTCACTA	ACTACCGTCC	TCAGTTCTAC	700
	TTCCGTACAA	CTGACGTAAC	TGGTGTTGTT	GATCTACCAG	AAGGTACTGA	750
	AATGGTAATG	CCTGGTGATA	ACGTAACAT	GGAAGTTGAA	TTAATCCACC	800
35	CAATCGCGAT	CGAAGACGGA	ACTCGTTTCT	CTATTC		836

## 2) INFORMATION FOR SEQ ID NO: 70

- 40 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 835 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 45 (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:  
 50 (A) ORGANISM: *Enterococcus raffinosus*  
 (B) STRAIN: ATCC 49427

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 70

55	CGGAGCTRTC	TTAGTAGTAT	CTGCTGCTGA	TGGCCCTATG	CCTCAAACCTC	50
	GTGAACACAT	CTTGTTATCT	CGTAACGTTG	GTGTTCTTA	CATCGTTGTA	100
	TTCTTAAACA	AAATGGATAT	GGTTGACGAT	GAAGAATTAC	TAGAATTAGT	150
	TGAAATGGAA	GTTTCGTGACT	TATTAACCTGA	ATACGACTTC	CCAGGCGACG	200
	ACACTCCAGT	TATCGCAGGT	TCAGCTTTGA	AAGCCTTAGA	AGGCGACGCT	250
60	TCATACGAAG	AAAAAATCTT	AGAATTAATG	GCTGCTGTTG	ATGAATACAT	300

	CCCAACACCA	GTTTCGTGATA	CTGACAAACC	ATTCATGATG	CCAGYGGAAG	350
	ACGTAYTCTC	AATCACTGGT	CGTGGAAGTG	TTGCAACTGG	TCGTGTTGAA	400
	CGTGGACAAG	TTCGCGTTGG	TGACGAAGTT	GAAATCGTAG	GTATTGCTGA	450
	AGAAACTGCT	AAAACAACCTG	TTACAGGTGT	TGAAATGTTC	CGTAAATTGT	500
5	TGGATTACGC	TGAAGCGGGC	GACAACATTG	GTGCATTATT	ACGTGGTGTT	550
	GCACGTGAAG	ACATCCAACG	TGGACAAGTA	TTGGCTAAAC	CAGCTTCAAT	600
	CACTCCACAT	ACAAAATTCT	CTGCAGAAGT	TTACGTTTTA	ACTAAAGAAG	650
	AAGGCGGACG	TCATACTCCA	TTCTTCACTA	ACTACCGTCC	TCAGTTCTAC	700
	TTCCGTACAA	CTGACGTAAC	TGGTGTAGTT	GATCTACCAG	AAGGTACTGA	750
10	AATGGTAATG	CCTGGTGATA	ACGTAACAT	GGAAGTTGAA	TTAATCCACC	800
	CAATCGCGAT	CGAAGACGGA	ACTCGTTTCT	CTATT		835

## 15 2) INFORMATION FOR SEQ ID NO: 71

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 835 bases

(B) TYPE: Nucleic acid

20 (C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

## 25 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Enterococcus saccharolyticus*

(B) STRAIN: ATCC 43076

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 71

30	CGGCGCGATC	TTAGTAGTAT	CTGCTGCTGA	TGGTCCTATG	CCTCAAACCTC	50
	GTGAACACAT	CTTGTTATCT	CGTAACGTAG	GTGTTCCCTTA	CATCGTTGTA	100
	TTCTTAAACA	AAATGGATAT	GGTTGATGAC	GAAGAATTAT	TAGAATTAGT	150
	AGAAATGGAA	GTTTCGTGACT	TATTATCAGA	ATACGATTTC	CCAGGCGATG	200
35	ACACTCCAGT	TATTGCAGGT	TCTGCTTTGA	AAGCTTTAGA	AGGCGATCCA	250
	GTTTACGAAG	AAAAAATCTT	CGAATTAATG	GCTGCAGTTG	ACGAATATAT	300
	CCCAACTCCA	GAACGTGATA	CTGAAAAACC	ATTCATGATG	CCAGTTGAGG	350
	ATGTATTCTC	AATCACTGGT	CGTGGTACTG	TTGCTACAGG	TCGTGTTGAA	400
	CGTGGACAAG	TTCGCGTTGG	TGACGTTGTA	GAAATCGTTG	GTATCGACGA	450
40	AGAAACAGCT	CAAACACTG	TAACAGGTGT	TGAAATGTTC	CGTAAATTAT	500
	TAGACTACGC	TGAAGCAGGC	GATAACATCG	GTGCTTTTATT	ACGTGGGGTT	550
	GCTCGTGAAG	ACATCCAACG	TGGACAAGTA	TTAGCTAAAC	CAGGAACAAT	600
	CACTCCTCAT	ACAAAATTCG	TAGCTGAAGT	TTACGTTTTA	ACTAAAGAAG	650
	AAGGTGGACG	TCATACTCCA	TTCTTCACTA	ACTACCGTCC	TCAATTCTAC	700
45	TTCCGTACAA	CTGACGTAAC	TGGTGTGTA	GAATTACGCG	AAGGTACTGA	750
	AATGGTAATG	CCTGGTGACA	ACGTAACAT	CGACGTTGAA	TTAATCCACC	800
	CAATCGCTAT	CGAAGACGGA	ACTCGTTTCT	CTATT		835

50

## 2) INFORMATION FOR SEQ ID NO: 72

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 823 bases

55 (B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

60

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus solitarius*  
 (B) STRAIN: ATCC 49428

## 5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 72

	GAGCTATCTT	GGTAGTTTCT	GCAGCTGATG	GCCCAATGCC	ACAAACTCGT	50
	GAACATATTT	TGTTGTCACG	TAATGTAGGT	GTACCTTACA	TCGTTGTGTT	100
	CTTGAACAAA	ATGGATATGG	TTGATGACGA	AGAATTACTT	GAGTTAGTTG	150
10	AAATGGAAGT	ACGTGATCTA	TTATCTGAAT	ACGACTTCCC	AGGAGATGAT	200
	ACTCCAGTTA	TTTCCGGTTC	AGCTTTGAAA	GCTTTAGAAG	GCGACGAAGA	250
	ATATGAACAA	AAAATTATGG	ACTTAATGGA	TGCAGTTGAT	GACTACATTC	300
	CAACTCCTGA	ACGTGACCAT	GACAAACCAT	TCATGATGCC	AATTGAAGAT	350
	GTATTTTCAA	TTACAGGCCG	TGGTACTGTT	GCTACAGGAC	GTGTTGAACG	400
15	CGGGACTATC	AAAGTCGGCG	ATGAAGTTGA	CATTATTGGT	ATTCATGAAG	450
	ACGTTAAAAA	GACAACAGTT	ACTGGTGTAG	AAATGTTCCG	TAAATTGTTG	500
	GACTACGCTG	AAGCAGGCGA	TAACATTGGT	ACTTTGTTAC	GTGGTGTTC	550
	TCGTGATGAT	ATCGAACGTG	GTCAGTATT	AGCTAAACCA	GGTTCATCA	600
	CACCACATAC	AAGATTCTCT	GCTGAAGTTT	ATGTTTTGAC	TAAAGAAGAA	650
20	GGCGGACGTC	ATACTCCATT	CTTCTCAAAC	TATCGTCCTC	AATTCTACTT	700
	CCGTACAAC	GATATCACTG	GTGTCATTGA	ATTGCCAGAA	GGTACTGAAA	750
	TGGTAATGCC	AGGTGATAAT	GTAACAATGG	ATGTTGAATT	AATCCACCCA	800
	GTGCTATCG	AAGAAGGAAC	TCG			823

25

## 2) INFORMATION FOR SEQ ID NO: 73

## (i) SEQUENCE CHARACTERISTICS:

- 30 (A) LENGTH: 835 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

## 35 (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus casseliflavus*  
 (B) STRAIN: ATCC 25788

40

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 73

	CGGTGCAATC	TTGGTCGTAT	CAGCGACAGA	TGGCCCAATG	CCACAAACAC	50
	GGGAGCATAT	TTTGCTTTCT	CGTCAAGTGG	GTGTGAAACA	TTTGATCGTC	100
45	TTTTTGAATA	AGACGGACCT	TGTCGATGAT	GACGAGTTGA	TCGATTTAGT	150
	TGAAATGGAA	GTCAGAGAA	TGCTGACTGA	ATATGATTTT	CCTGGCGACG	200
	ACATTCCTGT	GATCAAGGGC	TCTGCGTTAA	AAGCCTTGGA	AGGGGACCCA	250
	GATGCTGAAG	CAGCGATCTT	AACGCTGATG	GATACAGTAG	ATGAATATAT	300
	CCCAACGCCA	GAACGTGATA	CTGACAAACC	ATTGTTGTTA	CCGATCGAAG	350
50	ATGTCTTTTC	GATCACAGGA	CGGGGGACCG	TTGCTTCTGG	TCGGATCGAT	400
	CGCGGCATGG	TAAAAGTCGG	GGATGAAGTA	GAAATCGTCG	GAATCAAACC	450
	TGAAACACAA	AAAGCAGTCG	TGACAGGGGT	AGAAATGTTT	CGCAAAACGA	500
	TGGACTTCCG	AGAAGCTGGC	GATAACGTAG	GGGTATTGTT	ACGGGGCATC	550
	ACCCGTGATG	AAATTGAACG	TGGCCAAGTG	TTAGCAAAAC	CAGGTTCTAT	600
55	CACACCGCAT	ACGAAATTCC	AAGCGGAAGT	CTATGTGTTG	ACAAAAGAAG	650
	AAGGCGGTCG	CCATACCCCA	TTCTTTAATA	ATTATCGCCC	ACAATTTTAC	700
	TTCCGTACAA	CGGACGTAAC	TGGGAATATC	GTTTTACCAG	AAGGAACGGA	750
	AATGGTGATG	CCTGGTGACA	ACGTAACGAT	CGATGTGAA	TTGATCCATC	800
60	CGATCGCTGT	AGAAAATGGA	ACGACCTTCT	CGATT		835

## 2) INFORMATION FOR SEQ ID NO: 74

## 5 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 380 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

10

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus saprophyticus*  
 (B) STRAIN: ATCC 15305

15

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 74

	TAACGGGCGT	CTCGATAGAA	AAACACGTGA	AAATCCCAAT	GATTATAAAC	50
20	AATCAATATA	CGATTTTGCT	GAAGCTGTAA	CAAAAGGTAT	TAAGGAACAA	100
	ACAAATAAAA	ATTAATAGGC	AACTTAACCA	GAATCGTTAA	AACTATATGA	150
	AGATTCTGGT	TTTTTAAATT	CAAAAAGTTT	TCTAAAAAAT	TTACTTGCTT	200
	TTTTAAGTAT	AGGTATAAAA	TACGATTGAT	TAAAACAGTA	AAGGAAATGA	250
	ATCATGAAAC	AATTAACTAA	GCCTTTATAC	TTTACCTAT	TACTTTTAT	300
25	TACAACAACG	CTGATTGGCG	CGTTACTATT	ATATTTGCCA	ATCACAGGTA	350
	AACATCCTAT	TGATTTTGTG	GACGCCCGTT			380

## 30 2) INFORMATION FOR SEQ ID NO: 75

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 666 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

35

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus flavescens*  
 (B) STRAIN: ATCC 49996

40

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 75

45	GCAATCTTGG	TCGTATCAGC	GACAGATGGC	CCAATGCCAC	AAACACGGGA	50
	GCATATTTTG	CTTTCTCGTC	AAGTGGGTGT	GAAACATTTG	ATCGTCTTTT	100
	TGAATAAGAC	GGACCTTGTC	GATGATGACG	AGTTGATCGA	TTTAGTTGAA	150
	ATGGAAGTCA	GAGAATTGCT	GACTGAATAT	GATTTTCCTG	GCGACGACAT	200
50	TCCTGTGATC	AAGGGCTCTG	CGTTAAAAGC	CTTGGAAGGG	GACCCAGATG	250
	CTGAAGCAGC	GATCTTAACG	CTGATGGATA	CGGTAGATGA	ATATATCCCA	300
	ACGCCAGAAC	GTGATACTGA	CAAACCATTG	TTGTTACCGA	TCGAAGATGT	350
	CTTTTCGATC	ACAGGACGGG	GGACCGTTGC	TTCTGGTCGG	ATCGATCGCG	400
	GCATGGTAAA	AGTCGGGGAT	GAAGTAGAAA	TCGTCCGAAT	CAAACCTGAA	450
55	ACACAAAAAG	CAGTCGTGAC	AGGGGTAGAA	ATGTTCCGCA	AAACGATGGA	500
	CTTCGGAGAA	GCTGGCGATA	ACGTAGGGGT	ATTGTTACGG	GGCATCACCC	550
	GTGATGAAAT	TGAACGTGGC	CAAGTGTTAG	CAAAACCAGG	TTCTATCACA	600
	CCGCATACGA	AATTCCAAGC	GGAAGTCTAT	GTGTTGACAA	AAGAAGAAGG	650
60	CGGTCGCCAT	ACCCCA				666

## 2) INFORMATION FOR SEQ ID NO: 76

- 5 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 751 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear
- 10 (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: *Enterococcus gallinarum*  
 15 (B) STRAIN: ATCC 49573

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 76

	TGGTGC	GATT	TTAGTT	GTAT	CCGCAAC	AAGA	TGGTCC	AATG	CCTCAA	AACCC	50
20	GGGAAC	ATAT	CTTGCT	TTCG	AGACAAG	TTG	GTGTGA	AAACA	TCTGAT	TGTT	100
	TTCTTG	AACA	AAATCG	ATTT	AGTCGAT	GAC	GAAGAAT	TGA	TTGATT	TAGT	150
	AGAAAT	TGGAA	GTAAGA	GAAC	TGCTAT	CTGA	ATATAAT	TTTT	CCAGGG	GATG	200
	ACATTC	CCTGT	TATCAA	AGGT	TCGGC	ATTAA	AAGCGT	TGGA	AGGAG	ACCCT	250
	GATGC	AAG	CTGCC	ATCAT	GGAATTA	ATG	GATAC	AGTAG	ACAGC	TATAT	300
25	CCCAAC	CACCT	GAGCGT	GATA	CAGACAA	AACC	ATTACT	CTTG	CCAGTT	GAA	350
	ATGTCT	TTTTC	GATTACT	TGGA	CGAGGA	AACAG	TTGCTT	CCGG	ACGGAT	CGAT	400
	CGGGGA	AACAG	TTCGGG	TAGG	CGATGA	AGTA	GAAATC	GTCTG	GTATCA	AACC	450
	TGAAAC	CCCAA	AAAGCT	GTAG	TGACAG	GCGT	CGAAAT	GTTC	CGCAAG	ACGA	500
	TGGACT	TTTGG	GGAAGC	CGGT	GACAAT	GTAG	GTGTCT	TGCT	GAGAGG	GATC	550
30	ACTCGT	GACG	AAATTG	AACG	AGGACA	AGTG	TTGGCT	TAAAC	CAGGTT	CGAT	600
	CACACC	CACAT	ACAAA	ATTCC	AAGCAG	AAGT	TTATGT	TATTG	ACGAA	AGAAG	650
	AAGGTG	GTCG	TCATAC	ACCA	TTCTT	CAACA	ACTATC	GTCC	ACAAT	TTTAT	700
	TTCCGT	TACAA	CGGATG	TGAC	AGGGA	AACATT	ACATTG	CCTG	AAGGA	ACAGA	750
35	A										751

## 2) INFORMATION FOR SEQ ID NO: 77

- 40 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 834 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 45 (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: *Ehrlichia canis*  
 50 (B) STRAIN: Florida

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 77

	TGCAGC	AATA	TTAGTAG	TGT	CTGCAAC	TGA	TGGAGC	AATG	CCACAA	AACAA	50
55	GAGAAC	ATAT	ATTATT	AGCA	AAGCAAG	TAG	GTGTAAA	AGA	TATAGT	AGTG	100
	TGGATG	AATA	AGTGTG	ATGT	TGTAGAT	GAT	GAAGAA	ATGT	TGTCAT	TAGT	150
	TGAAAT	TGGAA	ATAAGG	GAAT	TGTTAT	CAAA	ATATGG	GTAT	CCTGGG	GATG	200
	ATATAG	ATGT	AGTTAG	AGGA	TCTGC	AGTTA	AAGCATT	AGA	AGAAG	AAACA	250
	GGCTC	AGGTG	TGTGG	AGTGA	AAAAATA	AATG	GAATTG	ATGA	ATGCTT	TAGA	300
60	AAAAAT	AAGT	TTACC	AGTAA	GAGAAA	AGA	TAAGCC	ATT	TTAATG	TCAA	350



	TAGAAGATGT	GTTTTCAATA	CCTGGAAGAG	GTACAGTAGT	AACAGGAAGA	400
	ATAGAAAGAG	GAGTAATTAG	AGTAGGGGAT	AAAATAGAGA	TAGTAGGATT	450
	GCGTGAGATA	CAAAGTACAG	TATGTACAGG	TGTTGAAATG	TTTCATAAAG	500
	CATTAGATGC	AGGAGAAGCA	GGGGATAATG	CTGGAATATT	GTTAAGAGGG	550
5	ATAAAAAAAG	AAGATGTAGA	AAGAGGGGCAA	GTATTGAGTG	CACCTGGACA	600
	GATACATTCA	TATAAGAGAT	TTAAGGCAGA	GGTATATATA	TTGAAAAAAG	650
	AAGAAGGAGG	AAGACATACT	CCATTTTTCT	CAAATTACCA	GCCGCAATTT	700
	TATGTTAGAA	CAACAGATGT	AACAGGGAAT	ATAAAGTTAC	CAGAAGGAGT	750
	AGAAATGGTA	ATGCCAGGGG	ATAATATAAA	TATCGAAGTG	AGTTTGGATA	800
10	AGCCTGTTGC	TATTGATCAA	GGATTGAGAT	TTGC		834

## 2) INFORMATION FOR SEQ ID NO: 78

15

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 817 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 20 (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- 25 (A) ORGANISM: *Escherichia coli*  
 (B) STRAIN: ATCC 23511

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 78

30	CGGCGCGATC	CTGGTAGTTG	CTGCGACTGA	CGGCCCGATG	CCGCAGACTC	50
	GTGAGCACAT	CCTGCTGGGT	CGTCAGGTAG	GCGTTCCGTA	CATCATCGTG	100
	TTCCTGAACA	AATGCGACAT	GGTTGATGAC	GAAGAGCTGC	TGGAAGCTGGT	150
	TGAAATGGAA	GTTCGTGAAC	TTCTGTCTCA	GTACGACTTC	CCGGGCGACG	200
	ACACTCCGAT	CGTTCGTGGT	TCTGCTCTGA	AAGCGCTGGA	AGGCGACGCA	250
35	GAGTGGGAAG	CGAAAATCCT	GGAAGTGGCT	GGCTTCTCTG	ATTCTTAYAT	300
	TCCGGAACCA	GAGCGTGCGA	TTGACAAGCC	GTTCTCTGCT	CCGATCGAAG	350
	ACGTATTCTC	CATCTCCGGT	CGTGGTACCG	TTGTTACCGG	TCGTGTAGAA	400
	CGCGGTATCA	TCAAAGTTGG	TGAAGAAGTT	GAAATCGTTG	GTATCAAAGA	450
	GAATCAGAAG	TCTACCTGTA	CTGGCGTTGA	AATGTTCCGC	AAACTGCTGG	500
40	ACGAAGGCCG	TGCTGGTGAG	AACGTAGGTG	TTCTGCTGCG	TGGTATCAAA	550
	CGTGAAGAAA	TCGAACGTGG	TCAGGTACTG	GCTAAGCCGG	GCACCATCAA	600
	GCCGCACACC	AAGTTCGAAT	CTGAAGTGTA	CATTCTGTCC	AAAGATGAAG	650
	GCGGCCGTCA	TACTCCGTTT	TTCAAAGGCT	ACCGTCCGCA	GTTCTACTTC	700
	CGTACTACTG	ACGTGACTGG	TACCATCGAA	CTGCCGGAAG	GCGTAGAGAT	750
45	GGTAATGCCG	GGCGACAACA	TCAAATGGT	TGTTACCCTG	ATCCACCCGA	800
	TCGCGATGGA	CGACGGT				817

## 50 2) INFORMATION FOR SEQ ID NO: 79

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 825 bases  
 (B) TYPE: Nucleic acid  
 55 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

## 60 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Escherichia fergusonii*  
 (B) STRAIN: ATCC 35469

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 79

5  
 CGATCCTGGT AGTTGCTGCG ACTGACGGCC CGATGCCGCA GACTCGTGAG 50  
 CACATCCTGC TGGGTCGTCA GGTAGGCGTT CCGTACATCA TCGTGTTCCT 100  
 GAACAAGTGC GACATGGTTG ATGACGAAGA GCTGCTGGAA CTGGTTGAAA 150  
 TGGAAGTTCG TGAACCTCTG TCTCAGTACG ACTTCCCGGG CGACGACACT 200  
 10 CCGATCGTTC GTGGTTCTGC TCTGAAAGCG CTGGAAGGCG ACGCAGAGTG 250  
 GGAAGCGAAA ATCCTGGAAC TGGCTGGCTT CCTGGATTCT TACATTCCGG 300  
 AACCAGAGCG TGCGATTGAC AAGCCGTTCC TGCTGCCGAT CGAAGACGTG 350  
 TTCTCCATCT CCGGTCGTGG TACCGTTGTT ACCGGTCGTG TAGAACGCGG 400  
 TATCATCAAA GTTGGTGAAG AAGTTGAAAT CGTTGCTATC AAAGAGACTC 450  
 15 AGAAGTCTAC CTGTACTGGC GTTGAAATGT FCCGCAAAC TCTGGACGAA 500  
 GGCCGTGCTG GTGAGAACGT AGGTGTTCTG CTGCGTGGTA TCAAACGTGA 550  
 AGAAATCGAA CGTGGTCAGG TACTGGCTAA GCCGGGCACC ATCAAGCCGC 600  
 ACACCAAGTT CGAATCTGAA GTGTACATTC TGTCCAAAGA TGAAGGCGGT 650  
 CGTCATACTC CGTTCTTCAA AGGCTACCGT CCGCAGTTCT ACTTCCGTAC 700  
 20 TACTGACGTG ACTGGTACCA TCGAACTGCC GGAAGGCGTA GAGATGGTAA 750  
 TGCCGGGCGA CAACATCAAA ATGGTTGTGA CCCTGATCCA CCCGATCGCG 800  
 ATGGACGACG GTCTGCGTTT CGCAA 825

25  
 2) INFORMATION FOR SEQ ID NO: 80

## (i) SEQUENCE CHARACTERISTICS:

30 (A) LENGTH: 829 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

35 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Escherichia hermannii*  
 (B) STRAIN: ATCC 33650

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 80

GGCGCGATCC TGGTTGTTGC TGCGACTGAC GGCCCGATGC CGCAGACCCG 50  
 TGAGCACATC CTGCTGGGTC GTCAGGTAGG CGTTCCGTAC ATCATCGTGT 100  
 TCCTGAACAA ATGCGACATG GTTGATGACG AAGAGCTGCT GGAAGTGGTT 150  
 45 GAGATGGAAG TTCGCGAACT GCTGTCCCAG TACGATTTCC CGGGCGACGA 200  
 CACCCCGATC GTTCGTGGTT CCGCGCTGAA AGCGCTGGAA GGCGAAGCAG 250  
 AGTGGGAAGA GAAAATCATC GAACCTGGCTG GCTACCTGGA TTCCTATATC 300  
 CCGGAACCAG AGCGTGCGAT TGACAAGCCG TTCTTGCTGC CTATCGAAGA 350  
 CGTATTCTCC ATCTCCGGCC GTGGTACCGT TGTTACCGGT CGTGTAGAGC 400  
 50 GCGGTATCAT CAAAGTGGGT GAAGAAGTTG AAATCGTGGG TATCAAAGAT 450  
 ACTGCGAAAT CAACCTGTAC CGGCGTTGAA ATGTTCCGCA AACTGCTGGA 500  
 CGAAGGCCGT GCGGGCGAGA ACGTGGGTGT TCTGCTGCGT GGTATCAAAC 550  
 GTGAAGAAAT CGAACGTGGT CAGGTACTGG CTAAGCCGGG TTCCATCAAG 600  
 CCKCACACCA AGTTCGAATC TGAAGTGATC ATTCTGTCCA AAGACGAAGG 650  
 55 CGGCCGTCAC ACTCCGTTCT TCAAAGGCTA CCGTCCGCAG TTCTACTTCC 700  
 GTACAATGTA CGTGAATGCG ACCATCGAAC TGCCGGAAGG CGTTGAGATG 750  
 GTAATGCCGG GCGACAACAT CAAAATGGTT GTTACCCTGA TCCACCCGAT 800  
 CGCGATGGAC GACGGTCTGC GTTTCGCAA 829

60

## 2) INFORMATION FOR SEQ ID NO: 81

## (i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 816 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

## 10 (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Escherichia vulneris*  
 (B) STRAIN: ATCC 33821

15

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 81

CGGCGCGATC CTGGTTGTTG CTGCGACTGA CGGCCCCGATG CCGCAGACCC 50  
 GTGAGCACAT CCTGCTGGGT CGTCAGGTAG GCGTTCCGTA CATCATCGTG 100  
 20 TTCCTGAACA AATGCGACAT GGTTGATGAC GAAGAGCTGC TGGAAGTGGT 150  
 TGAGATGGAA GTGCGTGAAC TTCTGTCCCA GTACGACTTC CCGGGCGACG 200  
 ACACCCCGAT CATTCTGGT TCTGCGCTGA AAGCGCTGGA AGGCGAAGCT 250  
 GAGTGGGAAG AGAAAATCGT TGAGCTGGCT GGCTACCTGG ATTCCTACAT 300  
 CCCGGAACCA GAGCGTGCGA TTGACAAGCC GTTCCTGCTG CCGATCGAAG 350  
 25 ACGTATTCTC CATCTCCGGT CGTGGTACCG TTGTTACCGG TCGTGTAGAG 400  
 CGCGGTATCA TCAARGTKGG TGAAGAAGTT GAAATCGTGG GTATCAAAGA 450  
 TACTGCGAAA TCTACCTGTA CCGGCGTTGA AATGTTCCGC AAAGTCTGG 500  
 ACGAAGGTCG TGCAGGCGAG AACTGCGGCG TTCTGCTGCG TGGTATCAAG 550  
 CGTGAAGAGA TCCAGCGTGG CCAGGTTCTG GCTAAGCCGG GCTCAATCAA 600  
 30 GCCGCACACC AAGTTCGAAT CCGAAGTGTA CATCCTGTCC AAAGACGAAG 650  
 GCGGCCGTCA CACTCCGTTT TTCAAAGGCT ACCGTCCGCA GTTCTACTTC 700  
 CGTACAACTG ACGTGACTGG CACCATCGAA CTGCCGGAAG GCGTAGAGAT 750  
 GGTAATGCCG GGCGACAACA TCAAATGGT TGTTACCCTG ATCCATCCGA 800  
 TCGCGATGGA CGACGG 816

35

## 2) INFORMATION FOR SEQ ID NO: 82

## (i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 828 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

45

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Eubacterium lentum*  
 50 (B) STRAIN: ATCC 43055

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 82

CGGCGCCTCC TCGTTATCGC CGCCACCGAC GGCCCGATGG CCCAGACCCG 50  
 55 CGAGCACATC CTGCTCGCCC GTCAGGTCGG CGTGCCCTAC ATCGTGGTCT 100  
 TCCTGAACAA GTGCGACATG GTCGACGACG AGGAGCTCCT CGAGCTCGTC 150  
 GAGATGGAAG TTCGCGAGCT GCTCGACTCT TACGAGTTCC CCGGCGACGA 200  
 CACCCCGATC ATCCGCGGCT CCGCTTTGAA GGCCCTCGAG GCGCACAAAG 250  
 AGTGGCAGGA GAAGGTCTGG GAGCTCATGG ACGCCGTCGA CTCCTACATC 300  
 60 CCGACGCCGG AGCGCATGGT CGACAAGCCG TTCCTGATGG CCGTCGAGGA 350

50

	CACGATGACC	ATCACCGGCC	GCGGCACCGT	TGCCACCGGT	CGTGTGGAGC	400
	GTGGTACGCT	GCATGTCAAC	GACCCGCTGG	AGATCGTCGG	TATCAAGGAG	450
	ACCCAGAACA	CGGTCTGCAC	CGGTATCGAG	ATGTTCCGCA	AGCTGCTCGA	500
	CGAGGCTCAG	GCCGGCGACA	ACATCGGCTG	CCTGCTCCGC	GGTGTCAAGC	550
5	GCGAGGAGAT	CGTTCGCGGC	CAGGTTCTCT	GCAAGCCCGG	TAGCGTGACC	600
	CCGCACACCG	AGTTCGAGGG	TCAGGTCTAC	ATCCTGACGA	AGGAAGAGGG	650
	CGGCCGCCAC	ACGCCGTTCT	TCGACGGCTA	CCGTCCGCAG	TTCTACTTCC	700
	GCACGACGGA	CGTGACGGGT	GTTGCCACAC	TTCCCGAGGG	CACCGAGATG	750
	GTCATGCCGG	GCGACAACGT	GGAGATCAAG	GGCGAGCTCA	TTCACCCGAT	800
10	CGCCAGGAAG	AGGGCTGCGT	TCGCTAAC			828

## 2) INFORMATION FOR SEQ ID NO: 83

15

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 835 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 20 (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- 25 (A) ORGANISM: *Eubacterium nodatum*  
 (B) STRAIN: ATCC 33099

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 83

30	GGAGCAATTC	TGGTTTGTGC	AGCAACKGAC	GGACCAATGC	CTCAGACAAG	50
	AGAACATATC	CTTTTGTCAA	GGCAGGTAGG	AGTGCCATAT	ATCATCGTAT	100
	TCCTGAATAA	ATGTGACATG	GTGGATGAYG	AAGAGCTTCT	GGACTTGGTA	150
	GAGATGGAAG	TAAGAGAACT	TCTCAGTGAG	TATGAATTCC	CGGGAGATGA	200
	TACCCCGATA	GTAAGAGGTT	CAGCCCTGAA	GGCACTGGAA	GAACCCCAATG	250
35	GAGAATGGGC	AGACAAGATT	GTAGAGCTGA	TGGAGGAAGT	AGATAAATAC	300
	ATTCTTGAAC	CAAAGAGAGA	TAACGACAAA	CCGTTCTCTGA	TGCCTGTAGA	350
	GGACGTATTC	TCAATAACAG	GAAGAGGAAC	AGTAGCGACA	GGAAGRGTTC	400
	AAAGAGGAAT	CCTGAAGGTC	GGTGATGAAG	TAGAAATCGT	GGGAATGAGC	450
	GAAGAGAGAA	GAAAGGTAGT	AGTAACGGGA	GTTGAAATGT	TCAGAAAGCT	500
40	TCTGGATGAA	GCAGAGACAG	GAGACAACAT	CGGAGCACTG	CTGAGAGGAG	550
	TTCAGAGAAC	RGAGATCCAG	AGAGGTCAGG	TATTGGCRGC	ACCTGGAACG	600
	ATCAACCCAC	ATACAAAGTT	CAAGGGTCAG	GTATATGTAC	TGAAGAAGGA	650
	AGAAGGAGGA	AGGCATACGC	CGTTCTTCAA	YGGATACAGW	CCACAGTTCT	700
	ACTTCAGAAC	AACAGACGTA	ACAGGAGATT	TGCAGCTGCC	GGAAGGARCA	750
45	GAGATGTGCA	TGCCGGGAGA	TAATGTGGTA	ATGAACRTCA	GCCTGATCAC	800
	TCCGATTGCT	ATAGAAGAGG	GWCTGAGATT	TGCCA		835

## 50 2) INFORMATION FOR SEQ ID NO: 84

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 826 bases  
 (B) TYPE: Nucleic acid  
 55 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

## 60 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Ewingella americana*  
 (B) STRAIN: ATCC 33852

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 84

5  
 GCGATCCTGG TTGTTGCTGC AACTGATGGC CCTATGCCAC AGACTCGTGA 50  
 GCACATCCTG TTGGGTCGYC AGGTTGGCGT TCCATTCATG ATCGTATTCA 100  
 TGAACAAATG CGACATGGTT GATGACGAAG AGCTGCTGGA ACTGGTAGAA 150  
 ATGGAAGTTC GYGAACCTCT GTCTGCTTAC GATTTCCCAG GCGACGACAT 200  
 10 CCCAGTTGTT AAAGGTTTCAG CGCTGAAAGC ACTGGAAGGC GAAGCAGAGT 250  
 GGGAAGCTAA GATCATCGAG CTGGCTGGCC ACCTGGATAG CTACATCCCA 300  
 GAACCAGAGC GTGCGATTGA CAAGCCATTC CTGCTGCCAA TCGAAGACGT 350  
 ATTCTCCATC TCCGGTCGTG GTACCGTTGT TACCGGTCGT GTAGAGCGCG 400  
 GTATCATCAA AGTTGGCGAA GAAGTTGAAA TCGTTGGTAT CAAGGACACT 450  
 15 GTTAAGTCTA CTTGTACTGG CGTTGAAATG TTCCGCAAAC TGCTGGACGA 500  
 AGGCCGTGCY GGTGAGAACG TTGGTGTTCT GCTGCGTGGT ATCAAGCGTG 550  
 AAGACATCGA ACGTGGTCAG GTTCTGGCTA AACCAGGTTT AATCAAACCA 600  
 CACACCACWT TYGACTCAGA AGTTTATATC CTGAGCAAAG ATGAAGGCGG 650  
 CCGTCATACT CCGTTCTTCA AAGGCTACCG TCCACAGTTC TACTTCCGTA 700  
 20 CAACTGACGT GACCGGTACC ATCGAAGTGC CAGAAGGCGT AGAGATGGTA 750  
 ATGCCAGGTG ACAACATCAA CATGRTAGTT ACCCTGATCC ACCCAATCGC 800  
 GATGGATGAC GGTCTGCGTT TCGCAA 826

25  
 2) INFORMATION FOR SEQ ID NO: 85

## (i) SEQUENCE CHARACTERISTICS:

30 (A) LENGTH: 828 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Francisella tularensis*  
 (B) STRAIN: LVS

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 85

40  
 TGGTGCTATT CTAGTATGTT CTGCTGCGGA TGGTCCTATG CCACAAACTC 50  
 GTGAGCACAT TCTGCTTTCT CGTCAAGTTG GTGTACCAA AATCGTTGTT 100  
 TTCTTAAACA AGTGTGACAT GGTGTGATGAT GAAGAGTTAT TAGAGCTAGT 150  
 45 TGAGATGGAA GTTCGTGAGC TTTTAGATCA GTATGAGTTC CCAGGTGATG 200  
 AACTCCAGT TATTATGGGT TCAGCTCTTA GAGCTATTGA AGGTGACGAA 250  
 GCTTACGTTG AGAAAATTGT TGAGCTAGTT CAAGCTATGG ATGACTATAT 300  
 TCCTGCTCCT GAGCGTGATA CTGAGAAGCC ATTTATTCTT CCGATCGAAG 350  
 ATGTATTCTC AATTTTCAGGT CGTGGTACTG TTGTAAGTGG TCGTATTGAG 400  
 50 CGCGGTGTAG TTAACGTTGG TGATGAAGTT GAAGTTGTTG GTATTTCGTC 450  
 AACTCAAAA ACTACAGTAA CTGGTGTGGA AATGTTCCGT AAGCTTTTAG 500  
 ATAGAGGGGA AGCTGGTGAT AACGTTGGTA TCCTAGTTTC TGGACTTAAG 550  
 AGAGATGATG TTGAGCGTGG ACAAGTATTA TGTAAGCCAG GTTCAATTAA 600  
 GCCACATACT AAGTTTGAAG CTGAGGTTTA TGTATTATCT AAAGAAGAGG 650  
 55 GTGGTAGACA TACTCCATTC TTCAAGGGAT ATAGACCACA ATTCTACTTC 700  
 CGTACTACAG ACATTACTGG AGCTGTTGAG CTTCCAGAGG GTGTAGAAAT 750  
 GGTATGCCT GGTGATAACG TTAAGATGAC TATCACTCTA ATTAACCCAA 800  
 TCGCTAGGAT GAAGGGTTAC GTTTTGCA 828

60

## 2) INFORMATION FOR SEQ ID NO: 86

## (i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 829 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

## 10 (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Fusobacterium nucleatum* subsp. *polymorphum*  
 (B) STRAIN: ATCC 10953

15

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 86

CGGTGCTATC ATCGTAGKTG CTGCTACTGA TGGTCCGATG CCTCARACTC 50  
 GTGAGCAYAT CYTGCTGGCT CGTCAGGTAA ACGTWCKKAG ACTGGTTGTA 100  
 20 TTCATGAACA AGTGYGACAT GGTAGACGAC GCTGAAATGY TGGAATCGT 150  
 TGAAATGGAA ATGCGTGAAC TGCTTTCAGC YTACGAATTC GAYGGYGACA 200  
 AACTCCKTT CATTGAGGGT TCTGCTCTTG GTGCRITGAA YGGCGTTGAA 250  
 AAGTGGGAAG AGAAGGTTAT GGANCTGATG GATGCTTGCG AACTTTGGAT 300  
 TCCTTTGCCT CCGCGTGATA TTGAYAAACC GTTCTTGATG CCGGTTGAAG 350  
 25 ACGTATTCTC AATCACTGGT CGTGGTACTG TAGCTACTGG TCGTATCGAA 400  
 GCTGGTGTTA TCCATGTAGG TGACGAAGTT GAAATCCTCG GTTGGGTGA 450  
 AGACAAGAAG TCTGTTGTAA CTGGTGTGTA AATGTTCCGC AAGTTGCTGG 500  
 ATCAAGGTGA AGCTGGTGAC AACGTAGGTY TGTGCTCCG TGGTATCGAC 550  
 AAGAACGAAA TCAAACGTGG TATGGTTCTT TGTAAGCCCG GTCAGATTAA 600  
 30 ACCTCACTCT AAGTTCAAAG CTTCTATCTA CGTTTGAAG AAAGAAGAAG 650  
 GTGGTCGTCA CACTCCGTTT CACAACAAAT ACCGTCCTCA GTTCTATCTG 700  
 CGTACTATGG ACTGTACAGG TGAAATCWCT CTTCCGGAAG GAACTGAAAT 750  
 GGTAAATGCCT GGTGATAACG TAGAAATCAC TGTAGAACTG ATCTACCCGG 800  
 TAGCATTGAA CGTAGGTTTG CGTTTCGCT 829

35

## 2) INFORMATION FOR SEQ ID NO: 87

## (i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 828 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 45 (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- 50 (A) ORGANISM: *Gemella haemolysans*  
 (B) STRAIN: ATCC 10379

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 87

CTATCTTAGT AATCGCTGCT ACAGATGGAC CAATGGCTCA AACTCGTGAG 50  
 55 CACATCCTAT TATCTCGTAA CGTTGGAGTA CCAAAAATCG TTGTATTCTT 100  
 AAACAAATGT GATATGGTTG ATGACGAAGA GTTATTAGAA TTAGTTGAAA 150  
 TGGAAGTTCG TGAACATTA TCTGAATACG GATTCGACGG AGATGAACTA 200  
 CCAGTAATCA AAGGTTCTGC TCTTAAAGCT CTTGAAGGAG ATGCAGATGC 250  
 AGAAAAAGCT ATCATCGAAT TAATGGAAC AGTTGACGAA TACATCCCAA 300  
 60 CTCCAGAACG TGATAACGCT AAACCATTCA TGATGCCAGT TGAGGACGTA 350

	TTCTCAATCA	CAGGTCGTGG	TACAGTTGCT	ACTGGACGTG	TTGAACGTGG	400
	ACAAGTTAAA	GTTGGAGACG	TAGTAGAAAT	CGTTGGATTA	ACTGAAGAAC	450
	CAGCTTCAAC	TACTGTAAAC	GGTGTTGAAA	TGTTCCGTAA	ATTATTAGAT	500
	TACGCTGAAG	CAGGAGATAA	CATCGGTGCA	TTATTACGTG	GTGTTGCTCG	550
5	TGAAGACATC	GAACGTGGAC	AAGTTTTAGC	AGCTCCTAAA	ACAATCACTC	600
	CACACACTCA	ATTCGTAGCT	GACGTGTACG	TATTATCTAA	AGAAGAAGGT	650
	GGACGTCACA	CTCCATTCTT	CACAACTAC	CGTCCTCAAT	TCTACTTCCG	700
	TACTACTGAC	GTAAC TGGTG	TAGTTACTTT	ACCAGAAGGT	ACTGAAATGG	750
	TAATGCCTGG	GGATAACGTA	TCAATCAACG	TAGAACTTAT	TTCTCCAATC	800
10	GCGATCGAAG	AAGGAAC TCG	TTTCTCAA			828

## 2) INFORMATION FOR SEQ ID NO: 88

15

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 823 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

20

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Gemella morbillorum*  
 (B) STRAIN: ATCC 27824

25

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 88

30	TCTTAGTAAT	CGCTGCTACA	GATGGTCCTA	TGGCTCAAAC	TCGTGAACAC	50
	ATCCTATTAT	CTCGTAACGT	TGGAGTACCT	AAAATTGTTG	TATTCTTAAA	100
	CAAATGTGAT	ATGGTTGATG	ACGAAGAGTT	ATTAGAATTA	GTAAGAAATGG	150
	AAGTTCGTGA	ACTATTATCT	GAATACGGAT	TTGATGGAGA	TGAACTACCA	200
	GTAATCAAAG	GTTCAGCTCT	TAAAGCTCTT	GAAGGAGATG	CAGATGCTGA	250
35	AAAAGCTATC	ATCGAATTAA	TGGAAACAGT	TGACGAGTAC	ATCCCAACTC	300
	CAGAACGTGA	TAACGCTAAA	CCATTTATGA	TGCCAGTTGA	GGACGTGTTT	350
	TCAATCACAG	GTCGTGGTAC	AGTTGCTACT	GGACGTGTTG	AACGTGGACA	400
	AGTTAAAGTT	GGTGACGTAG	TAGAAATCGT	TGGATTAACT	GAAGAACCAG	450
	CTTCAACTAC	TGTAACAGGT	GTTGAAATGT	TCCGTAAATT	ATTAGATTAC	500
40	GCTGAAGCAG	GAGATAACAT	CGGTGCATTA	TTACGTGGTG	TTGCTCGTGA	550
	AGATATCGAA	CGTGGACAAG	TTTTAGCAGC	TCCTAAAACA	ATCACTCCAC	600
	ATACTCAATT	CGTAGCTGAT	GTGTACGTAT	TATCTAAAGA	AGAAGGTGGA	650
	CGTCACACTC	CATTCTTCAC	AACTACCGT	CCACAATTCT	ACTTCCGTAC	700
	TACTGACGTA	ACTGGTGTAG	TTACTTTACC	AGAAGGTACT	GAAATGGTAA	750
45	TGCCTGGGGA	CAACGTATCA	ATCAACGTAG	AACTTATTTC	TCCAATCGCT	800
	ATCGAAGAAG	GAAC TCGTTT	CTC			823

## 50 2) INFORMATION FOR SEQ ID NO: 89

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 829 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

55

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

60

(A) ORGANISM: *Haemophilus actinomycetemcomitans*  
 (B) STRAIN: ATCC 33384

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 89

```

5      GCTATCTTAG TAGTAGCAGC AACCGACGGT CCTATGCCAC AAACCTCGTGA      50
      GCACATCTTA TTAGGTCGCC AAGTAGGTGT TCCTTACATC ATCGTATTCT      100
      TAAACAAATG CGACATGGTA GATGACGAAG AGTTATTAGA ATTAGTTGAA      150
      ATGGAAGTTC GTGAACTTCT TTCTCAATAT GACTTCCCGG GCGATGACAC      200
10     CCAATCGTA CGCGGTTCTG CATTAAAAGC GCTTGAAGGC GATGCCGCAT      250
      GGAAGAAAAA AATCCTTGAA TTAGCAAACC ATTTAGATAC TTACATCCCG      300
      GAACCTGAGC GTGCTATCGA CCAACCGTTC CTTCTTCCAA TTGAAGATGT      350
      GTTCTCTATC TCCGGTCGTG GTACCGTAGT AACGGGTCGT GTTGAGCGCG      400
      GTATCATCCG TACCGGTGAT GAAGTTGAAA TCGTGGGTAT CAAACCGACT      450
15     GCAAAAACCA CCGTAACCGG TGTGAAAATG TTCCGTAAAT TACTTGACGA      500
      AGGTCGTGCG GGTGAAAACA TCGGTGCATT ATTGCGTGGT ACTAAACGTG      550
      AAGAAATCGA ACGTGGTCAG GTATTGGCGA AACCGGGGTC AATCACCCCG      600
      CACACTGACT TCGAATCTGA AGTGACGTA TTGTCCAAAG AAGAAGGTGG      650
      TCGTCATACT CCATTCTTCA AAGGTTACCG TCCACAATTC TATTTCGGTA      700
20     CAACTGACGT AACCGGTACT ATCGAGTTAC CTGAAGGCGT GGAAATGGTT      750
      ATGCCTGGCG ATAACATCAA AATGACCGTA TCCTTAATTC ACCCAATTGC      800
      GATGGACCAA GGTTTACGTT TCGCTATCG      829
  
```

25 2) INFORMATION FOR SEQ ID NO: 90

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 833 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: *Haemophilus aphrophilus*  
 (B) STRAIN: ATCC 33389

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 90

```

      TGGTGCTATC TTAGTAGTAG CAGCAACTGA TGGTCCTATG CCACAAACTC      50
      GTGAGCACAT CTTATTAGGT CGCCAAGTAG GTGTTCTTCA CATCATCGTA      100
      TTCTTAAACA AATGCGACAT GGTAGATGAC GAAGAGTTAT TAGAATTAGT      150
45     TGAAATGGAA GTTCGTGAAC TTCTTTCTCA ATATGACTTC CCGGTGATG      200
      ATACACCAAT CGTACGTGGT TCTGCATTAC AAGCGTTAAA CGGCGTTGCA      250
      GAATGGGAAG AAAAAATCCT TGAATTAGCA AACCACTTAG ATACTTACAT      300
      TCCTGAGCCA CAACGTGCTA TCGACCAACC GTTCCTTCTT CCAATTGAAG      350
      ACGTGTTCTC TATCTCCGGT CGTGGTACTG TAGTAACAGG TCGTGTTGAG      400
50     CGTGGTATCA TCCGTACCGG TGATGAAGTT GAAATCGTAG GTATCAAACC      450
      GACTGCGAAA ACTACCGTAA CCGGTGTTGA AATGTTCCGT AAATTACTTG      500
      ACGAAGGTCG TGCAGGTGAA AACATCGGTG CATTATTACG TGGCACTAAA      550
      CGTGAAGAAA TCGAACGTGG TCAAGTATTG GCTAAACCGG GCTCAATCAC      600
      TCCGCACACT GATTTCGAAT CTGAAGTGTA CGTATTATCC AAAGAAGAAG      650
55     GTGGTCGTCA TACTCCATTC TTCAAAGGTT ACCGTCCACA ATTCTATTTT      700
      CGTACAACATG ACGTAACCGG TACTATCGAG TTACCGGAAG GCGTGGAAT      750
      GGTATGCCT GGCGATAACA TCAAAATGAC TGTATCCTTA ATCCACCCAA      800
      TCGCGATGGA CCAAGGTTTA CGTTTCGCTA TCG      833
  
```

60



## 2) INFORMATION FOR SEQ ID NO: 91

## (i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 815 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

## 10 (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Haemophilus ducreyi*  
 (B) STRAIN: DSM 8925

## 15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 91

	CGGCGCTATC	TTAGTTGTAG	CAGCAACTGA	TGGTCCTATG	CCTCAAACCTC	50
	GTGAACACAT	CTTATTAGGC	CGCCAAGTTG	GTGTTCCCTTA	CATCATCGTA	100
20	TTCTTAAATA	AATGCGATAT	GGTAGATGAT	GAAGAATTAT	TAGAATTAGT	150
	TGAAATGGAA	GTTCGTGAAC	TTCTTTCTCA	ATATGATTTC	CCAGGTGACG	200
	ATACTCCTAT	CGTTCGTGGT	TCAGCATTAC	AAGCATTAAA	TGGTGTGCCT	250
	GAGTGGGAAG	AAAAAATCAT	TGAATTAGCA	CAACACTTAG	ATTCTTATAT	300
	CCCTGAGCCT	GAGCGTGCGA	TTGATAAACC	TTTCTTATTA	CCAATCGAAG	350
25	ACGTATTCTC	AATTCAGGT	CGTGGTACAG	TAGTAACCGG	TCGTGTTGAG	400
	CGTGGTATCA	TCAAATCAGG	TGAAGAAGTT	GAAATCGTAG	GGATTAAAGA	450
	AACGACAAAA	ACAACAGTAA	CCGGTGTGTA	GATGTTCCGT	AAACTATTAG	500
	ACGAAGGTCG	TGCGGGTGAA	AACGTAGGTG	CCTTATTACG	TGGTACTAAA	550
	CGTGAAGAAA	TCGAACGTGG	TCAAGTATTA	GCGAAACCAG	GTACAATTAC	600
30	ACCACACACT	GATTTTGAAT	CAGAAGTTTA	TGTATTATCA	AAAGAAGAAG	650
	GTGGTCGTCA	TACTCCATTC	TTCAAAGGTT	ATCGTCCTCA	GTTCTACTTC	700
	CGYACAACGG	ACGTAACAGG	AACGATTGAA	TTACCTGAAG	ATGTTGAGAT	750
	GGTAATGCCT	GGTGATAATA	TCAAGATGAC	AGTAAGCTTA	ATTCACCCTA	800
35	TCGCGATGGA	CGAAG				815

## 2) INFORMATION FOR SEQ ID NO: 92

## (i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 830 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

## 45 (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Haemophilus haemolyticus*  
 50 (B) STRAIN: ATCC 33390

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 92

	TGGTGCTATC	TTAGTAGTAG	CAGCAACTGA	TGGTCCAATG	CCACAAACTC	50
55	GTGAGCACAT	CTTATTAGGT	CGCCAAGTAG	GTGTTCCATA	CATCATCGTA	100
	TTCTTAAACA	AATGCGACAT	GGTAGATGAC	GAAGAGTTAT	TAGAATTAGT	150
	AGAAATGGAA	GTTTCGTGAAC	TTCTTTCTCA	ATATGACTTC	CCAGGTGACG	200
	ATACACCAAT	CGTACGTGGT	TCTGCATTAC	AAGCATTAAA	TGGCGTAGCA	250
	GAATGGGAAG	AAAAAATCCT	TGAGTTAGCA	AACCACTTAG	ATACTTACAT	300
60	CCCAGAACCA	GAGCGTGCAA	TTGACCAACC	GTTCTTCTT	CCAATCGAAG	350

	ATGTGTTCTC	AATCTCAGGT	CGTGGTACAG	TAGTAACTGG	TCGTGTAGAA	400
	CGTGGTATCA	TCCGTACTGG	TGATGAAGTA	GAAATCGTAG	GTATCAAAGA	450
	TACAGCAAAA	ACTACTGTAA	CGGGTGTGTA	AATGTTCCGT	AAATTACTTG	500
	ACGAAGGTCG	TGCAGGTGAA	AACATCGGTG	CATTATTACG	TGGTACCAAA	550
5	CGTGAAGAAA	TCGAACGTGG	TCAAGTATTA	GCGAAACCAG	GTTCAATCAC	600
	GCCACACACT	GACTTTCGAAT	CAGAAGTTTA	TGTATTATCA	AAAGAAGAAG	650
	GTGGTCGTCA	TACTCCATTC	TTCAAAGGTT	ACCGTCCACA	ATTCTATTTT	700
	CGTACAACCTG	ACGTAACTGG	TACTATCGAG	TTACCAGAAG	GCGTAGAAAT	750
	GGTAATGCCA	GGCGATAACA	TCAAGATGAC	AGTAAGCTTA	ATCCACCCAA	800
10	TCGCGATGGA	CCAAGGTTTA	CGTTTCGCAA			830

## 2) INFORMATION FOR SEQ ID NO: 93

15

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 824 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 20 (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- 25 (A) ORGANISM: *Haemophilus parahaemolyticus*  
 (B) STRAIN: ATCC 10014

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 93

30	TCTTAGTAGT	AGCAGCAACA	GACGGTCCAA	TGCCACAAAC	TCGTGAGCAC	50
	ATCTTATTAG	GTCGCCAAGT	AGGTGTTCCA	TACATCATCG	TATTCTTAAA	100
	CAATGCGAT	ATGGTTGACG	ATGAAGAATT	ATTAGAATTA	GTTGAAATGG	150
	AAGTGCGTGA	ACTTCTTTCA	CAATATGACT	TCCCAGGTGA	TGACACGCCA	200
	GTAGTACGTG	GTTCAGCGTT	ACAAGCGTTA	AACGGCGTAG	CAGAGTGGGA	250
35	AGAAAAAATT	CTTGAATTAG	CAAACCACTT	AGATACATAC	ATCCCAGAGC	300
	CAGAGCGTGC	GATTGATAAA	CCATTCTTAT	TACCAATCGA	AGACGTATTC	350
	TCAATCTCAG	GTCGTGGTAC	AGTAGTAACA	GGTCGTGTTG	AGCGTGGTAT	400
	CATCAAAGCG	GGTGAAGAAG	TTGAAATCGT	AGGTATCAAA	GACACTGCCA	450
	AAACAACAGT	AACTGGCGTG	GAAATGTTCC	GTAAATTATT	AGACGAAGGT	500
40	CGTGCGGGTG	AAAACGTTGG	TGCATTATTA	CGTGGTACAA	AACGTGAAGA	550
	AATCGAACGT	GGTCAAGTGT	TAGCGAAACC	AGGTACAATT	ACACCACACA	600
	CAGACTTCGA	ATCAGAAGTG	TACGTATTAT	CAAAGAAGA	AGGTGGTCGT	650
	CACACTCCAT	TCTTCAAAGG	TTACCGTCCA	CAATTCTACT	TCCGTACAAC	700
	TGACGTAACT	GGTACTATTG	AATTACCAGA	AGGCGTAGAA	ATGGTAATGC	750
45	CAGGCGATAA	CATCAAAATG	ACAGTATCAT	TAATCCACCC	AATCGCGATG	800
	GACGAAGGTT	TACGTTTTGC	GATT			824

## 50 2) INFORMATION FOR SEQ ID NO: 94

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 833 bases  
 (B) TYPE: Nucleic acid  
 55 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

## 60 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Haemophilus parainfluenzae*  
 (B) STRAIN: ATCC 7901

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 94

5  
 TGGTGCTATC TTAGTAGTAG CAGCAACTGA TGGTCCTATG CCACAAACTC 50  
 GTGAGCACAT CTTATTAGGT CGCCAAGTAG GTGTTTCCTTA CATCATCGTG 100  
 TTCTTAAACA AATGCGACAT GGTAGATGAC GAAGAGTTAT TAGAATTAGT 150  
 TGAATGGAA GTTCGTGAAC TTCTTTCTCA ATATGACTTC CCGGGTGACG 200  
 10 ATACACCAAT CGTACGTGGT TCTGCATTAC AAGCGTTAAA CGGCGTWGCA 250  
 GAATGGGAAG AAAAAATCCT TGAATTAGCT AGCCACTTAG ATTCTTACAT 300  
 TCCTGAGCCT CAACGTGCTA TCGACCAACC GTTCCTTCTT CCAATCGAAG 350  
 ACGTGTTCTC TATCTCCGGT CGTGGTACAG TAGTAACAGG TCGTGTTGAG 400  
 CGTGGTATCA TCCGTACCGG TGATGAAGTT GAAATCGTAG GTATCAAACC 450  
 15 GACTGCGAAA ACTACCGTAA CCGGTGTTGA AATGTTCCGT AAATTACTTG 500  
 ACGAAGGTCG TGCAGGTGAA AACATCGGTG CATTATTACG TGGTACYAAA 550  
 CGTGAAGAAA TCGAACGTGG TCAAGTATTG GCTAAACCGG GTTCAATCAC 600  
 TCCACACACT GATTTCGAAT CTGAAGTGTA CGTATTATCC AAAGAAGAAG 650  
 GTGGTCGTCA TACTCCATTC TTCAAAGGTT ACCGTCCACA ATTCTATTTC 700  
 20 CGTACAACCTG ACGTAACCGG AACTATCGAA TTACCGGAAG GCGTGGAAT 750  
 GGTATGCCT GGTGATAACA TCAAAATGAC TGTATCCTTA ATCCACCCAA 800  
 TCGCGATGGA CCAAGGTTTA CGTTTCGCTA TCG 833

25  
 2) INFORMATION FOR SEQ ID NO: 95

## (i) SEQUENCE CHARACTERISTICS:

30 (A) LENGTH: 824 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

35 (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Haemophilus paraphrophilus*  
 (B) STRAIN: ATCC 29241

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 95

TGGTGCTATC TTAGTAGTAG CAGCAACTGA TGGTCCTATG CCACAAACTC 50  
 GTGAGCACAT CTTATTAGGT CGCCAAGTAG GTGTTTCCTTA CATCATCGTA 100  
 TTCTTAAACA AATGCGACAT GGTAGATGAC GAAGAGTTAT TAGAATTAGT 150  
 45 TGAATGGAA GTTCGTGAAC TTCTTTCTCA ATATGACTTC CCGGGTGACG 200  
 ATACGCCAAT CGTACGTGGT TCTGCATTAC AAGCGTTAAA CGGCGTTGCA 250  
 GAATGGGAAG AAAAAATCCT TGAATTAGCA AACCCTTGG ATACTTACAT 300  
 TCCTGAGCCA CAACGTGCTA TCGACCAACC GTTCCTTCTT CCAATCGAAG 350  
 ACGTGTTCTC TATCTCCGGT CGTGGTACAG TAGTAACAGG TCGTGTTGAG 400  
 50 CGTGGTATCA TCCGTACCGG TGATGAAGTT GAAATCGTAG GTATCAAACC 450  
 GACTGCGAAA ACTACCGTAA CCGGTGTTGA AATGTTCCGT AAATTACTTG 500  
 ACGAAGGTCG TGCAGGTGAA AACATCGGTG CATTATTACG TGGTACCAA 550  
 CGTGAAGAAA TCGAACGTGG TCAAGTATTG GCTAAACCGG GTTCAATCAC 600  
 TCCACACACT GATTTCGAAT CTGAAGTGTA CGTATTATCC AAAGAAGAAG 650  
 55 GTGGTCGTCA TACTCCATTC TTCAAAGGTT ACCGTCCACA ATTCTATTTC 700  
 CGTACAACCTG ACGTAACCGG TACTATCGAG TTACCGGAAG GTGTGGAAT 750  
 GGTAATGCCT GCGGATAACA TCAAAATGAC CGTATCCTTA ATCCACCCAA 800  
 TCGCGATGGA CCAAGGTTTA CGTT 824

60

## 2) INFORMATION FOR SEQ ID NO: 96

- (i) SEQUENCE CHARACTERISTICS:
- 5 (A) LENGTH: 818 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear
- 10 (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
- (A) ORGANISM: *Haemophilus segnis*
- (B) STRAIN: ATCC 33393
- 15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 96

	GCTATCTTAG	TAGTAGCAGC	AACTGATGGT	CCTATGCCAC	AAACTCGTGA	50
	GCACATCTTA	TTAGGTCGCC	AAGTAGGTGT	TCCTTACATC	ATCGTATTCT	100
20	TAAACAAATG	CGACATGGTA	GATGACGAAG	AGTTATTAGA	ATTAGTTGAA	150
	ATGGAAGTTC	GTGAACTTCT	TTCTCAATAT	GACTTCCCAG	GTGATGATAC	200
	TCCAATCATT	CGTGGTCTG	CATTACAAGC	GTAAACGGC	GTAGCAGAAT	250
	GGGAAGAAAA	AATCCTTGAA	TTAGCTCAAG	CATTAGATAC	TTACATTCTT	300
	GAACCTGAGC	GTGCAATCGA	CCAACCGTTC	CTTCTTCCAA	TTGAAGACGT	350
25	GTTCTCAATC	TCTGGTCGTG	GTACTGTAGT	AACAGGTCGT	GTAGAGCGTG	400
	GTATCATCCG	TACCGGTGAT	GAAGTTGAAA	TCGTTGGTAT	CAAACCAACT	450
	GCGAAAACAA	CCGTAACCGG	TGTTGAAATG	TTCCGTAAAT	TACTTGACGA	500
	AGGTCGTGCA	GGTGAAAACA	TCGGTGCAAT	ATTACGTGGT	ACTAAACGTG	550
	AAGAAATCGA	ACGTGGTCAA	GTATTAGCGA	AACCGGGTTC	AATCACTCCA	600
30	CACACTGACT	TCGAATCTGA	AGTGTACGTA	TTATCTAAAG	AAGAAGGTGG	650
	TCGTCATACT	CCATTCTTCA	AAGGTTACCG	TCCACAATTC	TATTTCCGTA	700
	CAACTGACGT	AACCGGTACT	ATCGAGTTAC	CGGAAGGCGT	GGAAATGGTT	750
	ATGCCTGGCG	ATAACATCAA	AATGACCGTA	TCCTTAATCC	ACCCAATCGC	800
35	GATGGACCAA	GGTTTACG				818

## 2) INFORMATION FOR SEQ ID NO: 97

- (i) SEQUENCE CHARACTERISTICS:
- 40 (A) LENGTH: 763 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear
- 45 (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
- (A) ORGANISM: *Hafnia alvei*
- 50 (B) STRAIN: ATCC 13337
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 97

	CGGCGCTATC	CTGGTTGTTG	CTGCGACTGA	CGGCCCTATG	CCTCAGACTC	50
55	GTGAGCACAT	CCTGCTGGGT	CGTCAGGTTG	GCGTTCCTTW	CATCATCGTR	100
	TTCTTGAACA	AATGCGACAT	GGTTGATGAT	GAAGAGCTGC	TGGAAGTGGT	150
	AGAAATGGAA	GTTCTGTGAAC	TCTGTCTCTA	GTACGACTTC	CCWGGYGATG	200
	ATACTCCAAT	CATCCGTGGT	TCTGCTCTGA	AAGCGCTGGA	AGGYGMACCT	250
	GAGTGGGAAG	CTAAGATCGT	AGAACTGGCT	GAAACTCTGG	ATTCTTACAT	300
60	YCCACARCCA	GAACGTGCTA	TCGAYAAGCC	ATTCTGCTG	CCAATCGAAG	350

```

ACGTATTCTC TATCTCTGGC CGTGGTACWG TTGTTACCGG TCGTGTAGAG      400
CGCGGTATCG TTAAAGTTGG TGAAGAAGTT GARATCGTTG GTATCAAAGA      450
TACCGTTAAA TCAACTTGTA CCGGCGTTGA AATGTTCCGT AAAGTGTCTG      500
ACGAAGGTCG TGCAGGCGAG AACGTTGGTG TTCTGCTGCG TGGTATCAAG      550
5  CGTGAAGACA TCGAACGTGG TCAGGTTCTG GCTAAACCAG GYTCYATCAA      600
GCCACACACC AAGTTCGAAT CAGAAGTTTA TATTCTGAGC AAAGATGAAG      650
GCGGYCGTCA TACTCCGTTT TTCAAAGGCT ACCGTCCACA GTTCTACTTC      700
CGTACAAC TG ACGTGACCGG TACCATCGAA TTGCCAGAAG GCGTGGAAAT      750
GGTAATGCCA GGC                                          763
10

```

## 2) INFORMATION FOR SEQ ID NO: 98

```

15  (i) SEQUENCE CHARACTERISTICS:
      (A) LENGTH: 828 bases
      (B) TYPE: Nucleic acid
      (C) STRANDEDNESS: Double
      (D) TOPOLOGY: Linear
20

```

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

```

25  (A) ORGANISM: Kingella kingae
      (B) STRAIN: ATCC 23330

```

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 98

```

30  CGGCGCAATC TTGGTATGTT CAGCAGCTGA CGGTCCTATG CCACAAACTC      50
    GCGAACACAT CTTGTTGGCT CGCCAAGTAG GTGTACCTTA TATCATCGTA      100
    TTCATGAACA AATGCGACAT GGTGCGATGAT GCTGAGTTGT TGGAATTGGT      150
    TGAAATGGA AATCCGTGACT TGTGTCTAG CTACGATTTT CCAGGCGACG      200
    ATGCCCCAAT CGTTCAAGGT TCTGCATTGC GYGCAATTGGA AGGCGACGCT      250
    GCATACAAAG AAAAAATCTT TGAATTGGCT GCTGCTTTGG ATAGCTACAT      300
35  TCCTACTCCA GAACGTGCTG TTGATAAACC ATTCTTGTTG CCAATCGAAG      350
    ATGTATTCTC TATCTCTGGT CGTGGTACAG TAGTTACTGG TCGTGTAGAG      400
    CGCGGTATCA TCAAAGTAGG CGAAGAGATT GAAATCGTTG GTTTGAAAGA      450
    CACGCAAAAA ACCACTTGTA CTGCGGTGGA AATGTTCCGC AAATTGTTGG      500
    ACGAAGGTCA AGCTGGTGAT AACGTTGGTG TATTATTGCG TGGTACGAAG      550
40  CGTGAAGACG TTGAACGTGG TCAGGTATTG GCTAAACCAG GTTCTATCAC      600
    TCCGCACACT AAATTTGAAG CTGAAGTGTA TGTGTTGAGC AAAGAAGAAG      650
    GTGGCCGTC TACGCCATTC TTCGCTAACCT ACCGCCCCACA ATTCTACTTC      700
    CGTACGACTG ACGTAACTGG TGCAGTTACT TTGTCTGAGG GTGTGGAAAT      750
    GGTATGCCA GCGGAAAACG TGAAAATCAC TGTGAGTTG ATTGCACCTA      800
45  TCGCTAGGAA AACGGTTTGC GTTTTGCG                                          828

```

## 2) INFORMATION FOR SEQ ID NO: 99

```

50  (i) SEQUENCE CHARACTERISTICS:
      (A) LENGTH: 828 bases
      (B) TYPE: Nucleic acid
      (C) STRANDEDNESS: Double
55  (D) TOPOLOGY: Linear

```

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

```

60  (A) ORGANISM: Klebsiella ornithinolytica

```

(B) STRAIN: ATCC 31898

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 99

5	GGCGCGATCC	TGGTTGTTGC	TGCGACTGAC	GGCCCGATGC	CGCAGACTCG	50
	TGAGCACATC	CTGCTGGGTC	GTCAGGTAGG	CGTTCCGTAC	ATCATCGTGT	100
	TCCTGAACAA	ATGCGACATG	GTTGATGACG	AAGAGCTGCT	GGAGCTGGTT	150
	GAAATGGAAG	TCCGTGAGCT	GCTGTCTCAG	TACGACTTCC	CGGGCGACGA	200
	CACGCCGATC	GTTCTGTTT	CCGCTCTGAA	AGCGCTGGAA	GGCGAAGCAG	250
10	ACTGGGAAGC	GAAAAATCATC	GAACTGGCTG	GCTACCTGGA	TTCTTACATC	300
	CCGGAACCAG	AGCGTGCGAT	TGACAAGCCG	TTCTTGCTGC	CGATCGAAGA	350
	CGTATTCTCC	ATCTCCGGTC	GTGGTACCGT	TGTTACCGGT	CGTGTAGAGC	400
	GCGGTATCAT	CAAAGTGGGC	GAAGAAGTTG	AAATCGTTGG	TATCAAAGAG	450
	ACTGCGAAGT	CTACCTGTAC	TGGCGTTGAA	ATGTTCCGCA	AACTGCTGGA	500
15	CGAAGGCCGT	GCTGGTGAGA	ACGTTGGTGT	TCTGCTGCGT	GGTATCAAAC	550
	GTGAAGAAAT	CGAACGTGGT	CAGGTACTGG	CTAAGCCGGG	CTCTATCAAG	600
	CCGCACACCA	AGTTCGAATC	TGAAGTGATC	ATTCTGTCCA	AAGACGAAGG	650
	CGCCCGTCAT	ACTCCGTTCT	TCAAAGGCTA	CCGTCCGCAG	TTCTACTTCC	700
	GTACAACCTGA	CGTGACTGGC	ACCATCGAAC	TGCCGGAAGG	CGTAGAGATG	750
20	GTCATGCCGG	GCGACAACAT	CAAAATGGTT	GTTACCCTGA	TTCACCCGAT	800
	CGCGATGGAC	GATGGTCTGC	GTTTCGCA			828

25 2) INFORMATION FOR SEQ ID NO: 100

(i) SEQUENCE CHARACTERISTICS:

	(A)	LENGTH: 749 bases
	(B)	TYPE: Nucleic acid
30	(C)	STRANDEDNESS: Double
	(D)	TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

35 (vi) ORIGINAL SOURCE:

	(A)	ORGANISM: <i>Klebsiella oxytoca</i>
	(B)	STRAIN: ATCC 33496

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 100

40	GATGCCGCAG	ACTCGTGAGC	ACATCCTGCT	GGGTCGTCAG	GTAGGCGTTC	50
	CGTACATCAT	CGTGTTCTCTG	AACAAGTGCG	ACATGGTTGA	TGACGAAGAG	100
	CTGCTGGAAC	TGGTTGAAAT	GGAAGTTCGT	GAAGTTCTGT	CTCAGTACGA	150
	TTTCCCGGGC	GACGACACTC	CGATCGTTCTG	TGGTTCTGCT	CTGAAAGCGC	200
45	TGGAAGGCGA	CGCWGAGTGG	GAAKCKAAAA	TCATCGAACT	GGCTGGCTTC	250
	CTGGATTCTT	ACATTCCGGA	ACCAGAGCGT	GCGATTGACA	AGCCGTTCTT	300
	GCTGCCGATC	GAAGACGTAT	TCTCCATCTC	CGGTCGTGGT	ACCGTTGTTA	350
	CCGGTCGTGT	AGAGCGCGGT	ATCATCAAAG	TTGGCGAAGA	AGTTGAAATY	400
	GTTGGTATYA	AAGACACTGC	TAAGTCTACC	TGTACTGGCG	TTGAAATGTT	450
50	CCGCAAACCTG	CTGGACGAAG	GCCGYGCTGG	TGAGAACGTT	GGTGTTCTGC	500
	TGCGTGGTAT	CAAACGTGAA	GAAATCGAAC	GTGGTCAGGT	ACTGGCTAAG	550
	CCGGGCTCTA	TCAAGCCGCA	CACCAAGTTC	GAATCTGAAG	TTTATATCCT	600
	GTCCAAAGAC	GAAGGCGGCC	GTCACACTCC	GTTCTTCAAA	GGCTACCGTC	650
	CGCAGTTCTA	CTTCCGTACA	ACTGACGTGA	CTGGCACCAT	CGAACTGCCG	700
55	GAAGGCGTAG	AGATGGTTAT	GCCGGGCGAC	AACATCAAAA	TGGTTGTTA	749

2) INFORMATION FOR SEQ ID NO: 101

60

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 830 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Klebsiella planticola*  
 (B) STRAIN: ATCC 33531

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 101

```

15  TGGCGCGATC CTGGTTGTTG CTGCGACTGA CGGCCCGATG CCGCAGACTC      50
    GTGAGCACAT CCTGCTGGGT CGTCAGGTAG GCGTTCCGTA CATCATCGTG      100
    TTCCTGAACA AATGCGACAT GGTTCGATGAC GAAGAGCTGC TGGAACCTGGT      150
    TGAAATGGAA GTTCGTGAGC TGCTGTCTCA GTACGACTTC CCGGGCGACG      200
    ACACTCCGAT CGTTCGTGGT TCCGCTCTGA AAGCGCTGGA AGGCGAAGCA      250
20  GACTGGGAAG CGAAAATCAT CGAACTGGCT GGCTACCTGG ATTCTTACAT      300
    CCCGGAACCA GAGCGTGCGA TTGACAAGCC GTTCCTGCTG CCTATCGAAG      350
    ACGTATTCTC CATCTCCGGT CGTGGTACCG TTGTTACCGG TCGTGTAGAG      400
    CGCGGTATCA TCAAAGTGGG CGAAGAAGTT GAAATCGTTG GTATCAAAGA      450
    TACTGCTAAR TCWACCTGTA CYGGCGTTGA AATGTTCCGC AAACCTGCTGG      500
25  ACGAAGGCCG TGCTGGTGAG AACGTTGGTG TTCTGCTGCG TGGTATCAAA      550
    CGTGAAGAAA TCGAACGTGG TCAGGTACTG GCTAAGCCGG GCTCTATCAA      600
    GCCGCACACC AAGTTCGAAT CTGAAGTGTA CATTCTGTCC AAAGACGAAG      650
    GCGGCCGTCA TACTCCGTTT TTCAAAGGCT ACCGTCCGCA GTTCTACTTC      700
    CGTACAACCTG ACGTGACTGG CACCATCGAA CTGCCGGAAG GCGTAGAGAT      750
30  GGTAAATGCCG GGCGACAACA TCAAATGGT TGTTACCCTG ATTCACCCRA      800
    TCGCGATGGA CGACGGTCTG CGTTTCGCAA                                830
  
```

## 2) INFORMATION FOR SEQ ID NO: 102

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 806 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Klebsiella pneumoniae* subsp. *ozaenae*  
 (B) STRAIN: ATCC 11296

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 102

```

50  CCTGGTTGTT GCTGCGACTG ACGGCCCGAT GCCGCAGACT CGTGAGCACA      50
    TCCTGCTGGG TCGTCAGGTA GCGTTCCGT ACATCATCGT GTTCCTGAAC      100
    AAATGCGACA TGGTTGATGA CGAAGAGCTG CTGGAACCTG TTGAGATGGA      150
    AGTTCGTGAA CTGCTGTCTC AGTACGATTT CCCGGGCGAC GACACCCCGA      200
55  TCGTTGCTGG TTCTGCTCTG AAAGCGCTGG AAGGCGACGC AGAGTGGGAA      250
    GCGAAAATCA TCGAACTGGC TGGCCACCTG GATACCTATA TCCCGGAACC      300
    AGAGCGTGCG ATTGACAAGC CGTTCCTGCT GCCGATCGAA GACGTATTCT      350
    CCATCTCCGG TCGTGGTACC GTTGTTACCG GTCGTGTAGA GCGCGGTATC      400
    ATCAAAGTAG GTGAAGAAGT TGAAATCGTT GGTATCAAAG AAACCGCGAA      450
60  AACCACCTGT ACTGGCGTTG AAATGTTCCG CAAACTGCTG GACGAAGGCC      500
  
```

GTGCTGGTGA GAACGTAGGT GTTCTGCTGC GTGGTATCAA ACGTGAAGAA 550  
 ATCGAACGTG GTCAGGTACT GGCTAAGCCG GGCACCATCA ACCCGCACAC 600  
 CAAGTTCGAA TCTGAAGTGT ACATCCTGTC CAAAGACGAA GCGGCCCGTC 650  
 A TACTCCGTT CTTCAAAGGC TACCGTCCGC AGTTCTACTT CCGTACTACT 700  
 5 GACGTGACTG GCACCATCGA ACTGCCCGAA GCGGTAGAGA TGGTAATGCC 750  
 GGGCGACAAC ATCAAAATGG TTGTTACCCT GATCCACCCG ATCGCGATGG 800  
 ACGACG 806

10

## 2) INFORMATION FOR SEQ ID NO: 103

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 743 bases  
 15 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

20 (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Klebsiella pneumoniae* subsp. *pneumoniae*  
 (B) STRAIN: ATCC 13883

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 103

GCAGACTCGT GAGCACATCC TGCTGGGTCG TCAGGTAGGC GTTCCGTACA 50  
 TCATCGTGTT CCTGAACAAA TGCGACATGG TTGATGACGA AGAGCTGCTG 100  
 GAACTGGTTG AGATGGAAGT TCGTGAACGT CTGTCTCAGT ACGATTTCCC 150  
 30 GGGCGACGAC ACTCCGATCG TTCGTGGTTC TGCTCTGAAA GCGCTGGAAG 200  
 GCGACGCAGA GTGGGAAGCG AAAATCATCG AACTGGCTGG CCACCTGGAT 250  
 ACCTATATCC CGGAACCAGA GCGTGCGATT GACAAGCCGT TCCTGCTGCC 300  
 GATCGAAGAC GTATTCTCCA TCTCCGGTCG TGGTACCGTT GTTACCGGTC 350  
 GTGTAGAGCG CCGTATCATC AAAGTAGGTG AAGAAGTTGA AATCGTTGGT 400  
 35 ATCAAAGAAA CCGCGAAAAC CACCTGTA CTGGTGAGAA CGTAGGTGTT CTGCTGCGTG 450  
 ACTGCTGGAC GAAGGCCGTG CTGGTGAGAA CGTAGGTGTT CTGCTGCGTG 500  
 GTATCAAACG TGAAGAAATC GAACGTGGTC AGGTACTGGC TAAGCCGGGC 550  
 ACCATCAACC CGCACACCAA GTTCGAATCT GAAGTGTACA TCCTGTCCAA 600  
 AGACGAAGGC GGCCGTCACA CTCCGTTCTT CAAAGGCTAC CGTCCGCAGT 650  
 40 TCTACTTCCG TACTACTGAC GTGACTGGCA CCATCGAACT GCCGGAAGGC 700  
 GTAGAGATGG TAATGCCGGG CGACAACATC AAAATGGTTG TTA 743

45 2) INFORMATION FOR SEQ ID NO: 104

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 819 bases  
 (B) TYPE: Nucleic acid  
 50 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

## 55 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Klebsiella pneumoniae* subsp.  
*rhinoscleromatis*  
 (B) STRAIN: ATCC 13884

60 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 104



	TGGTTGTTGC	TGCGACTGAC	GGCCCGATGC	CGCAGACTCG	TGAGCACATC	50
	CTGCTGGGTC	GTCAGGTAGG	CGTTCCGTAC	ATCATCGTGT	TCCTGAACAA	100
	ATGCGACATG	GTTGATGACG	AAGAGCTGCT	GGAAC TGGTT	GAGATGGAAG	150
5	TTCGTGAACT	RCTGTCTCAG	TACGATTTCC	CGGGCGACGA	CACCCCGATC	200
	GTTCGTGGTT	CTGCTCTGAA	AGCGCTGGAA	GGCGACGCAG	AGTGGGAAGC	250
	GAAAATCATC	GAAC TGGCTG	GCCACCTGGA	TACCTATATC	CCGGAACCAG	300
	AGCGTGGGAT	TGACAAGCCG	TTCCTGCTGC	CGATCGAAGA	CGTATTCTCC	350
	ATCTCCGGTC	GTGGTACCGT	TGTTACCGGT	CGTGTAGAGC	GCGGTATCAT	400
10	CAAAGTAGGT	GAAGAAGTTG	AAATCGTTGG	TATCAAAGAA	ACCGCGAAAA	450
	CCACCTGTAC	TGGCGTTGAA	ATGTTCCGCA	AACTGCTGGA	CGAAGGCCGT	500
	GCTGGTGAGA	ACGTAGGTGT	TCTGCTGCGT	GGTATCAAAC	GTGAAGAAAT	550
	CGAACGTGGT	CAGGTACTGG	CTAAGCCGGG	CACCATCAAC	CCGCACACCA	600
	AGTTCGAATC	TGAAGTGATC	ATCCTGTCCA	AAGACGAAGG	CGGCCGTCAC	650
15	ACTCCGTTCT	TCAAAGGCTA	CCGTCCGCAG	TTCTACTTCC	GTACTACTGA	700
	CGTGACTGGC	ACCATCGAAC	TGCCGGAAGG	CGTAGAGATG	GTAATGCCGG	750
	GCGACAACAT	CAAAATGGTT	GTTACCCTGA	TCCATCCGAT	CGCGATGGAC	800
	GACGGTCTGC	GTTTCGCAA				819

20

## 2) INFORMATION FOR SEQ ID NO: 105

(i) SEQUENCE CHARACTERISTICS:

25 (A) LENGTH: 832 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

30 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Kluyvera ascorbata*

(B) STRAIN: ATCC 33433

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 105

	CGGCGCGATC	CTGGTTGTTG	CTGCGACTGA	TGGCCCTATG	CCACAGACTC	50
	GTGAGCACAT	CCTGCTGGGT	CGTCAGGTAG	GCGTTCCTTA	CATCATCGTG	100
40	TTCCTGAACA	AATGYGACAT	GGTTGATGAC	GAAGAGCTGC	TGGAAC TGGT	150
	TGAAATGGAA	GTTCGTGAAC	TTCTGTCTCA	GTACGATTTT	CCAGGCGACG	200
	ATACTCCAAT	CATCCGTGGT	TCTGCTCTGA	AAGCGCTGGA	AGGCGATGCA	250
	GAGTGGGAAG	CGAAAATCAT	CGAACTGGCT	GGCTTCCTGG	ATTCTTACAT	300
	CCCAGAACCA	GAACGTGCTA	TCGATAAGCC	GTTCCTGCTG	CCAATCGAAG	350
45	ACGTATTCTC	CATCTCCGGT	CGTGGTACCG	TTGTTACCGG	TCGTGTAGAG	400
	CGCGGTATCA	TCAAAGTTGG	YGAAGAAGTT	GAAATCGTTG	GTATCAAAGA	450
	CACCGCTAAG	TCTACCTGTA	CCGGCGTTGA	AATGTTCCGC	AAACTGCTGG	500
	ACGAAGGCCG	TGCTGGTGAG	AACGTTGGTG	TTCTGCTGCG	TGGTATCAAA	550
	CGTGAAGAAA	TCGAACGTGG	TCAGGTTCTG	GCTAAGCCAG	GCTCTATCAA	600
50	GCCGCACACC	AAGTTCGAAT	CTGAAGTGTA	CATTCTGTCC	AAAGACGAAG	650
	GCGGCCGTC	TACTCCGTTT	TTCAAAGGCT	ACCGTCCACA	GTTCTACTTC	700
	CGTACTACTG	ACGTGACCGG	TACCATCGAA	CTGCCAGAAG	GCGTTGAGAT	750
	GGTAATGCCA	GGCGACAACA	TCAAGATGGT	TGTGACTCTG	ATCCACCCAA	800
55	TCGCGATGGA	CGACGGCCTG	CGTTTCGCAA	CC		832

## 2) INFORMATION FOR SEQ ID NO: 106

60 (i) SEQUENCE CHARACTERISTICS:

64

(A) LENGTH: 830 bases  
(B) TYPE: Nucleic acid  
(C) STRANDEDNESS: Double  
(D) TOPOLOGY: Linear

5

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Kluyvera cryocrescens*  
(B) STRAIN: ATCC 33435

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 106

15	TGGCGCGATC	CTGGTTGTTG	CTGCAACTGA	TGGCCCTATG	CCACAGACTC	50
	GTGAGCACAT	CCTGCTGGGT	CGTCAGGTAG	GCGTTCCTTA	CATCATCGTG	100
	TTCCTGAACA	AATGTGACAT	GGTTGATGAC	GAAGAGCTGC	TGGAAC TGGT	150
	TGAAATGGAA	GTTTCGTGAAC	TTCTGTCTCA	GTACGATTTT	CCAGGCGACG	200
	ACACTCCTAT	CGTTCGTGGT	TCCGCGCTGA	AAGCGCTGGA	AGGCGACGCT	250
	GAGTGGGAAG	CAAAAATCAT	CGAACTGGCT	GGCTTCCTGG	ATTCTTACAT	300
20	CCCAGAACCA	GAGCGTGCGA	TTGATAAGCC	GTTCTGCTG	CCAATCGAAG	350
	ACGTATTCTC	CATCTCCGGT	CGTGGTACCG	TTGTTACCGG	TCGTGTAGAG	400
	CGCGGTATCA	TCAAAGTTGG	TGAAGAAGTT	GAAATCGTGG	GTATCAAAGA	450
	CACTGCTAAG	TCTACCTGTA	CCGGCGTTGA	AATGTTCCGC	AAACTGCTGG	500
	ACGAAGGCCG	TGCTGGTGAG	AACGTTGGTG	TTCTGCTGCG	TGGTATCAAA	550
25	CGTGAAGAAA	TCGAACGTGG	TCAGGTTCTG	GCTAAGCCAG	GCTCCATCAA	600
	GCCGCACACC	AAATTCGAAT	CTGAAGTTTA	CATCCTGTCC	AAAGACGAAG	650
	GCGGCCGTCA	TACTCCGTTT	TTCAAAGGCT	ACCGTCCACA	GTTCTACTTC	700
	CGTACTACTG	ACGTGACTGG	TACCATCGAA	CTGCCAGAAG	GCGTAGAGAT	750
	GGTAATGCCG	GGCGACAACA	TCAAATGGT	TGTTACCCTG	ATCCACCCAA	800
30	TCGCGATGGA	CGACGGTCTG	CGTTTCGCAA			830

2) INFORMATION FOR SEQ ID NO: 107

35

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 826 bases  
(B) TYPE: Nucleic acid  
(C) STRANDEDNESS: Double  
(D) TOPOLOGY: Linear

40

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Kluyvera georgiana*  
(B) STRAIN: ATCC 51603

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 107

50	CGCGATCCTG	GTTGTTGCTG	CGACTGACGG	CCCGATGCCG	CAGACTCGTG	50
	AGCACATCCT	GCTGGGTCGT	CAGGTTGGCG	TTCCGTACAT	CATCGTGTTC	100
	CTGAACAAAT	GCGACATGGT	TGATGACGAA	GAGCTGCTGG	AACTGGTTGA	150
	AATGGAAGTT	CGTGAAC TTC	TGTCTCAGTA	CGACTTCCCG	GGCGACGACA	200
	CGCCGATCGT	TCGTGGTTCT	GCTCTGAAAG	CGCTGGAAGG	CGACGCTGAG	250
55	TGGGAAGCGA	AAATCATCGA	ACTGGCGGGC	TTCTTGGAAT	CTTACATCCC	300
	GGAACCAAG	CGTGCGATTG	ACAAGCCGTT	CCTGCTGCCG	ATCGAAGACG	350
	TATTCTCCAT	CTCCGGTCGT	GGTACCGTTG	TTACCGGTCG	TGTAGAACGC	400
	GGTATCATCA	AAGTTGGCGA	AGAAGTTGAA	ATCGTTGGTA	TCAAAGACAC	450
	CGCTAAGTCT	ACCTGTACTG	GCGTTGAAAT	GTTCCGCAAA	CTGCTGGACG	500
60	AAGGCCGTGC	TGGTGAGAAC	GTTGGTGTTC	TGCTGCGTGG	TATCAAACGT	550

65

	GAAGAAATCG	AACGTGGTCA	GGTACTGGCT	AAGCCGGGTT	CTATCAAGCC	600
	GCACACCAAG	TTCGAATCTG	AAGTGATACAT	TCTGTCCAAA	GACGAAGGCG	650
	GCCGTCATAC	TCCGTTCTTC	AAAGGCTACC	GTCCGCAGTT	CTACTTCCGT	700
	ACTACTGACG	TGACTGGCAC	CATCGAACTG	CCGGAAGGCG	TTGAGATGGT	750
5	AATGCCGGGC	GACAACATCA	AAATGGTTGT	TACCCTGATC	CACCCGATCG	800
	CGAAGGACGA	AGGTCTGCGT	TTCGCA			826

## 10 2) INFORMATION FOR SEQ ID NO: 108

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 803 bases  
 (B) TYPE: Nucleic acid  
 15 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

## 20 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Lactobacillus casei* subsp. *casei*  
 (B) STRAIN: ATCC 393

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 108

25	GCTGCTGATG	GCCCAATGCC	ACAAACTCGT	GAACATATCT	TACTTTCACG	50
	TCAAGTTGGT	GTTCCATACA	TCGTTGTATT	CATGAACAAA	TGTGACATGG	100
	TTGACGATGA	AGAATTACTA	GAATTAGTTG	AAATGGAAAT	TCGTGATCTA	150
	TTAACTGAAT	ATGAATTCCC	TGGCGATGAC	ATTCCTGTAA	TCAAAGGTTT	200
30	AGCTCTTAAA	GCACTTCAAG	GTGAAGCTGA	CTGGGAAGCT	AAAATTGACG	250
	AGTTAATGGA	AGCTGTAGAT	TCTTACATTC	CAACTCCAGA	ACGTGATACT	300
	GACAAACCAT	TCATGATGCC	AGTTGAGGAT	GTATTCTCAA	TCACTGGTCG	350
	TGGAACAGTT	GCAACTGGAC	GTGTTGAACG	TGGACAAGTT	AAAGTTGGTG	400
	ACGAAGTAGA	AGTTATCGGT	ATTGAAGAAG	AGAGCAAAAA	AGTAGTAGTA	450
35	ACTGGAGTAG	AAATGTTCCG	TAAATYACTA	GATTACGCTG	AAGCTGGCGA	500
	CAACATTGGC	GCACTTCTAC	GTGGTGTTCG	TCGTGAAGAT	ATCCAACGTG	550
	GTCAAGTATT	AGCTAAACCA	GGTTCGATTA	CTCCACACAC	TAACCTCAAA	600
	GCTGAAACTT	ATGTTTTAAC	TAAAGAAGAA	GGTGGACGTC	ACACTCCATT	650
	CTTCAACAAC	TACCGCCAC	AATTCTATTT	CCGTACTACT	GACGTAACGT	700
40	GTATTGTTAC	ACTTCCAGAA	GGTACTGAAA	TGGTAATGCC	TGGTGATAAC	750
	ATTGAGCTTG	CAGTTGANCT	AATTGCACCA	ATCGCTATCG	AAGACGGTAC	800
	TAA					803

45

## 2) INFORMATION FOR SEQ ID NO: 109

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 825 bases  
 50 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

55

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Lactococcus lactis* subsp. *lactis*  
 (B) STRAIN: ATCC 19435

## 60 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 109

```

CGGTGCAATC CTCGTTGTTG CTGCAACTGA TGGACCAATG CCACAAACTC      50
GTGAACACAT CTTGCTTTCA CGTCAAGTTG GTGTTAAATA CCTTATCGTC      100
TTCCTTAACA AGGCTGACCT TGTGATGAT GAAGAATTGA TGGAACTCGT      150
5  TGAAATGGAA GTTCGTGACC TCTTGAGCGA ATACGACTTC CCAGGTGACG      200
ATATTCCTGT AATCGCTGGT TCAGCACTTG GTGCTTTGAA CGGTGAACCA      250
CAATGGGTTG CTAAAGTTGA AGAATTGATG GACATCGTTG ATGAATACAT      300
CCCAACTCCA GAACGCGACA CTGACAAACC ACTCCTTCTT CCAGTCGAAG      350
ACGTATTCTC TATCACTGGT CGTGGTACAG TTGCTTCAGG ACGTATCGAA      400
10 CGTGTTACTG TTAAAGTTGG TGACGAAGTT GAAATCGTTG GTATCAAAGA      450
AGAAACTAAA AAAGCTGTTG TTAAGTGTAT CGAAATGTTT CGTAAAACAC      500
TTACTGAAGG TCTTGCTGGT GATAACGTCG GTGCACTTCT CCGTGGTATC      550
CAACGTGACG AAATCGAACG TGGTCAAGTT ATTGCTAAAC CAGGTTCAAT      600
CACTCCACAC AAACCTTTTCG AAGGTGAAGT TTACGTATTG AGCAAAGAAG      650
15 AAGGCGGACG TCACACTCCA TTCTTCGACA ACTACCGTCC TCAATTCTAC      700
TTCCACACAA CTGACGTTAC TGGTTCAGTT AAACCTCCAG AAGGAACTGA      750
AATGGTAATG CCTGGTGACA ACGTGCATAT CGACGTTGAA TTGATCCACC      800
CAGTTGCGAT CGAACAAGGT ACTAC                                     825

```

20

## 2) INFORMATION FOR SEQ ID NO: 110

## (i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 824 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

## 30 (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Leclercia adecarboxylata*  
 (B) STRAIN: ATCC 23216

35

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 110

```

GGCGCGATCC TGGTTGTTGC TGC GACTGAC GGCCCAATGC CTCAGACCCG      50
TGAGCACATC CTGCTGGGTC GTCAGGTAGG CGTTCCTTTC ATCATCGTGT      100
40 TCCTGAACAA ATGCGACATG GTTGATGACG AAGAGCTGCT GGAAGTGGTT      150
GAGATGGAAG TTCGTGAAC TCTGTCCCAG TACGACTTCC CGGGCGACGA      200
CACCCCAATC GTTCGTGGTT CTGCGCTGAA AGCGCTGGAA GCGGAAGCAG      250
AGTGGGAAGA GAAATCATC GARCTGGCTG GCTACCTGGA TTCCTACATC      300
CCAGAGCCAG AGCGTGCGAT TGACAAGCCG TTCCTGCTGC CTATCGAAGA      350
45 CGTATTCTCC ATCTCCGGTC GTGGTACCGT TGTTACCGGT CGTGTAGAGC      400
GCGGTATCAT CAARGTTGGC GAAGAAGTTG AAATCGTTGG TATCAAGGAC      450
ACTGCTAAGT CTACCTGTAC CGGCGTTGAA ATGTTCCGCA AACTGCTGGA      500
CGAAGGCCGT GCCGGTGAGA ACGTTGGTGT TCTGCTGCGT GGTATCAAAC      550
GTGAAGAAAT CGAACGTGGT CAGGTTCTGG CTAAGCCAGG CTCYATCAAG      600
50 CCGCACACCA AGTTCGAATC TGAAGTGTAC ATCCTGTCYA AAGACGAAGG      650
CGGCCGTCAT ACTCCGTTCT TCAAAGGCTA CCGTCCACAG TTCTACTTCC      700
GTACKACTGA CGTGACCGGT ACCATCGARC TGCCAGAAGG CGTTGAGATG      750
GTAATGCCAG GCGACAACAT CAAAATGGTT GTTACCCTGA TCCACCCAAT      800
CGCAATGGAC GATGGTCTGC GTTC                                     824

```

55

## 2) INFORMATION FOR SEQ ID NO: 111

## 60 (i) SEQUENCE CHARACTERISTICS:

67

(A) LENGTH: 838 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

5

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Legionella micdadei*  
 (B) STRAIN: ATCC 33218

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 111

	CGGAGCGATA	TTAGTAGTAT	CAGCAGCGGA	TGGCCCAATG	CCTCAAACGA	50
15	GAGAGCACAT	ACTYTTATCC	CGSCAGGTAG	GTGTTCCCTA	TATAGTAGTG	100
	TTCTTAAACA	AAGCTGACAT	GGTGGATGAT	GCGGAGTTAT	TAGAATTAGT	150
	TGAAATGGAA	GTACGCGAYT	TGTTGAGCAG	CTATGAATTT	CCAGGAGATG	200
	AGATCCCGAT	TGTAGTTGGT	TCAGCATTA	AAGCATTGGA	AGGCCGATACG	250
	AGTGATATAG	GTGTACCAGC	GATTGAGAAG	TTAGTTGAGA	CGATGGATTTC	300
20	TTATATACCT	GAGCCGGTAA	GAAACATCGA	TAAAAGTTTC	TTGTTACCGA	350
	TCGAAGACGT	GTTCTCAATA	TCTGGACGAG	GAACAGTAGT	AACAGGACGT	400
	ATCGAAAGCG	GGATCATCAA	AGTTGGTGAG	GAAGTCGAGA	TTGTTGGTAT	450
	ACGTGACACT	CAAAAGACGA	CATGCACAGG	CGTTGAAATG	TTCCGTAAAT	500
	TACTTGACGA	AGGTTCGAGCT	GGAGACAACG	TTGGTATATT	GCTACGTGGT	550
25	ACGAAGCGGG	ATGAAGTTGA	ACGCGGACAA	GTATTAGCTA	AGCCGGGAAG	600
	CATTAAACCG	CATACTAAAT	TTGAAGCTGA	AGTGTATGTG	TTGTCAAAAG	650
	ATGAAGGTGG	ACGTCATACC	CCATTCTTTA	ACGGATATCG	GCCTCAATTT	700
	TACTTCAGGA	CCACAGACGT	AACTGGTTCT	TGTGATTAC	CTGARGGTAT	750
	AGAAATGGTA	ATGCCAGGTG	ATAACGTCAA	GCTGATTGTT	AGCTTACACT	800
30	CACCGATTGC	TATGGACGAA	GGTTTGCGTT	TTGCAATC		838

2) INFORMATION FOR SEQ ID NO: 112

35

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 838 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

40

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Legionella pneumophila* subsp. *pneumophila*  
 (B) STRAIN: ATCC 33152

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 112

50	CGGAGCGATA	CTGGTTGTAT	CAGCAGCTGA	TGGTCCTATG	CCACAAACGA	50
	GGGAACACAT	TCTATTGTCT	CGCCAGGTAG	GTGTTCCATA	TATTGTTGTG	100
	TTCATGAACA	AAGCGGATAT	GGTTGATGAC	CCTGAGTTAT	TAGAGTTAGT	150
	GGAAATGGAA	GTGCGAGATT	TATTAAGCAG	TTACGATTTC	CCAGGGGATG	200
	ACATACCTAT	TGTTGTTGGT	TCAGCTTTGA	AAGCATTGGA	AGGTGAAGAC	250
55	AGTGATATAG	GCGTTAAGGC	TATTGAGAAA	TTGGTTGAAA	CAATGGATTTC	300
	ATACATTCTT	GAGCCAGTTA	GAAACATAGA	CAAGCCATTT	TTGTTGCCGA	350
	TTGAAGACGT	ATTTTCAATT	TCTGGACGCG	GAACAGTGGT	AACTGGTCGT	400
	GTAGAGAGTG	GAATTGTTAA	AGTTGGTGAG	GAAGTTGAAA	TTGTTGGAAT	450
	AAGAGACACC	CAAAAGACGA	CTTGACGGG	TGTTGAGATG	TTCCGTAAAT	500
60	TACTTGATGA	AGGTTCGAGCT	GGTGATAACG	TTGGTGTGTT	ATTACGAGGT	550

68

```

ACGAAGCGAG ATGAAGTGGG GCGTGGACAG GTATTGGCGA AGCCAGGAAC      600
CATCAAGCCA CACACCAAGT TTGAAGCAGA AGTGTATGTA TTATCCAAGG      650
AAGAAGGCGG ACGTCACACT CCATTCTTTA ATGGATACCG TCCACAATTC      700
TATTTTCAGAA CCACTGACGT GACAGGTACT TGTGACTTGC CATCAGGAGT      750
5  TGAAATGGTA ATGCCTGGAG ATAATGTGCA ATTAGTTGTT AGCTTGCATG      800
CTCCGATTGC GATGGATGAA GGTTTAAGAT TCGCAATT      838

```

10 2) INFORMATION FOR SEQ ID NO: 113

(i) SEQUENCE CHARACTERISTICS:

```

(A) LENGTH: 828 bases
(B) TYPE: Nucleic acid
15 (C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

```

(ii) MOLECULE TYPE: Genomic DNA

20 (vi) ORIGINAL SOURCE:

```

(A) ORGANISM: Leminorella grimontii
(B) STRAIN: ATCC 33999

```

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 113

```

25 GTGCAATCCT GGTAGTAGCA GCGACTGACG GCCCGATGCC TCAGACTCGC      50
GAGCACATCC TGCTGGGTCG TCAGGTAGGC GTTCCGTACA TCATCGTATT      100
CCTGAACAAG TGCGATATGG TTGATGACGA AGAGCTGCTG GAGCTGGTTG      150
ARATGGAAGT TCGCGAACTG CTGTCTCAGT ACGACTTCCC GGGCGACGAC      200
30 ACTCCGGTAG TCCGCGGTTT AGCGCTGAAA GCGCTGGAAG GCGAAGCCGA      250
GTGGGAARCG AAAATCATCG AGCTGGCAGG CCMTCTGGAT ACTTATATCC      300
CAGAACCTGA GCGTGCGATT GACAAGCCGT TCCTGCTGCC KATCGAAGAC      350
GTATTCTCTA TCTCCGGCCG TGGTACCGTT GTTACCGGTC GTGTAGAGCG      400
CGGCATCATC AAAGTCGGTG AAGAAGTGGA AATCGTCCGT ATCAAAGATA      450
35 CCACCAAGAC CACCTGTACC GCGGTTGAAA TGTTCCGTAA GCTGCTGGAC      500
GAAGGCCGTG CGGGCGAGAA CGTGGGCGTT CTGCTGCGCG GTACCAAGCG      550
TGACGAAATC GAACGTGGTC AAGTTCTGGC CAAGCCGGGC ACCATCACTC      600
CTCACACCCA GTTCGTGTCA GAAGTGTATA TCCTGAGCAA GGATGAAGGC      650
GGCCGTCATA CTCCGTTCTT CAAAGGCTAC CGTCCTCAGT TCTACTTCCG      700
40 TACGACTGAC GTGACAGGCA CCATCGAACT GCCGGAAGGC GTAGAGATGG      750
TAATGCCAGG CGACAACATT CAGATGACCG TAAGTCTGAT TCGCGCCGATC      800
GCAATGGACG AAGGTCTGCG CTTTCGCAA      828

```

45

2) INFORMATION FOR SEQ ID NO: 114

(i) SEQUENCE CHARACTERISTICS:

```

(A) LENGTH: 826 bases
50 (B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

```

(ii) MOLECULE TYPE: Genomic DNA

55

(vi) ORIGINAL SOURCE:

```

(A) ORGANISM: Leminorella richardii
(B) STRAIN: ATCC 33998

```

60 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 114

```

      GCTATCCTGG TTGTTGCTGC GACTGACGGC CCAATGCCTC AGACTCGTGA      50
      GCACATCCTG CTGGGTCGCC AGGTAGGCGT TCCTTACATC ATCGTGTTCC      100
      TGAACAAGTG CGACATGGTT GATGACGAAG AGCTGCTGGA ACTGGTAGAA      150
5     ATGGAAGTTC GTGAACTTCT GTCTCAATAC GACTTCCC GG GCGACGATAC      200
      GCCGGTTGTT CGCGGTTTCAG CGCTGAAAGC GCTGGAAGGT GACGCGYAGT      250
      GGGAARCGAA AATCATTGAA CTGGCGGAAT CCTTRGATAC TTAYATTCCA      300
      GAGCCAGAGC GTGCGATTGA CAAGCCGTTT CTGCTGCCTA TCGAAGACGT      350
      TTTCTCTATC TCTGGCCGTG GTACTGTAGT CACCGGTCGT GTAGAGCGCG      400
10    GCATCATCAA AGTTGGTGAA GAAGTGGAAA TCGTGGGAAT CAAAGACACC      450
      ACCAAGACCA CCTGTACTGG CGTTGAAATG TTCCGTAAGC TGCTGGACGA      500
      AGGCCGTGCA GGTGAGAACG TTGGTGTTCT GCTGCGYGGT ACTAAGCGTG      550
      ACGAAATCGA ACGTGCTCAG GTACTGGCTA AGCCAGGCAC CATCACTCCT      600
      CACACAGAAT TCGTGTCAGA AGTGTATATC CTGAGCAAGG ATGAAGGCGG      650
15    YCGTCATACT CCGTTCTTCA AAGGCTACCG TCCTCAGTTC TACTTCCGTA      700
      CGACTGACGT GACCGGCACC ATCGAACTGC CAGAAGGCGT AGAGATGGTA      750
      ATGCCAGGCG ATAACATCCA GATGGTAGTT ACGCTGATTG CCCCAATCGC      800
      GATGGACGAA GGTCTGCGCT TCGCAA      826

```

20

## 2) INFORMATION FOR SEQ ID NO: 115

```

      (i) SEQUENCE CHARACTERISTICS:
25      (A) LENGTH: 843 bases
      (B) TYPE: Nucleic acid
      (C) STRANDEDNESS: Double
      (D) TOPOLOGY: Linear

      (ii) MOLECULE TYPE: Genomic DNA
30

      (vi) ORIGINAL SOURCE:
      (A) ORGANISM: Leptospira interrogans
      (B) STRAIN: ATCC 23581
35

```

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 115

```

      TCGGCGGATT CTTGTAGTAT CCGCAACTGA CGGACCTATG CCACAAACAA      50
      AAGAACATAT CTTTCTTGCT CGTCAGGTAG GTGTTCCATA TGTAATTGTA      100
40    TTCATTAACA AAGCAGATAT GCTTGCTGCT GACGAAAGAG CAGAAATGAT      150
      CGAAATGGTT GAGATGGACG TTCGTGAACT TCTCAATAAG TATAGCTTCC      200
      CAGGAGATAC AACTCCTATC GTTCAITGGT TCTGCGGTAAA AGCACTTGAG      250
      GGCGATGAAT CTGAAATTGG GATGCCGTGCA ATTCTCAAAT TGATGGAAGC      300
      TCTGGATACT TTCGTTCCAA ATCCAAAACG TGTAATCGAC AAACCTTTCC      350
45    TTATGCCAGT AGAAGACGTT TTCTCGATCA CTGGTCGTGG AACTGTTGCA      400
      ACTGGAAGAG TGGAACAAGG TGTTTTGAAA GTGAACGACG AAGTTGAAAT      450
      TATCGGTATC CGCCCAACAA CAAAACTGT TGTTACCGGT ATCGAAATGT      500
      TCAGAAAAC TCTCGATCAA GCGGAAGCTG GCGACAACAT CGGCGCTCTT      550
      CTTCGTGGAA CTAAAAAAGA AGAAATCGAA AGAGGGCAAG TTCTTGCGAA      600
50    GCCAGGTTCT ATCACTCCTC AAAAAAGTT TGCCGCTGAG GTGTATGTAT      650
      TAACTAAGGA TGAAGGCGGA CGTCATACTC CGTTTATCAA TAACTACCGT      700
      CCTCAGTTTT ACTTTAGAAC AACTGACGTA ACCGGAGTTT GTAACCTTCC      750
      TAATGGTGTC GAAATGGTTA TGCCTGGTGA TAACGTTTCT TTGACGGTTG      800
      AATTGATTAG CCCGATCGCA ATGGACAAGG GTCTTAAGTT CGC      843
55

```

## 2) INFORMATION FOR SEQ ID NO: 116

```

60    (i) SEQUENCE CHARACTERISTICS:

```

70

(A) LENGTH: 832 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

5

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Megamonas hypermegale*  
 (B) STRAIN: ATCC 25560

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 116

15	CGGTGCTATC	CTCGTTGTTA	GTGCTGCTGA	TGGTCCTATG	CCTCAGACTC	50
	GTGAACACAT	CCTTCTCGCT	CGTCAGGTTG	GTGTTCCAGC	TATCGTTGTA	100
	TTCCTCAACA	AAGCTGACCA	GGTTGATGAC	CCTGAACTTC	TCGAACTTGT	150
	TGAAATGGAA	GTTCGTGAAC	TTCTTTCCAG	CTATGACTTC	CCAGGCGATG	200
	ACGTTCCAGT	AATCACTGGT	TCCGCTCTTC	AGGCTCTCGA	AGGCGACGAA	250
	GAAGCTAAAA	AGAAAATTCT	TGAATTAATG	GATGCTGTTG	ATGATTACAT	300
20	CCCAACTCCA	ACACGTGACA	CTGATAAACC	TTTCTTAATG	CCAGTTGAAG	350
	ACGTATTAC	AATTACTGGT	CGTGGTACTG	TTGCTACAGG	CCGTGTTGAA	400
	CGTGGCGAAC	TTAAACTTGG	TGACAGCGTT	GAAATCGTTG	GTCTTTCCGA	450
	TGAAAAGAAA	TCCACTACTG	TAAGTGGTAT	CGAAATGTTT	CGCAAAATGC	500
	TTGATAGCGC	TGTTGCTGGT	GATAACATCG	GTGCACTTCT	TCGTGGTATT	550
25	GACCGTAAAG	AAATCGAACG	TGGTCAAGTT	CTTGCTAAAC	CTGGCACAAT	600
	TCATCCACAC	AAAAAATTCA	AAGCTCAGGT	TTACGTATTA	ACTAAAGAAG	650
	AAGGTGGACG	TCATACTCCA	TTCTTCTCCA	ACTATCGTCC	ACAGTTCTAT	700
	TTCCGTAATA	CTGACGTTAC	TGGTGTTGTA	ACTCTTCCAG	AAGGTACTGA	750
	AATGGTTATG	CCTGGCGATA	ACATTGAAAT	GAGCATCGAA	CTCATCACTC	800
30	CAATCGCTAT	TGAAAAGGT	CTTCGCTTCG	CT		832

2) INFORMATION FOR SEQ ID NO: 117

35

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 820 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

40

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Mitsuokella multacida*  
 (B) STRAIN: ATCC 27723

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 117

50	TGGTGCTATC	CTCGTCGTTT	CCGCTGCTGA	TGGCCCGATG	CCGCAGACGC	50
	GTGAGCACAT	CCTGCTCGCT	CGCCAGGTCG	GTGTTCCGGC	AATCGTTGTC	100
	TTCCTCAACA	AGGTTGACCA	GGTTGACGAT	CCGGAGCTCC	TCGAGCTCGT	150
	CGAGATGGAA	GTTCGCGAGC	TGCTCTCCAG	CTACGACTTC	CCGGGCGATG	200
	ACATCCCTGT	AATCGCTGGT	TCCGCTCTGA	AGGCCCTCGA	AGGCGACGAA	250
55	GAGCAGAAGA	AGAATATCCT	CAAGCTCATG	GAAGCTGTCG	ATGAGTACAT	300
	CCCGACGCCG	GTCCGCGACA	ACGCTAAGCC	GTTCTTGATG	CCGGTTCGAGG	350
	ATGTCTTCAC	GATCACGGGC	CGTGGTACGG	TTGCAACGGG	CCGCGTTGAG	400
	CGTGGTGAGC	TCAAGATGAA	CGATACGGTT	GAGATCGTTG	GTCTGCAGGA	450
	CGAGCCGCGT	CAGACGGTTG	TCACGGGCAT	CGAGATGTTT	CGCAAGATGC	500
60	TTGATTTCGC	TGAGGCTGGC	GATAACATCG	GTGCTCTGCT	CCGTGGTATC	550



```

GACCGCAAGG AGATCGAGCG TGGCCAGGTT CTCGCAAAGC CGGGCACGAT      600
TCATCCGCAC ACGAAGTTCA AGGCTCAGGT CTATGTCCTG ACGAAAGAAG      650
AAGGCGGCCG TCATACGCCG TTCTTCACGA ACTATCGCCC GCAGTTCTAC      700
TTCCGCACGA CGGACGTAAC TGGCGTAGTC AAAGTGCCCG AAGGCACGGA      750
5 GATGGTTATG CCTGGCGATA ACGTCGAGAT GGAAGTTGAG CTCATCACCC      800
CGATCGCTAT CGAGAAGGGC                                     820

```

10 2) INFORMATION FOR SEQ ID NO: 118

(i) SEQUENCE CHARACTERISTICS:

```

(A) LENGTH: 831 bases
(B) TYPE: Nucleic acid
15 (C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

```

(ii) MOLECULE TYPE: Genomic DNA

20 (vi) ORIGINAL SOURCE:

```

(A) ORGANISM: Mobiluncus curtisii subsp. holmesii
(B) STRAIN: ATCC 35242

```

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 118

```

25 CGGCGCTATC CTCGTGGTGG CTGCTACTGA CGGTCCGATG GCTCAGACCA      50
AGGAACACAT CCTGTTGGCT AAGCAGGTTG GCGTGCCCTC CATCCTGGTC      100
GCTCTGAACA AGTGCGATTC TTCCGATGTG GACGAAGACA TGCTCGAAAT      150
CGTCGAGGAC GAAATCCGCG ATGACCTGGA GAAGCAGGGC TTCGATCGTG      200
30 ACTGCCCGAT TATCCACGTT TCCGCTCTGA AGGCCCTGGA AGGCGACCCC      250
GAGTGGACCA AGAAGATTGA AGAGCTCATG GAAGCGGTCG ATACCTACAT      300
TCCTGAGCCT GTTCGTGACC TCGACAAGCC GTTCTTGATG CCTATCGAAG      350
ACGTCTTCAC CATTACTGGT CGCGGTACCG TAGTGACCGG TCGTGTGGAA      400
CGCGGCAAGC TACCGTTGAA CGCCGAAGTG GAAATCGTAG GTATTTCGTCC      450
35 TACGCAAAAG ACCACCGTTA CCGGTATCGA AATGTTCCAC AAGTCCATGG      500
ACGAAGCCTA CGCCGGCGAG AACTGTGGTC TGTGCTGCG TGGCACCAAG      550
CGTGAGGACG TTGAGCGCGG TCAGGTTGTC TGCATTCCTG GCTCCGTGAC      600
CCCGCACACC AAGTTCGAGG GCAAGGTCTA CATCTTGAAG AAGGACGAAG      650
GTGGACGTCA CAAGTCGTTT TACGACGGCT ACCGCCCGCA GTTCTTCTTC      700
40 CGCACCACCG ACGTGACCGG TGTTATTCAC CTGCCCGAAG GCACCGAAAT      750
GGTTATGCCT GCGACACCA CCGAAATTAG CGTTGAGCTG ATTCAGCCTA      800
TCGCTATGGA GGAAGGTCTC GGCTTCGCTA 1' 831

```

45

2) INFORMATION FOR SEQ ID NO: 119

(i) SEQUENCE CHARACTERISTICS:

```

(A) LENGTH: 825 bases
50 (B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

```

(ii) MOLECULE TYPE: Genomic DNA

55

(vi) ORIGINAL SOURCE:

```

(A) ORGANISM: Moellerella wisconsensis
(B) STRAIN: ATCC 35017

```

60 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 119

```

      GGTGCAATTC TGGTTGTTGC TGCAACTGAT GGCCCTATGC CACAGACTCG      50
      TGAGCACATC CTGTTAGGTC GTCAGGTTGG CGTTCCATAC ATCATCGTTT      100
      TCCTGAACAA ATGTGACATG GTAGACGACG AAGAGCTGTT AGAACTGGTT      150
5     GAAATGGAAG TCCGTGAGCT GCTGTCTCAG TACGATTTCC CAGGCGATGA      200
      CACTCCAGTA ATCCGTGGTT CAGCGCTGAA AGCTCTGGAA GGCGAAGCTG      250
      AGTGGGAAGC TAAAATCATT GAACTGGCAG AAGCACTGGA TTCTTATATC      300
      CCAGAGCCAG AGCGTGACAT TGATAAGCCA TTCCTGTTAC CAATCGAAGA      350
      CGTATTCTCA ATTTCAGGCC GTGGTACAGT TGTTACTGGT CGTGTGAGC      400
10    GTGGTATCGT TAAAGTCGGT GAAGAAGTTG AAATCGTTGG TATCAAAGAT      450
      ACCGTGAAAA CAACATGTAC TGGCGTTGAA ATGTTCCGTA AACTGCTGGA      500
      CGAAGGCCGT GCTGGTGAGA ACGTTGGTGT TCTGCTGCGT GGTACTAAAC      550
      GTGATGATAT CGAACGTGGT CAAGTATTGG CTAAACCAGG TTCAATCACT      600
      CCGCATACAA CTTTCGAATC AGAAGTTTAC ATCCTGAGCA AAGATGAAGG      650
15    TGGCCGTCAT ACTCCATTCT TCAAAGGTTA CCGTCCACAG TTCTACTTCC      700
      GTACAACTGA CGTAACCGGT ACTATCGAAC TGCCAGAAGG CGTTGAGATG      750
      GTAATGCCAG GTGATAACAT CAAATGATC GTTACTCTGA TCCACCCAAT      800
      TGCAATGGAT GCAGGTCTGC GTTTTT      825

```

20

## 2) INFORMATION FOR SEQ ID NO:120

## (i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 827 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

## 30 (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Branhamella catarrhalis*  
 (B) STRAIN: ATCC 43628

35

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 120

```

      TGGTGCTATC TTGGTTGTTT CTGCAACTGA TGGTCCTATG CCACAAACTC      50
      GTGAGCATAT CCTACTATCT CGTCAGGTTG GTGTACCATA CATCATGGTA      100
40    TTCATGAACA AGTGCGATAT GGTGATGAT GAAGAGCTAC TAGAATTGGT      150
      TGAATGGAAG GTTCGTGAAC TTCTATCTGA CTATGATTTT CCTGGTGATG      200
      ATACCCCAAT CATCAAAGGT TCAGCACTAG AAGCATTGAA TGGTTCTGAT      250
      GGTAAATATG GCGAGCCTGC AGTTCTAGAA CTGCTAGACA CACTAGACAG      300
      CTATATCCCA GAGCCTGAGC GTGATATCGA TAAGTCATTC TTGATGCCAA      350
45    TTGAAGATGT CTTCTCGATC TCAGGTCGTG GTACAGTTGT GACTGGTCGT      400
      GTTGAATCAG GTATTATTAA AGTTGGTGAT GAAATTGAAA TCATCGGTAT      450
      CAAACCAACT GCTAAAACCA CCTGTACTGG TGTGAAATG TTCCGTAAAC      500
      TGTTAGACGA AGGTCGTGCA GGTGAGAACT GTGGTATCTT GTTGCCTGGT      550
      ACTAAGCGTG AAGAAGTTCA ACGCGGTCAA GTACTTGCAA AACCAGGTTT      600
50    AATCACCCCA CATACTAAGT TTGATGCTGA AGTTTATGTA CTGTCAAAG      650
      AAGAAGGTGG TCGTCACACC CCATTCTTAA ATGGCTATCG CCCACAGTTC      700
      TACTTCCGTA CCACAGATGT GACTGGTGCC ATCACTCTAC AAGAAGGTAC      750
      CGAAATGGTT ATGCCTGGTG ACAATGTTGA GATGAGTGTT GAGCTTATCC      800
      ACCCAATCGC CAGGATAAAG GTCTACG      827

```

55

## 2) INFORMATION FOR SEQ ID NO: 121

## 60 (i) SEQUENCE CHARACTERISTICS:

73

(A) LENGTH: 806 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

5

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Morganella morganii* subsp. *morganii*  
 (B) STRAIN: ATCC 25830

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 121

	CGGCGCTATC	CTGGTTGTTG	CTGCAACTGA	TGGCCCTATG	CCACAGACCC	50
15	GTGAGCACAT	CCTGTTAGGT	CGTCAGGTTG	GCGTTCCTTA	CATCATCGTA	100
	TTCCTGAACA	AATGTGACAT	GGTTGATGAT	GAAGAGCTGC	TGGAAGCTGGT	150
	TGAAATGGAA	GTTTCGTGAAC	TTCTGTCTCA	GTACGATTTC	CCTGGCGACG	200
	ACACGCCAAT	CGTTCGCGGT	TCAGCGCTGA	AAGCACTGGA	AGGCGAGCCA	250
	GAGTGGGAAG	CTAARATCGT	TGAAGTGGCA	GGTTTCCTGG	ATTCTTACAT	300
20	CCCTGAGCCA	GAGCGTGCAA	TTGACAAGCC	GTTCCCTGCTG	CCAATCGAAG	350
	ACGTATTCTC	AATCTCCGGC	CGTGGTACCG	TTGTTACCGG	TCGTGTTGAG	400
	CGCGGTATCA	TCAAGGTTGG	TGAGGAAGTT	GAAATCGTGG	GTATCAAAGA	450
	TACTGCGAAA	ACCACCTGTA	CCGGTGTGTA	AATGTTCCGC	AAACTGCTGG	500
	ACGAAGGCCG	TGCMGGTGAG	AACGTCGGTG	TTCTGCTGCG	TGGTACCAAG	550
25	CGTGAAGAAA	TCGAACGTGG	TCAGGTTCTG	GCTAAACCAG	GTTCAATCAA	600
	ACCACAYACC	AAATTGGAAT	CAGAAGTTTA	TATTCTGAGC	AAAGATGAAG	650
	GTGGTCGTCA	TACTCCATTTC	TTCAAAGGYT	ACCGTCCACA	GTTCTACTTC	700
	CGTACCACAG	ACGTAACAGG	TACTATCGAA	CTGCCGGAAG	GCGTTGAAAT	750
	GGTAATGCCG	GGCGACAACA	TCAAATGAT	CGTCACCCTG	ATCCACCCAA	800
30	TCGCAA					806

2) INFORMATION FOR SEQ ID NO: 122

35

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 825 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

40

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Mycobacterium tuberculosis*  
 (B) STRAIN: TB 299

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 122

50	GGTGCATCC	TGGTGGTCGC	CGCCACCGAC	GGCCCGATGC	CCCAGACCCG	50
	CGAGCACGTT	CTGCTGGCGC	GTCAAGTGGG	TGTGCCCTAC	ATCCTGGTAG	100
	CGCTGAACAA	GGCCGACGCA	GTGGACGACG	AGGAGCTGCT	CGAACTCGTC	150
	GAGATGGAGG	TCCGCGAGCT	GCTGGCTGCC	CAGGAATTCG	ACGAGGACGC	200
	CCCGGTTGTG	CGGGTCTCGG	CGCTCAAGGC	GCTCGAGGGT	GACGCGAAGT	250
55	GGGTTGCCCTC	TGTCGAGGAA	CTGATGAACG	CGGTCGACGA	GTCGATTCCG	300
	GACCCGGTCC	GCGAGACCGA	CAAGCCGTTC	CTGATGCCGG	TCGAGGACGT	350
	CTTCACCAT	ACCGGCCGCG	GAACCGTGGT	CACCGGACGT	GTGGAGCGCG	400
	GCGTGATCAA	CGTGAACGAG	GAAGTTGAGA	TCGTCGGCAT	TCGCCCATCG	450
	ACCACCAAGA	CCACCGTCAC	CGGTGTGGAG	ATGTTCCGCA	AGCTGCTCGA	500
60	CCAGGGCCAG	GCGGGCGACA	ACGTTGGTTT	GCTGCTGCGG	GGCGTCAAGC	550

	GCGAGGACGT	CGAGCGTGGC	CAGGTTGTCA	CCAAGCCCCG	CACCACCACG	600
	CCGCACACCG	AGTTCGAAGG	CCAGGTCTAC	ATCCTGTCCA	AGGACGAGGG	650
	CGGCCGGCAC	ACGCCGTTCT	TCAACAATA	CCGTCCGCAG	TTCTACTTCC	700
	GCACCACCGA	CGTGACCGGT	GTGGTGACAC	TGCCGGAGGG	CACCGAGATG	750
5	GTGATGCCCG	GTGACAAAC	CAACATCTCG	GTGAAGTTGA	TCCAGCCCGT	800
	CGCCATGGAC	GAAGGTCTGC	GTTTC			825

## 10 2) INFORMATION FOR SEQ ID NO: 123

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 806 bases  
 (B) TYPE: Nucleic acid  
 15 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

## 20 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Neisseria cinerea*  
 (B) STRAIN: ATCC 14685

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 123

25	CGGTGCGATC	TTGGTATGTT	CCGCAGCTGA	CGGTCCTATG	CCGCAAACCTC	50
	GCGAACACAT	CCTGTTGGCC	CGCCAAGTAG	GTGTACCTTA	CATCATCGTG	100
	TTCATGAACA	AATGCGACAT	GGTTGACGAT	GCCGAGCTGT	TGGAGCTGGT	150
	TGAAATGGAA	ATCCGTGACT	TGCTGTCAAG	CTACGACTTC	CCAGGTGACG	200
30	ACTGCCCCGAT	CGTACAAGGT	TCTGCACTGA	AAGCCTTGGA	AGGCGACGCA	250
	GCTTACGAAG	AAAAAATCTT	CGAATTGGCT	GCTGCATTGG	ACAGCTACAT	300
	CCCAACACCT	GAGCGTGCAG	TGGACAAACC	TTTCTTGTTG	CCTATCGAAG	350
	ACGTATTCTC	TATTTCCGGT	CGCGGTACAG	TAGTAACCGG	TCGTGTAGAG	400
	CGCGGTATCA	TCCACGTTGG	TGACGAGATC	GAAATCGTAG	GTCTGAAAGA	450
35	AACTCAAAAA	ACCACTTGTA	CCGGTGTGTA	AATGTTCCGC	AAACTGCTGG	500
	ACGAAGGTCA	AGCTGGTGAC	AACGTAGGTG	TATTGCTGCG	TGGTACTAAA	550
	CGTGAAGACG	TAGAGCGTGG	TCAAGTATTG	GCTAAACCGG	GTACTATCAC	600
	TCCTCACACC	AAGTTCAAAG	CAGAAGTATA	CGTACTGAGC	AAAGAAGAGG	650
	GTGGTCGTCA	CACTCCGTTC	TTCGCTAACT	ACCGTCCACA	ATTCTACTTC	700
40	CGTACTACCG	ACGTAACCGG	CGCGGTTACT	TTGGAAGAAG	GTGTAGAAAT	750
	GGTAATGCCG	GGTGAGAACG	TAACCATTAC	TGTAGAACTG	ATTGCGCCTA	800
	TCGCTA					806

45

## 2) INFORMATION FOR SEQ ID NO: 124

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 822 bases  
 50 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

55

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Neisseria elongata* subsp. *elongata*  
 (B) STRAIN: ATCC 25295

## 60 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 124

```

      CGGCGCAATC TTGGTATGTT CCGCTGCTGA CCGTCCTATG CCGCAAACCTC      50
      GCGAACACAT CCTGTTGGCC CGCCAAGTAG GCGTACCTTA CATCATCGTG      100
      TTCATGAATA AATGCGACAT GGTGAYGAT GCCGAACCTGC TGGAACTGGT      150
5     TGAATGGAA ATCCGTGACT TGCTGTCAAG CTACGACTTC CCAGGCGACG      200
      ACTGCCCGAT CGTACAAGGT TCCGCACTGA AAGCCTTGGA AGGCGACGCA      250
      GCTTACGAAG AAAAAATCTT CGAACTGGCT GCTGCATTGG ACAGCTACAT      300
      CCCGACACCT GAGCGTGCCG TGGACAAACC GTTCCTGTTG CCTATCGAAG      350
      ACGTATTCTC TATCTCCGGC CGTGGTACAG TAGTAACCGG TCGTGTAGAG      400
10    CGCGGTATCA TCCACGTCGG TGACGAGATC GAAATCGTAG GTCTGAAAGA      450
      AACCCAAAAA ACCACTTGTA CCGGTGTTGA AATGTTCCGC AAAGTGTCTG      500
      ACGAAGGTCA AGCAGGTGAC AACGTAGGCG TATTGCTGCG CGGTACCAAA      550
      CGTGAAGAAG TGGAACGCGG TCAAGTATTG GCTAAACCGG GTACCATCAC      600
      TCCTCACACC AAATTCAAAG CAGAAGTTTA CGTATTGAGC AAAGAAGAGG      650
15    GTGGTCGTCA TACTCCGTTT TTCGCTAACT ACCGTCCACA ATTCTACTTC      700
      CGTACTACCG ACGTAACCGG TGCGGTTACT TTGGAAGAAG GTGTAGAAAT      750
      GGTATGCCT GGTGAGAACG TGGCCATCAC TGTAGAACTG ATTGCACCTA      800
      TCGCTATGGA AGAAGGTCTG CG                                822

```

20

## 2) INFORMATION FOR SEQ ID NO: 125

```

      (i) SEQUENCE CHARACTERISTICS:
25      (A) LENGTH: 820 bases
      (B) TYPE: Nucleic acid
      (C) STRANDEDNESS: Double
      (D) TOPOLOGY: Linear

30      (ii) MOLECULE TYPE: Genomic DNA

      (vi) ORIGINAL SOURCE:
      (A) ORGANISM: Neisseria flavescens
      (B) STRAIN: ATCC 13120

```

35

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 125

```

      CGGCGCGACT TGGTATGTTC CGCAGCTGAC GGTCCTATGC CGAAACCCG      50
      CGAACACATC CTGTTGGCTC GCCAAGTAGG TGTACCTTAC ATCATCGTAT      100
40    TCATGAACAA ATGCGACATG GTAGACGATG CCGAGCTGTT GGAAGTGGTT      150
      GAAATGGAAA TTCGTGACTT GTTGTCAGC TACGACTTCC CAGGCGACGA      200
      CTGCCCAATC GTACAAGGTT CTGCACTGAA AGCTTTGGAA GGTGATGCTG      250
      CTTACGAAGA AAAAAATCTT GAATTGGCTG CTGCCTTGGA CAGCTACATC      300
      CCAACACCTG AGCGTGCTGT GGACAAACCT TTCTTGTTGC CTATCGAAGA      350
45    CGTATTCTCT ATCTCTGGTC GTGGTACAGT AGTAACCGGT CGCGTAGAGC      400
      GCGGTATCAT CCACGTTGGT GACGAGATCG AAATCGTAGG TCTGAAAGAA      450
      ACTCAAAAAA CCACTTGTAC CGGCGTTGAA ATGTTCCGCA AACTGCTGGA      500
      CGAAGGTCAA GCAGGTGACA ACGTAGGCGT ATTGCTGCGT GGTACTAAAC      550
      GTGAAGACGT AGAGCGTGGT CAAGTATTGG CTAAACCAGG TACCATCACT      600
50    CCTCACACCA AATTCAAAGC AGAAGTATAC GTACTGAGCA AAGAAGAGGG      650
      TGGTCGTCAC ACTCCATTTT TCGCTAACTA CCGTCCACAA TTCTACTTCC      700
      GTACTACCGA CGTAACTGGT GCAGTTACTT TGGAAGAAGG CGTAGAAATG      750
      GTAATGCCAG GTGAGAACGT AACCATTACT GTAGAACTGA TTGCGCCAAT      800
      CGCTATGGAA GAAGTCTGCG                                820

```

55

## 2) INFORMATION FOR SEQ ID NO: 126

```

60      (i) SEQUENCE CHARACTERISTICS:

```

(A) LENGTH: 830 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

5

(ii) MOLECULE TYPE: Genomic DNA.

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Neisseria gonorrhoeae*  
 (B) STRAIN: ATCC 49226

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 126

	GGTGCAATCC	TGGTATGTTT	TGCTGCCGAC	GGCCCTATGC	CGCAAACCCG	50
15	CGAACACATC	CTGCTGGCCC	GTCAAGTAGG	CGTACCTTAC	ATCATCGTGT	100
	TCATGAACAA	ATGCGACATG	GTCGACGATG	CCGAGCTGTT	GGAAGTGGTT	150
	GAAATGGAAA	TCCGCGACCT	GCTGTCCAGC	TACGACTTCC	CCGGCGACGA	200
	CTGCCCCGATC	GTACAAGGTT	CCGCACTGAA	AGCCTTGAA	GGCGATGCCG	250
	CTTACGAAGA	AAAAATCTTC	GAACTGGCTA	CCGCATTGGA	CAGCTACATC	300
20	CCGACTCCCG	AGCGTGCCGT	GGACAAACCA	TTCCTGCTGC	CTATCGAAGA	350
	CGTGTCTCTCC	ATTTCCGGCC	GCGGTACCGT	AGTCACCGGC	CGTGTAGAGC	400
	GAGGTATCAT	CCACGTTGGT	GACGAGATTG	AAATCGTCGG	TCTGAAAGAA	450
	ACCCAAAAAA	CCACCTGTAC	CGGCGTTGAA	ATGTTCCGCA	AACTGCTGGA	500
	CGAAGGTCAG	GCGGGCGACA	ACGTAGGCGT	ATTGCTGCGC	GGTACCAAAC	550
25	GTGAAGACGT	AGAACGCGGT	CAGGTATTGG	CCAAACCGGG	TACTATCACT	600
	CCTCACACCA	AGTTCAAAGC	AGAAGTGTAC	GTATTGAGCA	AAGAAGAGGG	650
	CGGCCGCCAT	ACCCCGTTTT	TCGCCAACTA	CCGTCCCCAA	TTCTACTTCC	700
	GTACCACTGA	CGTAACCGGC	GCGGTTACTT	TGGAAAAAGG	TGTGGAAATG	750
	GTAATGCCGG	GTGAGAACGT	AACCATTACT	GTAGAACTGA	TTGCGCCTAT	800
30	CGCTATGGAA	GAAGGTCTGC	GCTTTGCGAT			830

2) INFORMATION FOR SEQ ID NO: 127

35

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 816 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

40

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Neisseria lactamica*  
 (B) STRAIN: ATCC 23970

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 127

50	CGGCGCAATC	TTGGTATGTT	CCGCCGCCGA	CGGCCCTATG	CCGCAAACCC	50
	GCGAACACAT	TCTGTTGGCC	CGCCAAGTAG	GTGTACCTTA	CATCATCGTA	100
	TTCATGAACA	AATGCGATAT	GGTCGACGAT	GCCGAGCTGT	TGGAAGTGGT	150
	TGAAATGGAA	ATCCGCGACC	TGCTGTCAAG	CTACGACTTC	CCAGGCGACG	200
	ACTGCCCAAT	CGTACAAGGT	TCCGCACTGA	AAGCTTTGGA	AGGCGATGCC	250
55	GCTTACGAAG	AAAAAATCTT	CGAACTGGCT	GCCGCATTGG	ACAGCTACAT	300
	CCCGACTCCC	GAGCGTGCCG	TGGACAAACC	GTTCTTGCTG	CCTATCGAAG	350
	ACGTATTCTC	CATCTCCGGC	CGCGGTACGG	TAGTAACCGG	CCGTGTAGAG	400
	CGCGGTGTCA	TCCACGTTGG	CGACGAGATC	GAAATCGTCG	GTCTGAAAGA	450
	AACCCAAAAA	ACCACCTGTA	CCGGTGTCTGA	GATGTTCCGC	AAACTGCTGG	500
60	ACGAAGGTCA	GGCAGGCGAC	AACGTAGGCG	TATTGCTGCG	CGGTACCAAA	550

```

      CGTGAAGAAG TGGAACGCGG TCAGGTATTA GCCAAACCGG GTACCATCAC      600
      TCCGCACACC AAGTTCAAAG CAGAAGTGTA TGTATTGAGC AAAGAAGAGG      650
      GCGGTCGTCA CACTCCGTTC TTCGCCAACT ACCGTCCGCA ATTCTACTTC      700
      CGTACCACCG ACGTAACCGG CGCGGTTACT TTGGAAGAAG GCGTGGAAAT      750
5     GGTAATGCCC GGTGAGAACG TAACCATTAC TGTAGAAGT ATTGCGCCTA      800
      TCGCTATGGA AGAAGG      816

```

10 2) INFORMATION FOR SEQ ID NO: 128

(i) SEQUENCE CHARACTERISTICS:

```

      (A) LENGTH: 831 bases
      (B) TYPE: Nucleic acid
15     (C) STRANDEDNESS: Double
      (D) TOPOLOGY: Linear

```

(ii) MOLECULE TYPE: Genomic DNA

20 (vi) ORIGINAL SOURCE:

```

      (A) ORGANISM: Neisseria meningitidis
      (B) STRAIN: ATCC 13077

```

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 128

```

25     CGGTGCAATC CTGGTATGTT CCGCAGCCGA CGGTCCTATG CCGCAAACCC      50
      GCGAACACAT CCTGCTGGCC CGTCAAGTAG GCGTACCTTA CATCATCGTG      100
      TTCATGAACA AATGCGACAT GGTGACGAT GCCGAGCTGT TGGAACTGGT      150
      TGAAATGGAA ATCCGCGACC TGCTGTCCAG CTACGACTTC CCCGGCGACG      200
30     ACTGCCCCGAT CGTACAAGGT TCCGCACTGA AAGCCTTGGA AGGCGATGCC      250
      GCTTACGAAG AAAAAATCTT CGAATTGGCT GCTGCATTGG ACAGCTACAT      300
      CCCGACTCCC GAGCGTGCCG TGGACAAACC TTTCTTGTTG CCTATCGAAG      350
      ACGTATTCTC TATTTCGGGT CGTGGTACAG TAGTAACCGG TCGTGTAGAG      400
      CGCGGTATCA TCCACGTCGG TGACGAGATC GAAATCGTCG GTCTGAAAGA      450
35     AACTCAAAAA ACCACTTGTA CCGGTGTTGA AATGTTCCGC AAAGTGTGCTGG      500
      ACGAAGGTCA AGCAGGCGAC AACGTAGGCG TATTGCTGCG CCGTACCAAA      550
      CGTGAAGACG TAGAGCGTGG TCAAGTATTG GCTAAACCGG GTACAATCAC      600
      TCCTCACACC AAGTTCAAAG CAGAAGTATA CGTACTGAGC AAAGAAGAGG      650
      GCGGCCGCCA TACCCCGTTC TTCGCCAACT ACCGTCCCCA ATTCTACTTC      700
40     CGTACCACCG ACGTAACCGG CGCGGTTACT TTGGAAGAAG GTGTGGAAAT      750
      GGTAATGCCG GGCGAGAACG TAACCATCAC CGTAGAAGT ATTGCGCCTA      800
      TCGCTATGGA AGAAGGTTTG CGCTTTGCGA T      831

```

45

2) INFORMATION FOR SEQ ID NO: 129

(i) SEQUENCE CHARACTERISTICS:

```

      (A) LENGTH: 815 bases
50     (B) TYPE: Nucleic acid
      (C) STRANDEDNESS: Double
      (D) TOPOLOGY: Linear

```

(ii) MOLECULE TYPE: Genomic DNA

55

(vi) ORIGINAL SOURCE:

```

      (A) ORGANISM: Neisseria mucosa
      (B) STRAIN: ATCC 19696

```

60 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 129

	CGGCGCAATC	TTGGTATGTT	CTGCTGCTGAC	CGGTCCTATG	CCGCAAACCC	50
	GYGAACACAT	CCTGTTGGCC	CGTCAAGTAG	GYGTACCTTA	CATCATCGTG	100
	TTCATGAACA	AATGCGACAT	GGTTGACGAT	GCCGAAYTGT	TGGAACGGT	150
5	TGAAATGGAA	ATCCGTGACT	TGCTGTCAAG	CTACGACTTC	CCTGGYGACG	200
	ACTGCCCGAT	TGTACAAGGT	TCTGCACTGA	AAGCCTTGGA	AGGCGATGCC	250
	GCTTACGAAG	AAAAAATCTT	CGAACTGGCT	GCCGCATTGG	ACAGCTACAT	300
	CCCGACTCCC	GAGCGTGCCG	TAGACAAACC	GTTCTCTGTTG	CCTATCGAAG	350
	ACGTATTCTC	CATCTCCGGT	CGTGGTACAG	TAGTAACCGG	CCGTGTAGAG	400
10	CGCGGTGTTA	TCCACGTTGG	TGACGAGATC	GAAATCGTAG	GTCTGAAAGA	450
	AACCCAAAAA	ACCACATGTA	CCGGTGTTGA	AATGTTCCGC	AAACTGCTGG	500
	ACGAAGGTCA	AGCCGGTGAC	AACGTAGGCG	TATTGCTGCG	CGGTACCAA	550
	CGTGAAGAAG	TGGAACGCGG	TCAAGTATTG	GCTAAACCGG	GTACCATCAC	600
	TCCGCACACC	AAATTCAAAG	CAGAAGTGTA	CGTATTGAGC	AAAGAAGAGG	650
15	GTGGTCGTCA	TACTCCGTTT	TTCGCTAACT	ACCGTCCTCA	ATTCTACTTC	700
	CGTACTACCG	ACGTAACCGG	TGCGGTTACT	TTGGAAGAAG	GTGTAGAAAT	750
	GTTTATGCCT	GGTGAGAAYG	TAGCCATYAC	TGTAGAAGT	ATTGCGCCTA	800
	TYGCTATGGA	AGAAG				815

20

## 2) INFORMATION FOR SEQ ID NO: 130

## (i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 829 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

## 30 (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Neisseria sicca*  
 (B) STRAIN: ATCC 9913

35

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 130

	GGCGCAATCT	TGGTATGTTT	CGCTGCTGAC	GGTCCTATGC	CGCAAACCCG	50
	CGAACACATC	CTGTTGGCCC	GCCAAGTAGG	CGTACCTTAC	ATCATCGTGT	100
40	TCATGAACAA	ATGCGACATG	GTTGACGATG	CCGAGCTGTT	GGAAGTGGTT	150
	GAAATGGAAA	TCCGTGACTT	GCTGTCAAGC	TACGACTTCC	CTGGTGACGA	200
	CTGCCCCGATC	GTACAAGGTT	CTGCACTGAA	AGCCTTGGA	GGCGACGCCG	250
	CTTACGAAGA	AAAAATCTTC	GAAGTGGCTG	CTGCATTGGA	CAGCTACATC	300
	CCGACTCCTG	AGCGTGCCGT	GGACAAACCG	TTCCTGTTGC	CTATTGAAGA	350
45	CGTATTCTCC	ATCTCCGGTC	GCGGTACCGT	AGTAACCGGC	CGTGTAGAGC	400
	GCGGTGTTAT	CCACGTTGGT	GACGAGATTG	AAATCGTAGG	TCTGAAAGAA	450
	ACCCAAAAAA	CCACTTGTAC	CGGTGTTGAA	ATGTTCCGCA	AACTGCTGGA	500
	CGAAGGTCAA	GCCGGTGACA	ACGTAGGCGT	ATTGCTGCGC	GGTACCAAAC	550
	GTGAAGAAGT	GGAACGCGGT	CAAGTATTGG	CTAAACCGGG	TACCATCACT	600
50	CCTCACACTA	AATTCAAAGC	AGAAGTTTAC	GTATTGAGTA	AAGAAGAGGG	650
	TGGTCGTCAT	ACTCCGTTCT	TCGCTAACTA	CCGTCCTCAA	TTCTACTTCC	700
	GTACTACCGA	CGTAACCGGC	GCGGTTACTT	TGGAAGAAGG	TGTAGAAATG	750
	GTTATGCCTG	GTGAGAACGT	AGCCATCACT	GTAGAAGTGA	TTGCACCGAT	800
	CGCTATGGAA	GAAGGTCTGC	GCTTTGCGA			829

55

## 2) INFORMATION FOR SEQ ID NO: 131

## 60 (i) SEQUENCE CHARACTERISTICS:

79



(A) LENGTH: 814 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

5

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Neisseria subflava*  
 (B) STRAIN: ATCC 14221

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 131

	CGGCGCGACT	TGGTATGTTC	CGCAGCTGAT	GGTCCTATGC	CTCAAACCTCG	50
15	CGAACACATC	CTGTTGGCTC	GCCAAGTAGG	TGTACCTTAC	ATCATCGTAT	100
	TCATGAACAA	ATGCGACATG	GTTGACGATG	CCGAGCTGTT	GGAAGTGGTT	150
	GAAATGGAAA	TCCGTGACCT	GTTGTCAAGC	TACGACTTCC	CAGGCGACGA	200
	CTGCCCAATC	GTACAAGGTT	CTGCACTGAA	AGCTTTGGAA	GGTGACGCTG	250
	GTTACGAAGA	GAAAATCTTC	GAATTGGCTG	CTGCTCTGGA	CAGCTACATC	300
20	CCAACACCTG	AGCGTGCTGT	GGACAAACCT	TTCTTGTTGC	CTATCGAAGA	350
	CGTATTCTCT	ATCTCTGGCC	GTGGTACAGT	AGTAACTGGT	CGTGTAGAGC	400
	GCGGTATCAT	CCACGTTGGT	GACGAGATCG	AAATCGTAGG	TCTGAAAGAA	450
	ACCCAAAAAA	CCACTTGTAC	CGGCGTTGAA	ATGTTCCGCA	AACTGCTGGA	500
	CGAAGGTCAA	GCTGGTGACA	ACGTAGGCGT	ATTGCTGCGT	GGTACCAAAC	550
25	GTGAAGACGT	AGAGCGTGGT	CAAGTATTGG	CTAAACCAGG	TACCATTACT	600
	CCTCACACCA	AATTCAAAGC	AGAAGTATAC	GTAAGTACCA	AAGAAGAGGG	650
	TGGTCGTCAC	ACTCCATTCT	TCGCTAACTA	CCGTCCACAA	TTCTACTTCC	700
	GTACTACTGA	CGTAACTGGT	GCAGTTACTT	TGGAAGAAGG	CGTAGAAATG	750
	GTAATGCCAG	GTGAGAACGT	AACCATTACT	GTAGAACTGA	TTGCGCCTAT	800
30	CGCTATGGAA	GAAG				814

2) INFORMATION FOR SEQ ID NO: 132

35

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 818 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

40

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Neisseria weaveri*  
 (B) STRAIN: ATCC 51223

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 132

50	GCCATCTTGG	TATGTTCTGC	TGCTGACGGT	CCTATGCCGC	AAACCCGTGA	50
	GCACATCCTG	TTGGCTCGTC	AAGTAGGTGT	ACCCTACATC	ATCGTATTCA	100
	TGAACAAATG	CGATATGGTT	GATGATGCAG	AGCTGCTGGA	ATTGGTAGAA	150
	ATGGAAATCC	GTGATCTGCT	GAGCAGCTAC	GATTTCCCTG	GCGATGATTG	200
	YCCAATCGTG	CAAGGTTCTG	CTTTGAAAGC	TTTGGAAGGT	GATGCCGCTT	250
55	ACGAAGAAAA	AATCTTTGAA	TTAGCTGCTG	CATTGGATAG	CTATATTCCA	300
	ACWCCTGAGC	GYGCTGTTGA	TAAACCATTC	CTGTTGCCGA	TTGAAGATGT	350
	ATTCTCAATT	TCAGGTCGTG	GTACAGTAGT	AACTGGTCGT	GTAAGAGCGC	400
	GTATTATTCA	CGTAGGCGAT	GAAATTGAAA	TTGTAGGTTT	GAAAGARACY	450
	CAAAAAACTA	CTTGTAACCG	CGTTGAAATG	TTCCGTAAAT	TGCTGGATSA	500
60	AGGTCAGGCT	GGTGATAACG	TAGGCGTATT	GTTGCGTGGT	ACCAAACGTG	550

AAGACGTTGA GCGTGGTCAA GTATTGGCTA AGCCTGGTWC TATTACTCCG 600  
 CAYACCAAAT TCAAAGCAGA RGTKTATGTW TTGAGYAAGG AAGAAGGCGG 650  
 TCGTCATACT CCGTTCTTCG CTAACATATCG TCCGCAATTC TATTCCCGTA 700  
 CTACAGACGT TACCGGTGCK GTRACTTTAG AAGAAGGTGT GGAAATGGTA 750  
 5 ATGCCTGGTG AGAAYGTTGC CATTACTGTW GARYTGATYG CTCCGATTGC 800  
 KATGGAAGAA GGYTGCGT 818

10 2) INFORMATION FOR SEQ ID NO: 133

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 836 bases  
 (B) TYPE: Nucleic acid  
 15 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

20 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Ochrobactrum anthropi*  
 (B) STRAIN: ATCC 49188

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 133

25 CGGCGCAATT CTGGTTGTTT CGGCCGCTGA CGGCCCGATG CCGCAGACCC 50  
 GTGAGCACAT CCTGCTCGCT CGTCAGGTTG GCGTTCGGC AATCGTCGTG 100  
 TTCCTGAACA AGTGCGACCA GGTGACGAT GCAGAACTGC TCGAACTGGT 150  
 TGAAGTGGAA GTTCGCGAAC TTCTGTCGAA ATACGATTTC CCGGGCGACG 200  
 30 AAGTTCGAT CATCAAGGGC TCGGCTCTTG CTGCTCTGGA AGATTCTTCG 250  
 AAGGAACTGG GCGAAGACGC CGTTCGTTTC CTGATGGCCG CTGTTGACGA 300  
 CTACATTCCG ACCCCGGAAC GTCCGATCGA CCAGCCGTTT CTGATGCCGA 350  
 TCGAAGACGT TTTCTCGATC TCGGGCCGTG GTACGGTTGT GACGGGTCGC 400  
 GTTGAGCGCG GTATCGTCAA GGTGTTGTA GAAGTTGAAA TCGTCGGCAT 450  
 35 CAAGGCGACG GCGAAGACGA CGGTAACCGG CGTTGAAATG TTCCGCAAGC 500  
 TGCTCGAYCA GGGCCAGGCT GGCAGACAAC TCGGCGCTCT GATCCGCGGC 550  
 GTTGGCCGTG AAGACGTTGA ACGCGGCCAG GTTCTCTGCA AGCCGGGTTT 600  
 TGTGAAGCCG CACACCAAGT TCAAGGCAGA AGCCTACATT CTGACCAAGG 650  
 ACGAAGGTGG CCGTCATACG CCGTTCTTTA CGAACTACCG TCCGCAAGTT 700  
 40 TACTTCCGCA CGACGGACGT GACCGGTGTT GTCACGCTGC CGGAAGGCAC 750  
 GGAAATGGTT ATGCCTGGCG ACAACGTCGC TATGGACGTC ACCCTGATCG 800  
 TGCCGATCGC CATGGAAGAG AAGCTCCGCT TCGCTA 836

45

2) INFORMATION FOR SEQ ID NO: 134

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 805 bases  
 50 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

55

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Pantoea agglomerans*  
 (B) STRAIN: ATCC 27155

60 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 134

```

      CCTGGTTGTT GCTGCGACTG ATGGCCCAAT GCCACAGACC CGTGAGCACA      50
      TCCTGCTGGG TCGTCAGGTT GCGGTTTCCTT ACATCATCGT GTTCCTGAAC      100
      AAGTGTGACA TGGTTGATGA TGAAGAGCTG CTGGAAGCTGG TAGAGATGGA      150
5     AGTACGTGAC CTGCTGTCAC AGTACGACTT CCCAGGCGAT GACACCCCGA      200
      TCGTTCGTGG TTCTGCTCTG AAAGCGCTGG AAGGCGTTCC TGAGTGGGAA      250
      GCAAAAATCG TTGAGCTGGC TGAACACCTG GACAACTACA TCCC GGATCC      300
      AGTCCGTGCG ATCGACATGC CGTTCCTGCT GCCAATCGAA GACGTATTCT      350
      CAATCTCTGG CCGTGGTACC GTTGTTACCG GTCGTGTTGA GCGCGGCATC      400
10    GTTAAAGTCG GCGACGAAGT TGAAATCGTG GGTATCAAAG ATACTGCGAA      450
      ATCAACCTGT ACCGGTGTTG AGATGTTCCG TAAGCTGCTG GACCAGGGTC      500
      AGGCAGGCGA AAAGTGTGGT GTTCTGCTGC GCGGTATCAA GCGTGAAGAC      550
      ATCCAGCGTG GCCAGGTTCT GGCTAAGCCA GGCTCAATCA AGCCGCACAC      600
      CCAGTTCGAG TCAGAAAGTTT ACGTTCTGTC TAAAGACGAA GGTGGCCGCC      650
15    ATACTCCGTT CTTCAAAGGC TATCGTCCAC AGTTCTACTT CCGTACAAC      700
      GATGTAACCG GTTCAGTAGA GCTGCCAGAA GGCGTTGAGA TGGTCATGCC      750
      AGGCGACAAC ATCAAAATGG TTGTTACCCT GATCCACCCA ATCGCAATGG      800
      ACGAA                                         805

```

20

## 2) INFORMATION FOR SEQ ID NO: 135

```

      (i) SEQUENCE CHARACTERISTICS:
25      (A) LENGTH: 825 bases
      (B) TYPE: Nucleic acid
      (C) STRANDEDNESS: Double
      (D) TOPOLOGY: Linear

30      (ii) MOLECULE TYPE: Genomic DNA

      (vi) ORIGINAL SOURCE:
      (A) ORGANISM: Pantoea dispersa
      (B) STRAIN: ATCC 14589

35      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 135

```

```

      CGCGATCCTG GTTGTGCTG C GACTGATGG CCCAATGCCT CAGACCCGTTG      50
      AGCACATCCT GCTGGGCCGT CAGGTTGGCG TTCCTTACAT CATCGTGTTC      100
40    CTGAACAAGT GTGACATGGT TGATGACGAA GAGCTGCTGG AACTGGTTGA      150
      GATGGAAGTT CGCGATCTGC TGTCTCAGTA CGACTTCCCA GGCGACGATA      200
      -----
      CCCAATCGT ACGCGGTTCT GCGCTGAAAG CGTGGGAAGG CGACGCTGAG      250
      TGGGAAGCGA AAGTCGTTGA GCTGGCTGGT CACCTGGATA CTTACATTCC      300
      AGATCCAGTA CGTGCTATCG ATCTGCCGTT CCTGCTGCCA ATCGAAGACG      350
45    TATTCTCAAT CTCTGGCCGT GGTACCGTTG TTACCGGTCT TGTTGAGCGC      400
      GGCATCGTGA AAGTGGGCGA CGAAGTAGAA ATCGTTGGTA TCAAAGCGAC      450
      TGCCAAGTCT ACCTGTACCG GTGTTGAAAT GTTCCGCAA CTGCTGGACC      500
      AGGGTCAGGC AGGCGAGAAC TGTGGTGTTC TGCTGCGCGG TATCAAGCGT      550
      GAAGAGATCC AGCGTGGTCA GGTCTGGCT AAGCCAGGCA CCATCAAGCC      600
50    ACACACCAAG TTCGTATCAG AAGTGTACGT ACTGTCTAAA GACGAAGGCG      650
      GCCGTCATAC TCCGTTCTTC AAAGGCTACC GTCCACAGTT CTAATTCCGT      700
      ACYACTGATG TGACCGGCAM CATMGAAGT CCAGAAGGCG TTGAGATGGT      750
      AATGCCAGGC GACAACATCA AAATGRCCGT TGAGCTGATC CACCCAATCG      800
      CGATGGACCA GGGTCTGCGT TTCGC                                         825

```

55

## 2) INFORMATION FOR SEQ ID NO: 136

```

60      (i) SEQUENCE CHARACTERISTICS:

```

(A) LENGTH: 762 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

5

(ii) MOLECULE TYPE: Genomic DNA.

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Pasteurella multocida*  
 (B) STRAIN: NCTC 10322

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 136

	CACAAACACG	TGAGCACATC	CTTTTAGGTC	GCCAAGTAGG	CGTTCCTTAC	50
15	ATCATCGTAT	TCTTAAACAA	ATGCGACATG	GTGGATGATG	AAGAATTATT	100
	AGAATTAGTT	GAAATGGAAG	TGCGTGAAC	TCTTTCTCAA	TATGATTTC	150
	CAGGTGATGA	TACACCAATC	GTACGTGGTT	CAGCGTTACA	AGCGTTAAAC	200
	GGYGTAGCTG	AGTGGGAAGA	GAAAATTCTT	GAGTTAGCCA	ACCACTTAGA	250
	TACTTACATT	CCAGAGCCAC	AACGTGCAAT	CGACCAACCG	TTCCTTCTTC	300
20	CGATTGAAGA	CGTGTCTCA	ATTTCTGGTC	GTGGTACAGT	AGTAACAGGT	350
	CGTGTGAGC	GTGGTATCAT	CCGTACAGGT	GAAGAGGTTG	AAATTGTTGG	400
	TATTAAAGCG	ACAACGAAGA	CCACAGTAAC	AGGTGTTGAG	ATGTTCCGTA	450
	AATTATTAGA	CGAAGGTCGT	GCGGGTGAGA	ACGTTGGTGC	TTTATTACGT	500
	GGTACTAARC	GTGAAGAAAT	CGAACGTGGT	CAAGTGTTAG	CGAAACCGGG	550
25	TTCAATYACG	CCACACACTG	ATTTTGAATC	AGAAGTTTAC	GTGTTATCAA	600
	AAGAAGAAGG	TGGTCGTCAT	ACACCATTCT	TCAAAGGTTA	CCGTCCACAG	650
	TTCTACTTCC	GTACAACGGA	CGTAACAGGT	ACAATCGAAT	TACCGGAAGG	700
	TGTTGAGATG	GTGATGCCTG	GTGATAACAT	CAAGATGACT	GTAAGTTTGA	750
30	TTCACCCAAT	CG				762

2) INFORMATION FOR SEQ ID NO: 137

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 832 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

40

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Peptostreptococcus anaerobius*  
 (B) STRAIN: ATCC 27337

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 137

	TGGAGCTATC	TTAGTTGTAT	CAGCAGCGGA	TGGACCAATG	CCACAAACAA	50
50	GAGAACACAT	CTTATTATCA	AGACAAAGTAG	GAGTACCATA	TATCGTAGTA	100
	TATTTGAATA	AAGCAGATAT	GGTAGAAGAT	GAAGAATTAT	TAGAATTAGT	150
	AGAAATGGAA	GTAAGAGAAT	TACTATCTGA	ATATGGATTG	CCAGGAGATG	200
	AAATTCCAAT	CATAACAGGA	TCATCCTTAG	GAGCATTAAT	TGGAGAACAA	250
	AAATGGATAG	ATCAAATCAT	GGCATTGATG	AAAGCCGTAG	ATGAATATAT	300
55	TCCAACACCG	GAAAGAGCAG	TAGATCAACC	ATTCTTGATG	CCAATCGAAG	350
	ACGTATTTAC	AATTACAGGA	AGAGGAACTG	TAGTAACAGG	AAGAGTTGAA	400
	AGAGGAGTTG	TAAAAGTWGG	AGAAGAAGTT	GAAATCGTAG	GAATCAAAGC	450
	GACAACAAAG	ACAACCTGTA	CYGGAGTAGA	AATGTTCCGA	AAATTATTGG	500
	ATCAAGGACA	AGCAGGAGAT	AACATCGGAG	CTTTATTRAG	AGGAACCAAG	550
60	AAAGAAGATG	TAGAAAGAGG	ACAAGTATTG	GCAAAACCAG	GAACAATTCA	600

```

TCCTCATACA AACTTCAGTG GAGAAGTATA TGTATTGACA AAAGAAGAAG      650
GAGGAAGACA TACTCCATTC TTCTCAGGAT ACAGACCACA ATTTTACTTT      700
AGAACCACAG ATATTACAGG AGCAGTAACA TTACCAGAAG GAGTAGAAAT      750
GGTAATGCCR GGAGATAATA TCACAATGAC AGTAGAATTG ATTCACCCAA      800
5  TTGCAATGGA AACAGGATTA CGATTTGCAA TT                        832

```

## 2) INFORMATION FOR SEQ ID NO: 138

10

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 823 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 15 (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- 20 (A) ORGANISM: *Peptostreptococcus asaccharolyticus*  
 (B) STRAIN: LSPQ 2639

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 138

```

25 TAGTATGTTT AGCAGCAGAY GGTCCAATGC CACAAACAAG AGAACACATT      50
   CTACTAGCAA GACAAGTTGG TGTACCAAAG ATAGTAGTAT TCCTAAACAA      100
   AGAAGACCAA GTAGACGATC CAGAACTAAT TGAATTAGTA GAGATGGAAA      150
   TCAGAGACCT ACTATCAGAA TATGACTTCG AYGGAGACAA CACACCAATC      200
   GTAGTAGGAT CAGCATTAAT AGCCCTAGAC GATCCAGACG GAGAATGGGG      250
30 AGACAAAATC GTAAACTATA TGGGAAGMAGT AGACGAATAC ATCCCAACAC      300
   CAGTAAGAGA TACAGAACAC CCATTTCCTAA TGCCAATCGA AGACRTATTC      350
   TCAATYACAG GAAGAGGAAC AGTAGCAACA GGAAGAGTAG AACAAGGTGT      400
   AGTAAAAGTA GGMGACACAG TAGAACTAGT AGGCTTAACA GACGAAAGCA      450
   GACAAGTAGT AGTAACAGGT GTAGAAATGT TTAGAAAACA ACTAGACCTA      500
35 GCAGAAGCMG GAGACAACAT TGGAGCCCTA CTAAGAGGAG TACAAAGAGA      550
   AGAAATCCAA AGAGGACAAG TACTAGCAGC ACCAGGAACA ATCAAACCAC      600
   ACACAAAATT TGAAGCAGAA GTATACGTAC TAACAAAAGA AGAAGGTGGA      650
   AGACACACAC CATTCTTTAA CGGATACAGA CCACAATTCT ACTTCAGAAC      700
   AACAGACGTA ACAGGAGACA TCCAAC TAGC AGACGGAGTA GAAATGGTAA      750
40 TGCCAGGAGA CAACTCAACA TTTACAGTAA CACTAATCAC ACCAATCGCA      800
   ATGGACGAAG GACTAAGATT CGC                        823

```

## 45 2) INFORMATION FOR SEQ ID NO: 139

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 832 bases  
 (B) TYPE: Nucleic acid  
 50 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- 55 (A) ORGANISM: *Peptostreptococcus prevotii*  
 (B) STRAIN: ATCC 9321

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 139

60

	CTATCATCGT	AGTATCTGCA	GCAGACGGTC	CAATGCCCAA	ACAGAGAGAA	50
	CACATCCTAC	TAGCAAGACA	AGTAGGCGTT	CCAAAAATCG	CAGTATTCCT	100
	AAACAAAGAA	GACCAAGTAG	ACGATCCAGA	ACTAATCGAA	TTAGTAGAAA	150
	TGGAAATCAG	AGACCTACTT	TCAGAATACG	ACTTCGATGG	AGACAACGCT	200
5	CCAGTAGTAG	TAGGATCTGC	TCTTAAATCA	CTAGAAGAAG	GCGGAGAAGG	250
	CCCATGGTCA	GACAAAATCC	TTGACCTAAT	GGCACAAGTA	GACGAATACT	300
	TCGACATCCC	AGAAAGAGAC	AACGACCAAC	CATTTCCTAAT	GCCAGTAGAA	350
	GACGTAATGA	CAATCTCAGG	ACGTGGAACA	GTAGCAACAG	GAAGAGTTGA	400
	AAGAGGAACA	CTAAAAGTTG	GTGATACAGT	AGAAATCGTA	GGACTAACAG	450
10	AAGATACAAA	AGAAACAGTA	GTAACCTGGAG	TAGAAATGTT	CCACAAATCM	500
	CTAGACCAAG	CAGAATCTGG	AGATAACGTA	GGACTACTAC	TAAGAGGAGT	550
	AACAAGAGAT	CAAATCTCAA	GAGGACAAGT	ACTAGCAAAA	CCAGGWTCAG	600
	TAAACCCACA	CACAGAATTC	GAAGGTCAAG	TATACGTACT	AACAAAAGAA	650
	GAAGGTGGAC	GTCACACACC	ATTCTTCAGT	GGATATAGAC	CACAATTCTT	700
15	CTTTAGAACA	ACAGACGTAA	CAGGAGACAT	CGAACTAGAA	GAAGGCGTAG	750
	AAATGGTAAT	GCCAGGAGAC	AACGCAACAT	TCAAAATCAC	ACTCCAAAAA	800
	CCAATCGCTC	TAGAAGAAGG	ACTAAGATTC	GC		832

20

## 2) INFORMATION FOR SEQ ID NO: 140

## (i) SEQUENCE CHARACTERISTICS:

- |    |     |                      |
|----|-----|----------------------|
|    | (A) | LENGTH: 831 bases    |
| 25 | (B) | TYPE: Nucleic acid   |
|    | (C) | STRANDEDNESS: Double |
|    | (D) | TOPOLOGY: Linear     |

## (ii) MOLECULE TYPE: Genomic DNA

30

## (vi) ORIGINAL SOURCE:

- |  |     |  |
|--|-----|--|
|  | (A) | ORGANISM: <i>Porphyromonas asaccharolytica</i> |
|  | (B) | STRAIN: ATCC 25260                             |

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 140

	CGGTGCTATC	ATCGTAGTTG	CTGCAACTGA	TGGTCCTATG	CCTCAGACGC	50
	GTGAGCACAT	CCTACTAGCA	CGTCAGGTCA	ACGTACCTCG	TCTAGTTGTC	100
	TTTATGAACA	AGTGCGACCT	TGTTGATGAC	GAGGAGATGC	TCGAGCTCGT	150
40	AGAGATGGAT	ATGCGTGAGC	TACTAAGCTT	CTATGACTTT	GACGGCGACA	200
	ACACTCCTGT	CATCCGTGGT	TCTGCTCTTG	GTGCTCTCAA	TGGTGAGCCT	250
	AAGTGGGTAG	AGAAGGTTAT	GGAGCTCATG	GAGGCTGTAG	ACACTTGGAT	300
	CCCACTACCT	GAGCGCGACA	TCGACAAGCC	TTTCCTAATG	CCTGTAGAGG	350
	ACGTATTCTC	TATCACAGGT	CGTGGTACTG	TCGCTACTGG	TCGTATCGAG	400
45	ACTGGTGTCTG	TTAAGGTCAA	CGATGAGGTT	CAGATCATCG	GTCTAGGTGC	450
	TGAGGGTAAG	AAGAGCGTCG	TAAGTGGCGT	GGAAATGTTT	CGCAAGATCC	500
	TTGATGAGGG	TGAAGCTGGT	GATAACGTAG	GTCTCCTACT	CCGTGGTATC	550
	GACAAGGACG	AGATCAAGCG	CGGTATGGTC	CTAGCACACC	CAGGTCAGGT	600
	CAAGCCTCAC	GATCACTTCA	AGGCTGAGGT	CTATATCCTG	AAGAAGGAAG	650
50	AGGGTGTTCTG	TCACACACCA	TTCCACAACA	AGTACCGTCC	TCAGTTCTAC	700
	ATCCGTACGC	TAGACGTAAC	GGGCGAGATC	ACACTCCCAG	AGGGTGTAGA	750
	GATGGTTATG	CCTGGTGATA	ACGTCACCAT	CGATGTCAAG	CTCATCTCTC	800
	CAGTAGCTTG	TAGCGTAGGT	CTACGCTTCG	C		831

55

## 2) INFORMATION FOR SEQ ID NO: 141

## (i) SEQUENCE CHARACTERISTICS:

- |    |     |                   |
|----|-----|-------------------|
| 60 | (A) | LENGTH: 818 bases |
|----|-----|-------------------|

85

(B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

5 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Porphyromonas gingivalis*  
 (B) STRAIN: ATCC 33277

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 141

	CGGTGCTATA	ATCGTTGTAG	CAGCTACAGA	CGGTCCTATG	CCTCAGACTC	50
	GCGAGCACAT	CCTTTTGGCT	CGCCAGGTAA	ACGTTCCCTCG	TCTGGTTGTT	100
15	TTCATGAACA	AATGTGACAT	GGTAGACGAT	GAAGAGATGC	TCGAGCTTGT	150
	TGAAATGGAC	ATGCGCGAAC	TCCTTTCTTT	CTACGATTTC	GATGGTGACA	200
	ATACCCCTAT	CATCCGTGGT	TCTGCTCTGG	GCGCTTTGAA	TGGAGAGCCT	250
	CAGTGGGAAG	ACAAGGTGAT	GGAGCTTATG	GAAGCTGTTG	ACAACCTGGGT	300
	TCCCCTGCCT	GAGCGCGATA	TCGACAAACC	GTTCTTGATG	CCGGTTGAAG	350
20	ACGTGTTCTC	TATCACGGGT	CGTGGTACGG	TCGCTACAGG	ACGTATCGAA	400
	ACCGGTATTG	TGAAGACCGG	TGACGAAGTT	CAAATCATCG	GCCTCGGTGC	450
	AGAAGGAATG	AAGTCGGTTG	TTACGGGTGT	TGAAATGTTC	CGTAAGATTC	500
	TTGACGAAGG	TCAGGCTGGT	GACAACGTTG	GTCTCCTCCT	GCGTGGTATC	550
	GATAAGGATC	AGATCAAGCG	TGGTATGGTT	ATCTCTCACC	CGGGTAAGAT	600
25	TACTCCTCAC	AAGAGATTTA	AGGCCGAGGT	TTATATCTTG	AAGAAAGAAG	650
	AAGGTGGTTC	CCACACTCCT	TTCCACAACA	AATATCGTCC	GCAGTTCTAC	700
	ATCCGTACGC	TTGACGTGAC	CGGTGAAATC	ACTCTTCCCG	AAGGAACAGA	750
	AATGGTTATG	CCCGGTGACA	ACGTAACGAT	CACTGTAGAA	CTCATCTACC	800
30	CGGTTGCATG	TAATGTAG				818

2) INFORMATION FOR SEQ ID NO: 142

35 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 830 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

40

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Pragia fontium*  
 45 (B) STRAIN: ATCC 49100

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 142

	CGGCGCTATT	CTGGTTGTTG	CTGCAACTGA	TGGTCCTATG	CCTCAAACCTC	50
50	GTGAGCACAT	CCTGTTAGGY	CGCCAGGTTG	GCGTACCATA	CATCATTGTG	100
	TTCCTGAACA	AGTGTGACAT	GGTTGAYGAT	GAAGAGCTGT	TAGAAGCTGGT	150
	TGAAATGGAA	GTTCTGTGAGC	TTCTGTCTCA	GTACGATTTC	CCAGGTGATG	200
	ATACTCCAGT	TGTTCTGTGGT	TCTGCGCTGA	AAGCGTTTGA	AGGCGAAGCT	250
	GAGTGGGAAG	CTAAAATCAT	TGAATTGGCT	GAATCCCTGG	AYAGCTACAT	300
55	TCCACAGCCA	GAGCGTGCAA	TTGATAAGCC	GTTCTGTCTG	CCAATCGAAG	350
	ACGTTTTTCTC	AATCTCTGGC	CGTGGTACAG	TAGTAACCGG	TCGTGTAGAG	400
	CGCGGTATCG	TTAAAGTTGG	TGAAGAAGTT	GAAATCGTTG	GTATCAAAGA	450
	TACTGTGAAA	ACAACCTTGT	CTGCGGTTGA	AATGTTCCGT	AARTTACTGG	500
	ATGAAGGCCG	TGCGGGTGAG	AACGTTGGTG	TTCTGCTGCG	TGGTACTAAG	550
60	CGTGATGAAA	TCGAACGTGG	TCAAGTATTA	GCAAAACCAG	GTTCAATCAA	600

```

      CCCGCATACT AACTTCGTAT CAGAAGTTTA TATCCTGAGC AAAGATGAAG      650
      GTGGTCGTCA TACTCCATTC TTCAAAGGCT ACCGTCCACA GTTYTACTTC      700
      CGTACAAC TG ACGTGACCGG TACCATCGAA CTGCCAGAAG GCGTAGAGAT      750
      GGTAAATGCCA GGTGATAACA TTCAGATGAC TGTAAC TCTG ATTGCCCCAA      800
5     TCGCGATGGA CGAAGGTTTA CGCTTTCGCTA      830

```

## 2) INFORMATION FOR SEQ ID NO: 143

10

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 821 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 15 (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- 20 (A) ORGANISM: *Prevotella melaninogenica*  
 (B) STRAIN: ATCC 25845

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 143

```

25  TGGTGCTATC TTGGTTGTAG CTGCTACTGA TGGTCCTATG CCTCAGACTC      50
      GTGAGCACGT ATTGCTCGCT CGTCAGGTAA ACGTACCTCG CTTGGTTGTA      100
      TTCTTGAACA AGTGTGATAT GGTGACGAT GCTGAGATGC TTGACCTCGT      150
      TGAGATGGAG GTTCGTGAGA TCCTCGAGCA GTACGGTTAT GAGGAGGATA      200
      CTCCTATTAT TCGTGGTTCT GCACTCGGTG CTTTGAACGG TGTGAGAAG      250
30  TGGGTAGACT CTGTAATGGA GCTCATGGAT ACTGTTGACA CTTGGATTGA      300
      AGAGCCAGAG CGTGAGATTG ACAAGCCATT CTTGATGCCT GTTGAGGACG      350
      TATTCTCTAT CACAGGTCGT GGTACTGTAG CTACTGGTCG TATCGAGACT      400
      GGTATCTGTA AGGTAGGTGA TGAGGTTTCAG TTGCTCGGTC TCGGTGAGGA      450
      CAAGAAGTCT GTTATCACTG GTGTTGAGAT GTTCCGTAAG AACCTTCCAA      500
35  CAGGTCAGGC TGGTGACAAC GTAGGTCTCC TCCTTCGTGG TATCGATAAG      550
      GCTGAGGTTA AGCGTGGTAT GGTGTTGTGT CACCCAGGTG CTATTACTCC      600
      TCACGATCAC TTCAAGGCAT CTATCTATGT ATTGAAGAAG GAAGAGGGTG      650
      GTCGTCATAC TCCATTCCGT AACAAAGTATC GTCCACAGTT CTACCTCCGT      700
      ACAATGGACT GTACAGGTGA AATCCACCTC CCAGAGGGCG TTGAGATGGT      750
40  TATGCCAGGT GACAACGTAG AGATTGAAGT TGTATTGATC TATAAGGTTG      800
      CTTTGAACGA GGGTCTTCGT T      821

```

## 45 2) INFORMATION FOR SEQ ID NO: 144

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 827 bases  
 (B) TYPE: Nucleic acid  
 50 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- 55 (A) ORGANISM: *Prevotella oralis*  
 (B) STRAIN: ATCC 33269

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 144

60



```

      TGGTGCTATT CTTGTAGTAG CTGCTACTGA CGGTCCTATG CCTCAAACCTC      50
      GTGAACACGT GCTTCTTGCT CGTCAGGTGA ACGTACCTCG TTTGGTCGTT      100
      TTCTTGAACA AGTGCGATAT GGTTGACGAT GAAGAAATGC TTGAGCTCGT      150
      AGAAATGGAG CTTTCATGAAC TTCTCGAGCA GTATGAATAT GAGGAGGATA      200
5     CTCCTATTGT TCGTGGTTCG GCACTTGGCG CTCTGAATGG AGTAGAGAAG      250
      TGGGTTGACA GCGTGATGAA GTTGATGGAT ACCGTTGATG AATGGATACA      300
      GGAACCACCG CGTGATCTTG ATAAGCCTTT CTTGATGCCG GTAGAGGATG      350
      TATTTTCTAT TACTGGTCGT GGAACGGTTG TTACAGGCCG TATTGAAACT      400
      GGTAAGGTTA AGGTGGGCGA TGAAGTTCAA CTTCTTGGTC TCGGTGAAGA      450
10    TAAGAAGTCC GTTGTGACAG GCGTTGAGAT GTTCCGTAAG ATTCTTGACG      500
      AAGGTGAAGC TGGTGATAAT GTAGGCTTGC TGCTTCGTGG TATCGATAAG      550
      ACGGAAGTAA AGCGTGGTAT GGTGTGTCGTA CATCCGGGGG CTATTACTCC      600
      TCACGATCAT TTCAAGGCTT CAGTTTACGT ATTGAAGAAA GAAGAAGGCG      650
      GTCGCCATAC TCCGTTTGGT AMCAAGTATC GTCCACAGTT CTATCTTCGT      700
15    ACCATGGACT GTACTGGTGA AATTACTCTT CCGGAAGGAG TTGAGATGGT      750
      AATGCCGGGT GATAACGTCG AAATTGAAGT TAAGTTGATC TATCCGGTAG      800
      CTTTGAACGA GGGACTTCGT TTCGCTA      827

```

20

## 2) INFORMATION FOR SEQ ID NO: 145

## (i) SEQUENCE CHARACTERISTICS:

```

      (A) LENGTH: 833 bases
25    (B) TYPE: Nucleic acid
      (C) STRANDEDNESS: Double
      (D) TOPOLOGY: Linear

```

```

      (ii) MOLECULE TYPE: Genomic DNA
30

```

## (vi) ORIGINAL SOURCE:

```

      (A) ORGANISM: Propionibacterium acnes
      (B) STRAIN: ATCC 6919

```

```

35    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 145

```

```

      CGGCGCCATC CTCGTGGTTG CTGCTACCGA CGGCCCGATG CCTCAGACTC      50
      GCGAGCACGT TCTGCTCGCT CGTCAGGTGG GCGTGCCCGC CATCGTCGTC      100
      GCCCTCAACA AGTGCGACAT GGTTGACGAT GAGGAGCTCA TTGAGCTCGT      150
40    CGAGATGGAG GTCCGCGAGC TGCTGACCTC GCAGGAGTTC GACGGCGACA      200
      ACTGCCCTGT CGTTTCGCATC TCCGCCTTCC AGGCCCTCCA GGGTGATGAG      250
      AAGTGGACCC AGTCGATCCT CGACCTCATG GACGCCGTGG ACGAGTACAT      300
      CCCGCAGCCT GAGCGCGATC TCGACAAGCC CTTCTTATG CCGATCGAGG      350
      ACGTCTTCAC CATCACCAGC CGTGGCACC GGTGTCACCG TCGTGTGCGAG      400
45    CGCGGCGTCG TCAAGACTGG CGAAGAGGTC GAGATCGTCG GTATCCACGA      450
      GAAGACCCAG AAGACCACCG TTACCGGTGT CGAGATGTTC CGCAAGATCC      500
      TCGACGAGGG CCGCGCTGGT GAGAACGTCG GCGTTCTGCT CCGTGGCACC      550
      AAGAAGGAGG ATGTCGTTTC CGGCATGGTC CTCTCCAAGC CTGGTTCCAC      600
      CACCCCCAC ACCGACTTCG AGGGCCAGGT CTACGTCCTC AAGAAGGATG      650
50    AGGGTGGCCG CCACAAGCCG TTCTTCTCCC ACTACAGCCC CCAGTTCTAC      700
      TTCCGTACCA CGGACGTGAC TGGCACTGTT GAGCTCCCCG AGGGCACCAG      750
      GATGGTCATG CCTGGCGACA ACACCGACAT GACTGTGCAC CTGATTCACC      800
      CGGTTGCCAT GGAGGATCAG CTCAAGTTTC CTA      833

```

55

## 2) INFORMATION FOR SEQ ID NO: 146

## (i) SEQUENCE CHARACTERISTICS:

```

60    (A) LENGTH: 745 bases

```

(B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

5 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Proteus mirabilis*  
 (B) STRAIN: ATCC 35659

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 146

	CACAAACTCG	TGAGCACATC	CTGTTAGGTC	GTCAGGTTGG	TGTTCCCTTAC	50
	ATCATCGTAT	TCCTGAACAA	ATGTGACATG	GTAGATGATG	AAGAGCTGTT	100
15	AGAATTAGTT	GAAATGGAAG	TTCGTGAACT	TCTGTCTCAA	TACGATTTCC	150
	CAGGTGATGA	CACTCCAGTA	ATCCGTGGTT	CAGCGCTGAA	AGCACTGGAA	200
	GGCGAAGCAG	AGTGGGAAGC	AAAAATTGTT	GAATTAGCAG	AAGCACTGGA	250
	TTCTTATATC	CCAGAGCCAG	AGCGTGCAAT	TGACAAACCA	TTCCTGTTAC	300
	CAATCGAAGA	TGTATTCTCA	ATCTCAGGCC	GTGGTACAGT	AGTTACTGGT	350
20	CGTGTAGAGC	GTGGTATCAT	CAAAGTAGGT	GATGAAGTTG	AGATTGTTGG	400
	TATCAAAGAA	ACCGCCAAAA	CAACTTGTAC	TGGCGTTGAA	ATGTTCCGTA	450
	AATTACTTGA	CGAAGGTCGT	GCAGGTGAGA	ACGTAGGTGT	TCTGCTGCGT	500
	GGTACAAAAC	GTGAAGAAAT	CGAACGTGGA	CAAGTACTGG	CRAAACCAGG	550
	CTCAATCAAC	CCACACAACA	AATTTGAATC	AGAAGTTTAT	ATTCTGAGCA	600
25	AAGATGAAGG	TGGTCGTCAC	ACTCCATTCT	TCAAAGGCTA	CCGTCCACAG	650
	TTCTACTTCC	GTACAACTGA	CGTAACTGGT	ACTATCGAAT	TACCAGAAGG	700
	CGTAGAAATG	GTAATGCCAG	GCGACAACGT	GAACATGATC	GTTGA	745

30

2) INFORMATION FOR SEQ ID NO: 147

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 829 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

40

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Proteus penneri*  
 (B) STRAIN: ATCC 33519

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 147

	GGAGCTATCC	TGGTTGTTGC	TGCGACAGAT	GGCCCAATGC	CACAAACTCG	50
	TGAGCACATC	CTGTTAGGTC	GTCAGGTTGG	TGTTCCCTTAC	ATCATCGTAT	100
	TCCTGAACAA	ATGTGACATG	GTAGATGATG	AAGAGTTACT	GGAATTAGTM	150
50	GAAATGGAAG	TTCGTGAACT	TCTGTCTCAG	TACGATTTCC	CAGGTGATGA	200
	CACTCCAGTA	ATCCGTGGTT	CAGCGCTGAA	AGCACTGGAA	GGCGAAGCAG	250
	AGTGGGAAGC	AAAAATTGTT	GAATTAGCAG	AAGCACTGGA	TTCATACATC	300
	CCAGARCCAG	AGCGTGCAAT	TGACAAACCA	TTCCTGTTAC	CAATTGAAGA	350
	CGTATTCTCA	ATTTCAAGGCC	GTGGTACAGT	AGTAACAGGT	CGTGTGAGC	400
55	GTGGCGTAAT	CAAAGTTGGT	GAAGAAGTTG	AAATCGTTGG	TATTAAACCA	450
	ACAGCGAAAA	CAACTTGTAC	TGGCGTTGAA	ATGTTCCGTA	AATTACTTGA	500
	CGAAGGTCGT	GCAGGTGAGA	ACGTAGGTGT	TCTTCTGCGT	GGTACTAAAC	550
	GTGAAGAAAT	CGAACGTGGA	CAAGTACTGG	CGAAACCAGG	TTCAATCAAC	600
	CCACACACTA	AATTTGAATC	AGAAGTTTAT	ATTCTGAGCA	AAGATGAAGG	650
60	TGGTCGTCAT	ACTCCATTCT	TCAAAGGCTA	CCGTCCACAG	TTCTACTTCC	700

GTACAACTGA	CGTAACTGGT	ACTATCGAAT	TACCAGAAGG	CGTAGAAATG	750
GTAATGCCAG	GTGACAACAT	CAACATGATC	GTTGAACTGA	TTCACCCAAT	800
CGCGATGGAC	GACGGTTTAC	GTTTCGCTA			829

5

## 2) INFORMATION FOR SEQ ID NO: 148

## (i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 824 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

15 (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Proteus vulgaris*  
 (B) STRAIN: ATCC 13315

20

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 148

CGGAGCTATT	CTGGTTGTTG	CTGCGACTGA	TGGCCCAATG	CCACAAACTC	50
GTGAGCACAT	CCTGTTAGGT	CGCCAGGTTG	GTGTACCTTA	CATCATCGTA	100
25 TTCCTGAACA	AATGTGACAT	GGTTGATGAT	GAAGAACTGC	TGGAATTAGT	150
AGAAATGGAA	GTTCTGTGAAC	TTCTGTCTCA	GTACGATTTT	CCAGGTGATG	200
ACACTCCAGT	AATCCGTGGT	TCAGCGCTGA	AAGCACTGGA	AGGCGAAGCT	250
GAGTGGGAAG	CAAAAATTGT	TGAATTAGCA	GAAGCACTGG	ATTCTTACAT	300
CCCAGAACCA	GAGCGTGCAA	TTGACAAACC	ATTCCTGCTG	CCTATCGAAG	350
30 ACGTATTCTC	AATCTCTGGT	CGTGGTACAG	TAGTAACAGG	CCGTGTAGAG	400
CGTGGTGTTC	TTAAAGTTGG	TGAAGAAGTT	GAGATTGTTG	GTATTAAAGA	450
CACAGTTAAA	ACAACTTGTA	CTGGCGTTGA	AATGTTCCGT	AAATTACTTG	500
ACGAAGGTCG	TGCAGGTGAG	AACGTAGGTG	TTCTTCTGCG	TGGTACTAAA	550
CGTGAAGAAA	TCGAACGTGG	ACAAGTACTG	GCTAAACCAG	GTTCAATCAA	600
35 GCCACACACT	AAATTCGAAT	CAGAAGTTTA	TATCCTGAGC	AAAGATGAAG	650
GTGGTCGTCA	CACTCCATTC	TTCAAAGGTT	ACCGTCCACA	GTTCTACTTC	700
CGTACAACCTG	ACGTAACTGG	TACTATCGAA	TTACCAGAAG	GCGTAGAAAT	750
GGTAATGCCA	GGTGACAACA	TCAACATGAT	CGTTGAACTG	ATTACCCCTA	800
40 TCGCGTAGGA	CGACGGTTTA	CGTT			824

## 2) INFORMATION FOR SEQ ID NO: 149

## (i) SEQUENCE CHARACTERISTICS:

- 45 (A) LENGTH: 745 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

50

(ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Providencia alcalifaciens*  
 55 (B) STRAIN: ATCC 9886

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 149

CACAAACTCG	TGAGCACATC	CTGTTAGGTC	GCCAAGTAGG	TGTTCTTAC	50
60 ATCATCGTTT	TCCTGAACAA	ATGTGACATG	GTAGACGACG	AAGAACTGTT	100

```

    AGAATTAGTT GAAATGGAAG TTCGTGAACT TCTGTCTCAG TACGATTTCC      150
    CAGGCGATGA CACTCCAGTT GTTCGCGGTT CAGCACTGAA AGCGCTGGAA      200
    GGCAACCCAG AGTGGGAAGC AAAAATTGTT GAATTAGCAG GTTACCTGGA      250
    TTCTTACATC CCAGAACCAG AGCGTGCAAT TGACAAGCCA TTCCTGCTGC      300
5   CAATCGAAGA CGTATTCTCA ATCTCTGGTC GTGGTACAGT AGTAACAGGC      350
    CGTGTGAGC GTGGTATCAT CAAAGTTGGT GAAGAAGTTG AAATCGTTGG      400
    TATTCAAGCG ACTGCGAAAA CAACTTGATC TGGCGTTGAA ATGTTCCGTA      450
    AACTGCTGGA TGAAGGTCGT GCGGGTGAGA ACGTTGGTGT TCTGCTGCGT      500
    GGTACTAAAC GTGAAGAAAT TCAACGTGGT CAAGTACTGG CTAAACCAGG      550
10  TTCAATCAAG CCACACACTC AATTCGAATC AGAAGTATAT ATTCTGAGCA      600
    AAGATGAAGG TGGTCGTCAT ACTCCATTCT TCAAAGGCTA CCGTCCACAG      650
    TTCTACTTCC GTACAACTGA CGTAACCGGT ACTATCGAAC TGCCAGAAGG      700
    CGTAGAGATG GTAATGCCAG GCGACAACAT CAACATGATC GTGAC           745

```

15

## 2) INFORMATION FOR SEQ ID NO: 150

## (i) SEQUENCE CHARACTERISTICS:

- 20 (A) LENGTH: 830 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

## 25 (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Providencia rettgeri*  
 (B) STRAIN: ATCC 9250

30

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 150

```

    CGGTGCAATC CTGGTTGTTG CTGCGACTGA TGGCCCAATG CCACAACTC      50
    GTGAGCACAT CCTGTTAGGY CGCCAAGTAG GTGTWCCTTA CATATCGTT      100
35  TTCCTGAACA AATGTGACAT GGTAGACGAC GAAGAACTGT TAGAATTAGT      150
    TGAAATGGAA GTTCGTGAAC TTCTGTCTCA ATACGATTTT CCAGGCGACG      200
    ACACTCCAGT TGTCCGTGGT TCAGCTCTGA AAGCGCTGGA AGGCAACCCA      250
    GAGTGGGAAG CGAAAATTGT TGAATTAGCA GGTCACCTGG ATTCTTACAT      300
    CCCAGAACCA GAGCGTGCAA TTGACAAACC ATTCCTGCTG CCAATCGAAG      350
40  ACGTATTCTC AATCTCTGGT CGTGGTACAG TAGTAACAGG CCGTGTGAG      400
    CGTGGTATCA TCAAAGTTGG TGAAGAAGTT GAAATCGTTG GTATCCAAGA      450
    CACGGTTAAA ACAACTTGTA CTGGCGTTGA AATGTTCCGT AAAGTCTGG      500
    ACGAAGGTCG TGCGGGTGAG AACGTTGGTG TTCTGCTGCG TGGTACTAAA      550
    CGTGAAGAAA TTCAACGTGG TCAAGTACTG GCAAAACCAG GTTCAATCAA      600
45  GCCACACACT AAATTCGAAT CAGAAGTCTA TATTCTGAGC AAAGATGAAG      650
    GTGGTCGTCA CACTCCATTC TTCAAAGGTT ACCGTCCACA GTTCTACTTC      700
    CGTACAACCTG ACGTAACAGG TACTATCGAA CTGCCAGAAG GCGTAGAGAT      750
    GGTAAATGCCA GGTGATAACA TCAACATGAT CGTTACCCTG ATCCACCCAA      800
    TCGCGATGGA CGACGGTTTA CGTTTCGCAA           830

```

50

## 2) INFORMATION FOR SEQ ID NO: 151

## 55 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 826 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

60

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Providencia rustigianii*  
 5 (B) STRAIN: ATCC 33673

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 151

	CGGTGCAATC	CTGGTTGTTG	CTGCGACTGA	TGGCCCAATG	CCACAAACTC	50
10	GTGAGCACAT	CCTGTTAGGT	CGCCAAGTAG	GTGTTCTTA	CATCATCGTT	100
	TTCCTGAACA	AATGTGACAT	GGTTGACGAC	GAAGAACTGT	TAGAATTAGT	150
	TGAAATGGAA	GTTCTGTGAAC	TTCTGTCTCA	GTACGATTTC	CCAGGCGACG	200
	ACACTCCAGT	TGTTTCGYGGT	TCAGCACTGA	AAGCGCTGGA	AGGTATCCCT	250
	GAGTGGGAAG	CGAAAATTGT	TGAATTAGCC	GGTTACCTGG	ACAGCTACAT	300
15	CCCAGAACCA	GAGCGCGCAA	TTGACCGTCC	ATTCCTGCTG	CCAATCGAAG	350
	ACGTATTCTC	AATCTCTGGT	CGTGGTACAG	TAGTAACAGG	SCGTGTTGAG	400
	CGTGGTATCG	TTAAAGTTGG	TGAAGAAGTT	GAAATCGTTG	GTATCCAAGA	450
	CACRGTAA	ACAACTTGTA	CTGGCGTTGA	AATGTTCCGT	AAACTGCTTG	500
	ACGAAGGTCG	TGCTGGTGAG	AACGTTGGTG	TTTTACTGCG	TGGTACTAAG	550
20	CGTGAAGAAA	TTCAACGTGG	TCAAGTACTG	GCTAAACCAG	GTTCAATCAA	600
	GCCACACACT	ACTTTTGAAT	CAGAAGTTTA	TATTCTGAGC	AAAGATGAAG	650
	GTGGTCGTCA	TACTCCATTC	TTCAAAGGCT	ACCGTCCACA	GTTCTACTTC	700
	CGTACAACCTG	ACGTAACCGG	TACTATCGAA	CTGCCAGAAG	GCGTAGAGAT	750
	GGTAATGCCA	GGCGACAACA	TCAACATGAT	CGTGACACTG	ATTCACCCAA	800
25	TCGCGATGGA	TGATGGTTTA	CGTTTC			826

2) INFORMATION FOR SEQ ID NO: 152

30

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 830 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 35 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 40 (A) ORGANISM: *Providencia stuartii*  
 (B) STRAIN: ATCC 33672

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 152

45	CGGTGCAATC	CTAGTTGTTG	CGGCAACAGA	TGGCCCAATG	CCACAAACTC	50
	GTGAGCACAT	CCTGTTAGGT	CGTCAGGTTG	GCGTTCCTTA	CATCATCGTG	100
	TTCCTGAACA	AATGTGACAT	GGTAGACGAC	GAAGAGCTGC	TGGAAGTGGT	150
	TGAAATGGAA	GTTCTGTGAAC	TTCTGTCTCA	ATACGATTTC	CCAGGTGATG	200
	ACACTCCAGT	TATCCGTGGT	TCAGCGCTGA	AAGCGTTGGA	AGGCAACCCA	250
50	GAGTGGGAAG	CGAAAATCGT	TGAACTAGCA	GAAGCACTGG	ACAGCTACAT	300
	CCCAGAGCCA	GAGCGTGCAA	TTGACAAGCC	ATTCCTGCTG	CCAATCGAAG	350
	ACGTATTCTC	AATCTCAGGT	CGTGGTACAG	TAGTCACAGG	CCGTGTTGAG	400
	CGTGGTATCA	TCAAAGTTGG	TGAAGAAGTT	GAAATCGTAG	GTATCAAAGA	450
	GACTGCGAAA	ACCACTTGTA	CTGGCGTTGA	AATGTTCCGT	AAACTGCTGG	500
55	ACGAAGGCCG	TGCGGGTGAG	AACGTAGGTG	TTCTGCTGCG	TGGTACTAAG	550
	CGTGAAGAAA	TCGAACGTGG	TCAAGTTCTG	GCGAAACCAG	GTTCAATCAA	600
	GCCACACACA	ACTTTCGAAT	CAGAAGTTTA	TATTCTGAGC	AAAGATGAAG	650
	GTGGTCGTCA	CACGCCATTC	TTCAAAGGYT	ATCGTCCACA	GTTCTACTTC	700
	CGTACAACCTG	ACGTAACAGG	TACTATCGAA	CTGCCAGAAG	GCGTAGAGAT	750
60	GGTAATGCCA	GGCGACAACG	TGAACATGAA	AGTAACTCTG	ATTCACCCAA	800

TCGCGATGGA CGATGGTTTG CGTTTCGCAA

## 5 2) INFORMATION FOR SEQ ID NO: 153

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 827 bases  
 (B) TYPE: Nucleic acid  
 10 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

## 15 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Pseudomonas aeruginosa*  
 (B) STRAIN: ATCC 35554

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 153

20 CCTGGTTTGC TCGGCTGCCG ACGGCCCCAT GCCGCAGACC CGCGAGCACA 50  
 TCCTGCTGTC CCGCCAGGTA GCGTTCCCT ACATCGTCGT GTTCCTGAAC 100  
 AAAGCCGACA TGGTCGACGA CGCCGAGCTG CTGGAACTGG TCGAGATGGA 150  
 AGTTCGCGAT CTGCTGAACA CCTACGACTT CCCGGGCGAC GACACTCCGA 200  
 25 TCATCATCGG TTCCGCGCTG ATGGCGCTGG AAGGCAAGGA TGACAACGGC 250  
 ATCGGCGTAA GCGCCGTGCA GAAGCTGGTA GAGACCTGG ACTCCTACAT 300  
 TCCGGAGCCG GTTCGTGCCA TCGACCAGCC GTTCCTCATG CCGATCGAAG 350  
 ACGTGTTCTC GATCTCCGGT CGCGGTACCG TGGTAACCGG TCGTGTAGAG 400  
 CGCGGCATCA TCAAGGTCCA GGAAGAAGTG GAAATCGTCG GCATCAAGGC 450  
 30 GACCACCAAG ACCACCTGCA CCGGCGTTGA AATGTTCCGC AAGCTGCTCG 500  
 ACGAAGGTCG TGCTGGTGAG AACGTTGGTA TCCTGCTGCG TGGCACCAAG 550  
 CGTGAAGACG TAGAGCGTGG CCAGGTACTG GCCAAGCCGG GCACCATCAA 600  
 GCCGCACACC AAGTTCGAGT GCGAAGTGTA CGTGCTGTCC AAGGAAGAAG 650  
 GTGGTCGTCA CACCCCGTTC TTCAAGGGCT ACCGTCCGCA GTTCTACTTC 700  
 35 CGTACCACKG ACGTGACCGG TAMCTGCGAG CTGCCGGAAG GCGTAGAGAT 750  
 GGTAATGCCG GCGGACAACA TCAAGATGGT TGTCACCCTG ATCGCTCCGA 800  
 TCGCCATGGA AGATGGCTGC GTTCGCG 827

40

## 2) INFORMATION FOR SEQ ID NO: 154

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 841 bases  
 45 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

50

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Pseudomonas fluorescens*  
 (B) STRAIN: ATCC 13525

55

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 154

CGGCGCAATC CTGGTTTGCT CGGCCGCTGA TGGTCCGATG CCACAAACCC 50  
 GTGAACACAT CCTGCTGTCC CGTCAGGTTG GCGTTCCGTA CATCGTGTT 100  
 TACCTGAACA AGGCTGACCT GGTAGACGAC GCTGAGCTGC TGGAACCTGGT 150  
 60 TGAGATGGAA GTGCGCGATC TGCTGAGCAC TTACGACTTC CCAGGCGACG 200

```

          ACACTCCGAT CATCATCGGT TCTGCTCGTA TGGCTCTGGA AGGCAAAGAC      250
          GACAACGAAA TGGGCACCAC GTCCGTTCGT AAACCTGGTTG AAACCTCTGGA      300
          CAGCTACATC CCAGATCCAG TTCGTGTTAT CGACAAGCCG TTCCTGATGC      350
          CAATCGAAGA CGTGTTCTCG ATCTCCGGTC GCGGTACTGT TGTGACTGGT      400
5         CGTATCGAGC GCGGTATCGT TAAGGTTCAA GATCCACTGG AAATCGTTGG      450
          TCTGCGTGAC ACTACCGTCA CCACCTGCAC CGGTGTTGAA ATGTTCCGTA      500
          AGCTGCTCGA CGAAGGTCGT GCTGGCGAGA ACTGCGGCGT TCTGCTGCGT      550
          GGTACCAAGC GTGACGACGT TGAGCGTGGC CAGGTTCTGG TTAAGCCAGG      600
          TTCGGTTAAG CCGCACACCA AGTTCGAAGC TGAAGTCTAC GTACTGAGCA      650
10        AAGAAGAAGG CGGTCGTCAC ACTCCGTTCT TCAAAGGCTA CCGTCCACAG      700
          TTCTACTTCC GTACTACTGA CGTGACTGGT AACTGCGAGC TGCCGGAAGG      750
          CGTTGAAATG GTTATGCCAG GCGACAACAT CAAAATGGTT GTTACCCTGA      800
          TCAAAACCAT CGCAATGGAA GACGGTCTGC GTTTCGCTAT T              841

```

15

## 2) INFORMATION FOR SEQ ID NO: 155

## (i) SEQUENCE CHARACTERISTICS:

- 20 (A) LENGTH: 841 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

25

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Pseudomonas stutzeri*  
 (B) STRAIN: ATCC 17588

## 30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 155

```

          CGGCGCGATC CTGGTCTGCT CGGCTGCTGA CGGCCCCATG CCGCAGACTC      50
          GCGAGCACAT CCTGCTGTCC CGTCAGGTTG GTGTTCCGTA CATCGTTCGTG      100
          TTCCTGAACA AGGCCGACAT GGTGATGAC GCCGAGCTGC TCGAGCTGGT      150
35        CGAGATGGAA GTTCGYGACC TGCTGTGCAC CTACGACTTC CCGGGTGAYG      200
          ACACCTCCGAT CATCATCGGC TCCGCGCTGA TGGCGCTGAA CGGCGAAGAC      250
          GACAACGAGC TCGGCACCAC TCGGTGAAG AAGCTGGTCG AGACCTGGA      300
          CAGCTACATT CCCGAGCCGG TTCGTGCCAT CGACAAGCCG TTCCTGATGC      350
          CGATCGAAGA CGTGTTCTCG ATCTCCGGTC GCGGCACSGT GGTAACCGGT      400
40        CGCGTAGAGC GCGGCATCGT CAAGGTTTCA GAAGAGATCG AGATCGTTCGG      450
          TCTGCGTCCG ACCACCAAGA CTACCTGCAC CGGCGTTGAG ATGTTCCGCA      500
          AGCTGCTCGA YGARGGTCGT GCTGGCGAGA ACTGCGGYGT GCTGCTGCGT      550
          GGCACCAAGC GTGACGAAGT GGAGCGTGGT CAGGTTCTGG CCAAGCCGGG      600
          CACCATCAAG CCGCACACCA AGTTCGAAGC CGAAGTGTAC GTGCTGTCCA      650
45        AGGAAGAAGG TGGTCGTCAC ACCCCGTTCT TYAAGGGCTA CCGTCCCKCAG      700
          TTCTACTTCC GTACCACTGA YGTGACYGGW TCGTGCGARC TGCCGGAAGG      750
          CGTCGAGATG GTAATGCCGG GCGACAACGT GAAGATGGTT GTCACCCTGA      800
          TCAAGCCGAT CGCCATGGAA GACGGCCTGC GCTTCGCGAT T              841

```

50

## 2) INFORMATION FOR SEQ ID NO: 156

## (i) SEQUENCE CHARACTERISTICS:

- 55 (A) LENGTH: 833 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

## 60 (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Psychrobacter phenylpyruvicus*  
 (B) STRAIN: ATCC 23333

5

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 156

	GCTATTCTAG	TAGTATCAGC	AACTGACGGT	CCAATGCCAC	AAACACGTGA	50
	GCACATTCTA	TTATCACGTC	AGGTTGGTGT	ACCATACATC	ATCGTATTCA	100
10	TGAACAAATG	TGACATGGTA	GATGACGAAG	AGTTACTAGA	GCTAGTAGAA	150
	ATGGAAGTGC	GTGAATTACT	TTCAGACTAC	GACTTCCCAG	GTGATGACAC	200
	TCCAATCATC	AAAGGTTTCA	CTTTAGAAGC	GTTAAATGGT	AACGACGGTA	250
	AGTACGGTGA	GCCAGCAGTT	ATCGAACTAC	TAAACACTCT	AGACACTTAC	300
	ATTCCAGAGC	CAGAGCGTGA	CATCGATAAG	CCATTCTTAA	TGCCAATCGA	350
15	AGACGTATTC	TCAATCTCAG	GTCGTGGTAC	AGTAGTAACA	GGCCGTGTTG	400
	AATCTGGTAT	CATCAAAGTT	GGTGACGAAA	TCGAAATCGT	TGGTATCAAA	450
	GACACAGTTA	AAACAACCTG	TACTGGTATC	GAGATGTTCC	GTAAGTTACT	500
	AGACGAAGGT	CGTGCTGGTG	AGAAGTGTGG	TGTACTATTA	CGTGGTACTA	550
	AGCGTGAAGA	CGTACAACGT	GGTCAAGTAC	TTGCTAAGCC	AGGTTCAATC	600
20	ACTCCACACA	CCAACTTCGA	CGCAGAAGTA	TACGTACTAT	CAAAAGAAGA	650
	AGGTGGTCGT	CACACTCCAT	TCTTAAATGG	TTACCGTCCA	CAGTTCTACT	700
	TCCGTACTAC	TGACGTAACA	GGTGCAATCA	CGTTACAAGA	AGGTACTGAA	750
	ATGGTAATGC	CAGGCGATAA	CGTTGAGATG	AGCGTAGAGC	TAATCCACCC	800
25	AATCGCTAGG	ACAAAGGTTT	ACGTTTCGCA	ATC		833

## 2) INFORMATION FOR SEQ ID NO: 157

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 825 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

35

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Rahnella aquatilis*  
 (B) STRAIN: ATCC 33071

40

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 157

	GGCGCTATCC	TGGTTGTTGC	TGCAACTGAC	GGCCCTATGC	CTCAGACTCG	50
45	TGAGCACATC	CTGCTGGGTC	GCCAGGTTGG	CGTTCCATAC	ATGATCGTGT	100
	TCATGAACAA	ATGCGACATG	GTAGATGACG	AAGAGCTGCT	GGAAGTGGTA	150
	GAAATGGAAG	TTGCGGAACT	TCTGTCTGCT	TACGAATTCC	CAGGCGACGA	200
	CATCCCGGTC	ATCAAAGGTT	CAGCGCTGAA	AGCACTGGAA	GGCGATGCTA	250
	CTTGGAAGC	GAAAATCATC	GAACTGGCAG	AAGCACTGGA	CAGCTACATT	300
50	CCATTGCCAG	AGCGTGCTAT	CGATAAGCCA	TTCTTGCTGC	CAATCGAAGA	350
	CGTATTCTCC	ATCTCCGGTC	GTGGTACAGT	GGTTACCGGT	CGTGTAGAGC	400
	GCGGTATCGT	TAAAGTGGGC	GAAGAAGTTG	AAATCGTCGG	TATCAAGGAC	450
	ACTGTTAAGT	CTACTTGCTA	TGGCGTTGAA	ATGTTCCGCA	AACTGCTGGA	500
	CGAAGGCCGT	GCGGGCGAGA	ACGTGGGTGT	TCTGCTGCGT	GGTATCAAGC	550
55	GTGAAGACAT	CGAACGTGGT	CAGGTTCTGG	CTAAACCAGG	TTCAATCAAA	600
	CCACACACCA	AGTTTGATTG	CGAAGTGTAC	ATCCTGAGCA	AAGATGAAGG	650
	TGGTCGCTAC	ACTCCATTCT	TCAAAGGCTA	CCGTCCACAG	TTCTACTTCC	700
	GTACAACCTGA	CGTGACCGGT	ACTATCGAAC	TGCCAGAAGG	CGTTGAGATG	750
	GTTATGCCTG	GTGACAACGT	GAACATGGTT	GTTACCCTGA	TCCACCCCAAT	800
60	CGCGATGGAT	GACGGTCTGC	GTTTC			825



## 2) INFORMATION FOR SEQ ID NO: 158

5

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 830 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

10

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Salmonella choleraesuis* subsp. *arizonae*  
 (B) STRAIN: ATCC 13314

15

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 158

```

20  CGGCGCGATC CTGGTTGTTG CTGCGACTGA CGGCCCGATG CCGCAGACCC      50
    GTGAGCACAT CCTGCTGGGC CGTCAGGTAG GCGTTCCGTA CATCATCGTG      100
    TTCCTGAACA AATGCGACAT GGTGATGAC GAAGAGCTGC TGGAAGTGGT      150
    TGAAATGGAA GTTCGTGAAC TTCTGTCTCA GTACGACTTC CCGGGCGACG      200
    ATACCCCGAT CGTTCGTGGT TCTGCTCTGA AAGCGCTGGA AGGCGACGCA      250
25  GAGTGGGAAG CGAAAATCAT CGAACTGGCT GGCTTCCTGG ACTCTTACAT      300
    CCCGGAACCA GAGCGTGCGA TTGACAAGCC GTTCCTGCTG CCGATCGAAG      350
    ACGTATTCTC CATCTCCGGT CGTGGTACCG TTGTTACCGG TCGTGTAAGAA      400
    CGCGGTATCA TCAAAGTGGG CGAAGAAGTT GAAATCGTTG GTATCAAAGA      450
    GACTCAGAAG TCTACCTGTA CTGGCGTTGA AATGTTCCGC AAAGTCTGGG      500
30  ACGAAGGCCG TGCCGGTGAG AACGTAGGTG TTCTGCTGCG TGGTATCAAA      550
    CGTGAAGAAA TCGAACGTGG TCAGGTACTG GCTAAGCCGG GCACCATCAA      600
    GCCGCACACC AAGTTCGAAT CTGAAGTGTA CATTCTGTCC AAAGATGAAG      650
    GCGGCCGTCA TACTCCGTTT TTCAAAGGCT ACCGTCCGCA GTTCTACTTC      700
    CGTACTACTG ACGTGACTGG CACCATCGAA CTGCCGGAAG GCGTGGAGAT      750
35  GGTAATGCCG GGCGACAACA TCAAATGGT TGTTACCCTG ATCCACCCGA      800
    TCGCGATGGA CGACGGTCTG CGTTTCGCAA      830
  
```

## 40 2) INFORMATION FOR SEQ ID NO: 159

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 832 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

45

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Salmonella choleraesuis* subsp. *choleraesuis*  
 serotype *Choleraesuis*  
 (B) STRAIN: ATCC 7001

50

## 55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 159

```

    CGGCGCGATC CTGGTTGTTG CTGCGACTGA CGGYCCGATG CCGCAGACCC      50
    GTGAGCACAT CCTGCTGGGT CGTCAGGTAG GCGTTCCGTA CATCATCGTG      100
    TTCCTGAACA AATGCGACAT GGTGATGAC GAAGAGCTGC TGGAAGTGGT      150
60  TGAAATGGAA GTTCGTGAAC TTCTGTCTCA GTACGACTTC CCGGGCGACG      200
  
```

	ACACGCCGAT	CGTTCGTGGT	TCTGCTCTGA	AAGCGCTGGA	AGGTGACGCA	250
	GAGTGGGAAG	CGAAAATCAT	CGAACTGGCT	GGCTTCCTGG	ATTCTTACAT	300
	TCCGGAACCA	GAGCGTGCGA	TTGACAAGCC	GTTCCCTGCTG	CCGATCGAAG	350
	ACGTATTCTC	CATCTCCGGT	CGTGGTACCG	TTGTTACCGG	TCGTGTAGAG	400
5	CGCGGTATCA	TCAAAGTGGG	YGAAGAAGTT	GAAATCGTTG	GTATCAAAGA	450
	GACTCAGAAG	TCTACCTGTA	CTGGCGTTGA	AATGTTCCGC	AAACTGTTGG	500
	ACGAAGGCCG	TGCCGGTGAG	AACGTAGGTG	TTCTGCTGCG	TGGTATCAAA	550
	CGTGAAGAAA	TGGAACGTGG	TCAGGTACTG	GCTAAGCCGG	GCACCATCAA	600
	GCCGCACACC	AAGTTCGAAT	CTGAAGTGTA	CATTCTGTCC	AAAGATGAAG	650
10	GCGGCCGTCA	TACTCCGTTT	TTCAAAGGCT	ACCGTCCGCA	GTTCTACTTC	700
	CGTACTACTG	ACGTGACTGG	CACCATCGAA	CTGCCGGAAG	GCGTAGAGAT	750
	GGTAATGCCG	GGCGACAACA	TCAAATGGT	TGTTACCCTG	ATCCACCCGA	800
	TCGCAATGGA	CGACGGTCTG	CGTTTCGCAA	TC		832

15

## 2) INFORMATION FOR SEQ ID NO: 160

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 807 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Salmonella choleraesuis* subsp. *diarizonae*

(B) STRAIN: ATCC 43973

30

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 160

	CCTGGTTGTT	GCTGCGACTG	ACGGCCCCGAT	GCCGCAGACC	CGTGAGCACA	50
	TCCTGCTGGG	TCGTCAGGTA	GGCGTTCCGT	ACATTATCGT	GTTCTGAAC	100
35	AAATGCGACA	TGGTTGATGA	CGAAGAGCTG	CTGGAAGTGG	TAGAAATGGA	150
	AGTTCTGTAA	CTTCTGTCTC	AGTACGACTT	CCCGGGCGAC	GACACGCCAA	200
	TCGTTTCGTGG	TTCTGCTCTG	AAAGCGCTGG	AAGGCGACGC	AGAGTGGGAA	250
	GCGAAAATCA	TGGAAGTGGC	TGGCTTCCTG	GATTCTTACA	TCCCGGAACC	300
	AGAGCGTGCG	ATTGACAAGC	CGTTCTGTCT	GCCGATCGAA	GACGTATTCT	350
40	CCATCTCCGG	TCGTGTTACC	GTTGTTACCG	GTCGTGTAGA	GCGCGGTATC	400
	ATCAAAGTGG	GCGAAGAAGT	TGAAATCGTT	GGTATCAAAG	AGACTCAGAA	450
	GTCTACCTGT	ACTGGCGTTG	AAATGTTCCG	CAARCTGCTG	GACGAAGGCC	500
	GTGCWGGTGA	GAACGTAGGT	GTTCTGCTGC	GTGGTATCAA	ACGTGAAGAA	550
	ATCGAACGTG	GTCAGGTACT	GGCTAAGCCG	GGCACCATCA	AGCCGCACAC	600
45	CAAGTTCGAA	TCTGAAGTGT	ATATTCTGTC	CAAAGATGAA	GGCGGCCGTC	650
	ATACTCCGTT	CTTCAAAGGC	TACCGTCCGC	AGTTCTACTT	CCGTACCACT	700
	GACGTGACTG	GCACCATCGA	ACTGCCGGAA	GGCGTGGAGA	TGGTAATGCC	750
	GGGCGACAAC	ATCAAAATGG	TTGTTACCCT	GATCCACCCG	ATCGCGATGG	800
	ACGACGG					807

50

## 2) INFORMATION FOR SEQ ID NO: 161

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 832 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

60

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Salmonella choleraesuis* subsp. *choleraesuis*  
 serotype Heidelberg  
 (B) STRAIN: ATCC 8326

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 161

10	CGGCGCGATC	CTGGTTGTTG	CTGCGACTGA	CGGCCCGATG	CCGCAGACCC	50
	GTGAGCACAT	CCTGCTGGGT	CGTCAGGTAG	GCGTTCCGTA	CATCATCGTG	100
	TTCCTGAACA	AATGCGACAT	GGTTGATGAC	GAAGAGCTGC	TGGAACGGT	150
	TGAAATGGAA	GTTCTGTGAAC	TTCTGTCTCA	GTACGACTTC	CCGGGCGACG	200
	AACTCCGAT	CGTTCGTGGT	TCTGCTCTGA	AAGCGCTGGA	AGGCGACGCA	250
15	GAGTGGGAAG	CGAAAATCAT	CGAACTGGCT	GGCTTCCTGG	ATTCTTACAT	300
	CCCGGAACCA	GAGCGTGCGA	TTGACAAGCC	GTTCCTGCTG	CCGATCGAAG	350
	ACGTATTCTC	CATCTCCGGT	CGTGGTACCG	TTGTTACCGG	TCGTGTAGAA	400
	CGCGGTATCA	TCAAAGTGGG	CGAAGAAGTT	GAAATCGTTG	GTATCAAAGA	450
	GACTCAGAAG	TCTACCTGTA	CTGGCGTTGA	AATGTTCCGC	AAACTGCTGG	500
20	ACGAAGGCCG	TGCCGGTGGG	AACGTAGGTG	TTCTGCTGCG	TGGTATCAAA	550
	CGTGAAGAAA	TCGAACGTGG	TCAGGTACTG	GCTAAGCCGG	GCACCATCAA	600
	GCCGCACACC	AAGTTCGAAT	CTGAAGTGTA	CATTCTGTCC	AAAGATGAAG	650
	GCGGCCGTCA	YACTCCGTTT	TTCAAAGGCT	ACCGTCCGCA	GTTCTACTTC	700
	CGTACTACTG	ACGTGACTGG	CACCATCGAA	TTGCCGGAAG	GCGTAGAGAT	750
25	GGTAATGCCG	GGCGACAACA	TCAAAATGGT	TGTTACCCTG	ATCCACCCGA	800
	TCGCGATGGA	CGACGGTCTG	CGTTTCGCAA	TC		832

30 2) INFORMATION FOR SEQ ID NO: 162

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 807 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

40 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Salmonella choleraesuis* subsp. *houtenae*  
 (B) STRAIN: ATCC 43974

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 162

45	CCTGGTTGTT	GCTGCGACTG	ACGGCCCGAT	GCCGCAGACC	CGTGAGCACA	50
	TCCTGCTGGG	TCGTCAGGTA	GGCGTTCCGT	ACATCATCGT	GTTCTGAAC	100
	AAATGCGACA	TGGTTGATGA	CGAAGAGCTG	CTGGAACGGT	TAGAAATGGA	150
	AGTTCGTGAA	CTTCTGTCTC	AGTACGATTT	CCCGGGCGAC	GACACGCCGA	200
50	TCGTGCGTGG	TTCTGCTCTG	AAAGCGCTGG	AAGGCGACGC	AGAATGGGAA	250
	GCGAAAATCA	TCGAACTGGC	TGGCTACCTG	GATTCTTACA	TCCCGGAACC	300
	AGAGCGTGCG	ATTGACAAAC	CGTTCCTGCT	GCCGATCGAA	GACGTATTCT	350
	CTATCTCCGG	TCGTGGTACC	GTTGTTACCG	GTCGTGTAGA	GCGCGGTATC	400
	ATCAAAGTGG	GCGAAGAAGT	TGAAATCGTT	GGTATCAAAG	AGACTCAGAA	450
55	GTCGACCTGT	ACTGGCGTTG	AAATGTTCCG	CAAACGCTG	GACGAAGGCC	500
	GTGCTGGCGA	GAACGTAGGT	GTTCTGCTGC	GTGGTATCAA	ACGTGAAGAA	550
	ATCAAACGTG	GTCAGGTACT	GGCTAAGCCG	GGCACCATCA	AGCCGCACAC	600
	CAAGTTTCGA	TCTGAAGTGT	ACATTCTGTC	CAAAGATGAA	GGCGGCCGTC	650
	ATACTCCGTT	CTTCAAAGGC	TACCGTCCGC	AATTCTACTT	CCGTACGACT	700
60	GACGTGACTG	GCACCATCGA	ACTGCCGGA	GGCGTGAGA	TGGTAATGCC	750

GGGCGACAAC ATCAAAATGG TTGTTACCCT GATCCACCCG ATCGCGATGG 800  
ACGACGG 807

5

## 2) INFORMATION FOR SEQ ID NO: 163

## (i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 827 bases  
(B) TYPE: Nucleic acid  
(C) STRANDEDNESS: Double  
(D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

15

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Salmonella choleraesuis* subsp. *indica*  
(B) STRAIN: ATCC 43976

20

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 163

CGCGATCCTG GTTGTGCTG C GACTGACGG CCCGATGCCG CAGACCCGTG 50  
AGCACATCCT GCTGGGTCGT CAGGTAGGCG TTCCGTACAT CATCGTGTTC 100  
CTGAACAAAT GCGACATGGT TGATGACGAA GAGCTGCTGG AACTGGTTGA 150  
25 AATGGAAGTT CGTGAAC TTC TGTCTCAGTA CGACTTCCCG GGTGACGACA 200  
CGCCGATCGT GCGTGGTTCT GCTCTGAAAG CGCTGGAAGG CGACGCAGAG 250  
TGGAAGCGA AAATCATCGA ACTGGCTGGC TTCCTGGATT CTTACATTCC 300  
GGAACCAGAG CGTGCGATTG ACAAGCCGTT CCTGCTGCCG ATCGAAGACG 350  
TATTCTCCAT CTCCGGTCGT GGTACGTTG TTACCGGTCG TGTAGAGCGC 400  
30 GGTATCATCA AAGTGCGCA AGAAGTTGAA ATCGTTGGTA TCAAAGAGAC 450  
TCAGAACTCT ACCTGTACTG GCGTTGAAAT GTTCCGCAA CTGCTGGACG 500  
AAGGCCGTGC CCGTGAGAAC GTAGGTGTTT TGCTGCGTGG TATCAAACGT 550  
GAAGAAATCG AACGTGGTCA GGTACTGGCT AAGCCGGGCA CCATCAAGCC 600  
GCACACCAAG TTCGAATCTG AAGTGATCAT TCTGTCCAAA GATGAAGGCG 650  
35 GCCGTCATAC TCCGTTCTTC AAAGGCTACC GTCCGCAGTT CTAATTCCGT 700  
ACTACTGACG TGACTGGCAC CATCGAACTG CCGGAAGGCG TAGAGATGGT 750  
AATGCCGGGC GACAACATCA AAATGGTTGT TACCCTGATC CATCCGATCG 800  
CRATGGACGA CCGTCTGCGT TTCGCAA 827

40

## 2) INFORMATION FOR SEQ ID NO: 164

## (i) SEQUENCE CHARACTERISTICS:

- 45 (A) LENGTH: 807 bases  
(B) TYPE: Nucleic acid  
(C) STRANDEDNESS: Double  
(D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

50

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Salmonella choleraesuis* subsp. *salamae*  
(B) STRAIN: ATCC 43972

55

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 164

CCTGGTTGTT GCTGCGACTG ACGGCCCGAT GCCGCAGACC CGTGAGCACA 50  
TCCTGCTGGG TCGTCAGGTA GCGGTTCCGT ACATCATCGT GTTCTGTAAC 100  
60 AAATGCGACA TGGTTGATGA CGAAGAGCTG CTGGAAGTGG TAGAAATGGA 150

```

AGTTCGTGAA CTTCTGTCTC AGTACGACTT CCCGGGCGAC GACACGCCGA 200
TCGTGCGTGG TTCCGCTCTG AAAGCGCTGG AAGGCGAMGC TGAGTGGGAA 250
GMGAAAATCA TCGAACTGGC TGGCTWCCTG GATTCTTACA TTCCGGAACC 300
AGAGCGTGCG ATTGACAAGC CGTTCCTGCT GCCGATCGAA GACGTATTCT 350
5 CCATCTCCGG TCGTGGTACC GTTGTTACCG GTCGTGTAGA GCGCGGTATC 400
ATCAAAGTGG GCGAAGAAGT TGAAATCGTT GGTATCAAAG AGACTCAGAA 450
GTCTACCTGT ACTGGCGTTG AAATGTTCCG CAAACTGCTG GACGAAGGCC 500
GTGCCGGTGA GAACGTAGGT GTTCTGCTGC GTGGTATCAA ACGTGAAGAA 550
ATCGAACGTG GTCAGGTACT GGCTAAGCCG GGCACCATCA AGCCGCACAC 600
10 CAAGTTCGAA TCTGAAGTGT ACATTCTGTC CAAAGATGAA GGCGGCCGTC 650
ATACTCCGTT CTTCAAAGGC TACCGTCCGC AGTTCTACTT CCGTACCACT 700
GACGTGACTG GCACCATCGA ACTGCCGGAA GCGGTGGAGA TGGTAATGCC 750
GGGCGACAAC ATCAAATGG TTGTTACCCT GATCCACCCG ATCGCGATGG 800
ACGACGG 807
15

```

## 2) INFORMATION FOR SEQ ID NO: 165

```

20 (i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 832 bases
    (B) TYPE: Nucleic acid
    (C) STRANDEDNESS: Double
    (D) TOPOLOGY: Linear
25 (ii) MOLECULE TYPE: Genomic DNA
    (vi) ORIGINAL SOURCE:
    (A) ORGANISM: Salmonella choleraesuis subsp. choleraesuis
30 serotype Typhi
    (B) STRAIN: ATCC 10749

```

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 165

```

35 CGGCGCGATC CTGGTTGTTG CTGCGACTGA CGGCCCGATG CCGCAGACCC 50
GTGAGCACAT CCTGCTGGGT CGTCAGGTAG GCGTTCCGTA CATCATCGTG 100
TTCCTGAACA AATGCGACAT GGTTGATGAC GAAGAGCTGC TGGAACGGT 150
TGAAATGGAA GTTCGTGAAC TTCTGTCTCA GTACGACTTC CCGGGCGACG 200
ACACGCCGAT CGTTCGTGGT TCTGCTCTGA AAGCGCTGGA AGGCGACGCA 250
40 GAGTGGGAAG CGAAAATCAT CGAATGGCT GGCTTCCTGG ATTCTTACAT 300
CCCGGAACCA GAGCGTGCGA TTGACAAGCC GTTCCTGCTG CCGATCGAAG 350
ACGTATTCTC CATCTCCGGT CGTGGTACCG TTGTTACCGG TCGTGTAGAA 400
CGCGGTATCA TCAAAGTGGG CGAAGAAGTT GAAATCGTTG GTATCAAAGA 450
GACTCAGAAG TCTACCTGTA CTGGCGTTGA AATGTTCCGC AAACTGCTGG 500
45 ACGAAGGCCG TGCNNGTGAG AACGTAGGTG TTCTGCTGCG TGGTATCAAA 550
CGTGAAGAAA TCGAACGTGG TCAGGTACTG GCTAAGCCGG GCACCATCAA 600
GCCGCACACY AAGTTCGAAT CTGAAGTGTA CATTCTGTCC AAAGATGAAG 650
CGGCGCGTCA TACTCCGTTT TTCAAAGGCT ACCGTCCGCA GTTCTACTTC 700
CGTACTACTG ACGTGACTGG CACCATCGAA CTGCCGGAAG GCGTAGAGAT 750
50 GGTAATGCCG GCGGACAACA TCAAATGGT TGTTACCCTG ATCCACCCGA 800
TCGCAATGGA CGACGGTCTG CGTTTCGCAA TC 832

```

## 55 2) INFORMATION FOR SEQ ID NO: 166

```

    (i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 817 bases
    (B) TYPE: Nucleic acid
60 (C) STRANDEDNESS: Double

```

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

5 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Serratia fonticola*

(B) STRAIN: DSM 4576

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 166

10 CGGCGCTATC CTGGTTGTAG CTGCGACTGA CGGCCCTATG CCTCAGACTC 50  
 GTGAGCACAT CCTGCTGGGT CGTCAGGTTG GCGTTCCTTA CATCATCGTA 100  
 TTCATGAACA AATGCGACAT GGTTGATGAT GAAGAGCTGC TGGAAGTGGT 150  
 AGAAATGGAA GTTCGTGAAC TTCTGTCTGC TTATGACTTC CCTGGTGATG 200  
 15 ACCTGCCGGT TGTTCGTGGT TCAGCGCTGA AAGCACTGGA AGGCGAAGCT 250  
 GAGTGGGAAG CTAAAATCAT CGAGCTGGCC GGTCACCTGG ATTCCTACAT 300  
 CCCAGAACCA GAGCGTGCTA TCGATCAGCC GTTCCTGCTG CCAATCGAAG 350  
 ACGTATTCTC CATCTCCGGT CGTGGTACCG TAGTTACCGG TCGTGTGAG 400  
 CGCGGTATCG TTAAAGTTGG CGAAGAAGTT GAAATCGTTG GTATCAAAGA 450  
 20 CACCGTTAAG TCTACCTGTA CTGGCGTTGA AATGTTCCGC AAAGTCTGG 500  
 ACGAAGGCCG TGCTGGTGAG AACGTTGGTG TTCTGCTGCG TGGTATCAAG 550  
 CGTGAAGACA TCGAACGTGG TCAGGTACTG GCTAAACCAG GTTCCATCAA 600  
 GCCGCACACT CAGTTCGATT CAGAAGTGTA TATCCTGAGC AAAGAAGAAG 650  
 GTGGTCGTCA TACTCCATT TCAAAGGCT ACCGTCCACA GTTCTACTTC 700  
 25 CGTACAACCTG ACGTGACCGG TACCATCGAA CTGCCAGAAG GCGTAGAGAT 750  
 GGTAATGCCA GCGGATAACG TGAACATGGT TGTTACCCTG ATCCACCCAA 800  
 TCGCTATGGA CCAAGGC 817

30 2) INFORMATION FOR SEQ ID NO: 167

(i) SEQUENCE CHARACTERISTICS:

35 (A) LENGTH: 787 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

40 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Serratia liquefaciens*

(B) STRAIN: ATCC 27592

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 167

50 GCTGCGACTG ACGGCCCAAT GCCTCAGACC CGTGAGCACA TCCTGCTGGG 50  
 TCGTCAGGTT GCGGTTTCCTT TCATCATCGT ATTCATGAAC AAATGCGACA 100  
 TGTTTGATGA TGAAGAGCTG CTGGAAGTGG TAGAAATGGA AGTTCGTGAA 150  
 CTTCTGTCTG CTTACGACTT CCCTGGTGAT GACCTGCCGG TTGTTCGTGG 200  
 TTCAGCGCTG AAAGCACTGG AAGGCGAAGC TGAGTGGGAA GCTAAAATCA 250  
 TCGAGCTGGC CGGTTACCTG GATTCTTACA TCCCAGAACC AGAGCGTGCT 300  
 ATCGACAAGC CGTTCCTGCT GCCAATCGAA GACGTCTTCT CCATCTCCGG 350  
 TCGTGGTACC GTTGTTACCG GTCGTGTTGA GCGCGGTATC GTTAAAGTTG 400  
 55 GCGAAGAAGT TGAAATCGTT GGTATCAAAG ACACCGTTAA GTCTACCTGT 450  
 ACTGGCGTTG AAATGTTCCG CAAACTGCTG GACGAAGGCC GTGCTGGTGA 500  
 GAACGTTGGT GTTCTGCTGC GTGGTATCAA GCGTGAAGAC ATCGAACGTG 550  
 GTCAGGTACT GGCTAAACCA GGTTCATCA AGCCACACAC CAAGTTCGAC 600  
 TCAGAAGTGT ACATCCTGAG CAAAGAAGAA GGTGGTCGTC ATACTCCATT 650  
 60 CTTCAAAGGC TACCGTCCAC AGTTCTACTT CCGTACAAC TACGCTGACCG 700

GTACCATCGA ACTGCCAGAA GCGTTGAAA TGGTAATGCC AGGTGACAAC 750  
 GTGAACATGG TTGTTACCCT GATCCACCCA ATCGCGA 787

5

## 2) INFORMATION FOR SEQ ID NO: 168

## (i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 745 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

15

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Serratia marcescens*  
 (B) STRAIN: ATCC 13880

20

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 168

GCCTCAGACT CGTGAGCACA TCCTGCTGGG TCGTCAGGTT GCGTTCCTT 50  
 TCATCATCGT ATTCATGAAC AAATGCGACA TGGTTGATGA TGAAGAGCTG 100  
 YTGGAAGTGG TAGAAATGGA AGTTCGCGAA CTGCTGTCCG CTTACGACTT 150  
 25 CCCTGGCGAC GACCTGCCGG TAATCCGCGG TTCCGCGCTG AAAGCGCTGG 200  
 AAGGCGAAGC TGAGTGGGAA GCGAAAATCA TCGAACTGGC CGAAGCCCTG 250  
 GACAGCTACA TCCCAGAGCC AGAGCGTGCT ATCGACAAGC CGTTCCTGCT 300  
 GCCAATCGAA GACGTATTCT CCATCTCCGG TCGTGGTACC GTTGTTACCG 350  
 GTCGTGTTGA GCGCGGCATC ATCAAAGTTG GCGAAGAAGT TGAAATCGTT 400  
 30 GGTATCAAAG ACACCGTTAA GTCTACCTGT ACTGGCGTTG AAATGTTCCG 450  
 CAAACTGCTG GACGAAGGCC GTGCTGGTGA GAACGTAGGT GTTCTGCTGC 500  
 GTGGTATCAA ACGTGAAGAA ATCGAACGTG GTCAGGTACT GGCTAAGCCA 550  
 GGCTCCATCA AGCCGCACAC CCAGTTCGAA TCTGAAGTGT ACATCCTGAG 600  
 CAAAGATGAA GGTGGTCGTC ACACKCCATT CTTCAAAGGC TACCGTCCAC 650  
 35 AGTTCTACTT CCGTACCACT GACGTGACCG GTACCATCGA ACTGCCAGAA 700  
 GGCGTAGAGA TGGTAATGCC AGGCGACAAC GTGAACATGG TTGTA 745

## 40 2) INFORMATION FOR SEQ ID NO: 169

## (i) SEQUENCE CHARACTERISTICS:

- 45 (A) LENGTH: 829 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

50

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Serratia odorifera*  
 (B) STRAIN: ATCC 33077

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 169

55

GGCGCAATCC TGGTTGTTGC TGCGACTGAC GGCCCTATGC CTCAGACCCG 50  
 TGAGCACATC CTGCTGGGTC GCCAGGTTGG CGTTCCTTTC ATCATCGTGT 100  
 TCATGAACAA ATGTGACATG GTTGATGACG AAGAGCTGCT GGAAGTGGTA 150  
 GAAATGGAAG TTCGCGAGCT GCTGTCTGCT TACGATTTC CTGGCGACGA 200  
 60 CCTGCCAGTA ATCCGCGGTT CTGCGCTGAA AGCGCTGGAA GGCGAAGCAG 250

	AGTGGGAAGC	TAAGATTGTA	GAAGTGGCTG	AAGCGCTGGA	TTCTTACATC	300
	CCAGAACCAG	AGCGTGCTAT	CGACAAGCCG	TTCTTGCTGC	CAATCGAAGA	350
	CGTATTCTCC	ATCTCCGGTC	GTGGTACCGT	TGTTACCGGT	CGTGTTGAGC	400
	GCGGTATCAT	CAAAGTTGGC	GAAGAAGTTG	AAATCGTTGG	TATCAAAGAC	450
5	ACCGTTAAGT	CTACCTGTAC	CGGTGTAGAA	ATGTTCCGCA	AACTGCTGGA	500
	CGAAGGCCGT	GCTGGTGAGA	ACGTTGGTGT	TCTGCTGCGT	GGTATCAAGC	550
	GTGAAGACAT	CGAACGTGGT	CAGGTTCTGG	CTAAACCAGG	TTCTATCAAG	600
	CCGCACACCA	AATTCGACTC	AGAAGTGTAC	ATCCTGAGCA	AAGAAGAAGG	650
	TGGTCGTCAC	ACGCCATTCT	TCAAAGGCTA	CCGTCCACAG	TTCTACTTCC	700
10	GTACTACTGA	CGTGACCGGT	ACCATCGAAC	TGCCAGAAGG	CGTAGAGATG	750
	GTAATGCCAG	GCGATAACGT	GAACATGGTT	GTTACCCTGA	TTCACCCAAT	800
	CGCAATGGAC	GACGGTCTGC	GTTTCGCAA			829

15

## 2) INFORMATION FOR SEQ ID NO: 170

## (i) SEQUENCE CHARACTERISTICS:

20	(A)	LENGTH: 830 bases
	(B)	TYPE: Nucleic acid
	(C)	STRANDEDNESS: Double
	(D)	TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

25

## (vi) ORIGINAL SOURCE:

(A)	ORGANISM: <i>Serratia plymuthica</i>
(B)	STRAIN: DSM 4540

30

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 170

	CGGCGCAATC	CTGGTTGTTG	CTGCGACTGA	CGGCCCAATG	CCTCAGACCC	50
	GTGAGCACAT	CCTGCTGGGT	CGTCAGGTTG	GCGTTCCTTT	CATCATCGTA	100
	TTCATGAACA	AATGCGACAT	GGTTGATGAT	GAAGAGCTGC	TGGAAGCTGGT	150
35	AGAAATGGAA	GTTTCGTGAAC	TTCTGTCTGC	TTACGACTTC	CCTGGTGATG	200
	ACCTGCCGGT	TGTTTCGTGGT	TCAGCGCTGA	AAGCACTGGA	AGGCGAACCA	250
	GAGTGGGAAG	CTAAAATCAT	CGAGCTGGCT	GGTTTCCTGG	ATTCTTACAT	300
	CCCAGAACCA	GAGCGTGCTA	TCGACAAGCC	GTTCTGCTG	CCAATCGAAG	350
	ACGTATTCTC	CATCTCCGGT	CGTGGTACCG	TTGTTACCGG	TCGTGTTGAG	400
40	CGCGGTATCG	TTAAAGTTGG	CGAAGAAGTT	GAAATCGTGG	GTATCAAAGA	450
	CACCGTTAAG	TCTACCTGTA	CCGGCGTTGA	AATGTTCCGC	AAACTGCTGG	500
	ACGAAGGCCG	TGCTGGTGAG	AACGTGGGTG	TTCTGCTGCG	TGGTATCAAG	550
	CGCGAAGATA	TCGAACGTGG	TCAGGTCCTG	GCTAAACCAG	GTTCAATCAA	600
	GCCACACACC	AAGTTTGACT	CAGAAGTGTA	CATCCTGAGC	AAAGAAGAAG	650
45	GTGGTCGTCA	TACTCCATTC	TTCAAAGGCT	ACCGTCCACA	GTTCTACTTC	700
	CGTACAACCTG	ACGTGACCGG	TACCATCGAA	CTGCCAGAAG	GCGTAGAGAT	750
	GGTAATGCCA	GGTGACAACG	TGAACATGGT	TGTAACCCTG	ATCCACCCAA	800
	TCGCGATGGA	CGACGGCCTG	CGTTTCGCAA			830

50

## 2) INFORMATION FOR SEQ ID NO: 171

## (i) SEQUENCE CHARACTERISTICS:

55	(A)	LENGTH: 829 bases
	(B)	TYPE: Nucleic acid
	(C)	STRANDEDNESS: Double
	(D)	TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

103



## (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Serratia rubidaea*

(B) STRAIN: ATCC 27593

5

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 171

	GGCGCAATCC	TGGTAGTAGC	AGCGACTGAC	GGCCCAATGC	CTCAGACCCG	50
	TGAGCACATC	CTGCTGGGCC	GCCAGGTAGG	CGTACCTTAC	ATCATCGTAT	100
10	TCATGAACAA	ATGCGACATG	GTAGATGATG	AAGAGCTGCT	GGAAC TGGT A	150
	GAGATGGAAG	TTCGCGAACT	GCTGTCTGCT	TACGACTTCC	CAGGCGACGA	200
	CCTGCCGGTA	ATCCGTGGTT	CCGCGCTGAA	AGCGCTGGAA	GGCGAAGCCG	250
	AGTGGGAAGC	GAAAATCGTT	GAGCTGGCAG	AAGCGCTGGA	CAGCTACATC	300
	CCAGAGCCAG	AGCGTGCTGT	AGACAAGCCG	TTCCTGCTGC	CAATCGAAGA	350
15	CGTATTCTCC	ATCTCCGGTC	GTGGTACCGT	TGTTACCGGT	CGTGTAGAGC	400
	GCGGTATCAT	CAAAGTTGGT	GAAGAAGTAG	AAATCGTAGG	TATCAAAGAC	450
	ACCGTTAAGT	CTACCTGTAC	TGGCGTAGAA	ATGTTCCGCA	AACTGCTGGA	500
	CGAAGGCCGT	GCTGGTGAGA	ACGTAGGTGT	TCTGCTGCGT	GGTATCAAGC	550
	GTGAAGAAAT	CGAACGTGGT	CAGGTACTGG	CGAAGCCAGG	TTCAATCAAG	600
20	CCGCACACCC	AGTTCGAATC	TGAAGTGTAC	ATTCTGTCCA	AAGACGAAGG	650
	CGGCCGTCAT	ACTCCGTTCT	TCAAAGGCTA	CCGTCCACAG	TTCTACTTCC	700
	GTACAAC TGA	CGTGACCGGT	ACCATCGAAC	TGCCAGAAGG	CGTAGAGATG	750
	GTAATGCCAG	GCGACAACGT	GAACATGAAA	GTTACTCTGA	TTCACCCAAT	800
	CGCAATGGAC	GACGGTCTGC	GTTTCGCAA			829

25

## 2) INFORMATION FOR SEQ ID NO: 172

## 30 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 826 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

35

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Shigella boydii*

40

(B) STRAIN: ATCC 9207

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 172

	CGGCGCGATC	YTGGTAGTTG	CTGCGACTGA	CGGCCCGATG	CCGCAGACTC	50
45	GTGAGCACAT	CCTGCTGGGT	CGTCAGGTAG	GCGTTCCGTA	CATCATCGTG	100
	TTCCTGAACA	AATGCGACAT	GGTTGATGAC	GAAGAGCTGC	TGGAAC TGGT A	150
	TGAAATGGAA	GTTCGTGAAC	TTCTGTCTCA	GTACGACTTC	CCGGGCGACG	200
	ACACTCCGAT	CGTTCGTGGT	TCTGCTCTGA	AAGCGCTGGA	AGGCGACGCA	250
	GAGTGGGAAG	CGAAAATCCT	GGAAC TGCT A	GGCTTCCTGG	ATTCTTACAT	300
50	TCCGGAACCA	GAGCGTGCGA	TTGACAAGCC	GTTCTGCTG	CCGATCGAAG	350
	ACGTATTCTC	CATCTCCGGT	CGTGGTACCG	TTGTTACCGG	TCGTGTAGAA	400
	CGCGGTATCA	TCAAAGTTGG	TGAAGAAGTT	GAAATCGTTG	GTATCAAAGA	450
	GACTCAGAAG	TCTACCTGTA	CTGGCGTTGA	AATGTTCCGC	AAACTGCTGG	500
	ACGAAGGCCG	TGCTGGTGAG	AACGTAGGTG	TTCTGCTGCG	TGGTATCAAA	550
55	CGTGAAGAAA	TGAACGTGG	TCAGGTACTG	GCTAAGCCGG	GCACCATCAA	600
	GCCGCACACC	AAGTTCGAAT	CTGAAGTGTA	CATTCTGTCC	AAAGATGAAG	650
	GCGGCCGTCA	TACTCCGTTT	TTCAAAGGCT	ACCGTCCGCA	GTTCTACTTC	700
	CGTACTACTG	ACGTGACTGG	TACCATCGAA	CTGCCGGAAG	GCGTAGAGAT	750
	GGTAATGCCG	GGCGACAACA	TCAAATATGGT	TGTTACCCTG	ATCCACCCGA	800
50	TCGCGATGGA	CGACGGTCTG	CGTTTC			826

## 2) INFORMATION FOR SEQ ID NO: 173

5

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 818 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

10

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Shigella dysenteriae*  
 (B) STRAIN: ATCC 11835

15

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 173

20	TGGTAGTTGC	TGCGACTGAC	GGCCCGATGC	CGCAGACTCG	TGAGCACATC	50
	CTGCTGGGTC	GTCAGGTAGG	CGTTCCGTAC	ATCATCGTGT	TCCTGAACAA	100
	ATGCGACATG	GTTGATGACG	AAGAGCTGCT	GGAAGTGGTT	GAAATGGAAG	150
	TTCGTGAACT	TCTGTCTCAG	TACGACTTCC	CGGGCGACGA	CACTCCGATC	200
	GTTTCGTGGT	CTGCTCTGAA	AGCGCTGGAA	GGCGACGCAG	AGTGGGAAGC	250
25	GAAAATCCTG	GAAGTGGCTG	GCTTCCTGGA	TTCYTAYATT	CCGGAACCAG	300
	AGCGTGCGAT	TGACAAGCCG	TTCCTGCTGC	CGATCGAAGA	CGTATTCTCC	350
	ATCTCCGGTC	GTGGTACCGT	TGTTACCGGT	CGTGTAGAAC	GCGGTATCAT	400
	CAAAGTTGGT	GAAGAAGTTG	AAATCGTTGG	TATCAAAGAG	ACYCAGAAGT	450
	CTACCTGTAC	TGGCGTTGAA	ATGTTCCGCA	AACTGCTGGA	CGAAGGCCGT	500
30	GCTGGTGAGA	ACGTAGGTGT	TCTGCTGCGT	GGTATCAAAC	GTGAAGAAAT	550
	CGAACGTGGT	CAGGTACTGG	CGAAGCCRGG	CACCATCAAG	CCGCACACCA	600
	AGTTCGAATC	TGAAGTGTAC	ATTCTGTCCA	AAGATGAAGG	CGGCCGTCAT	650
	ACTCCGTTCT	TCAAAGGCTA	CCGTCCGCAG	TTCTACTTCC	GTACTACTGA	700
	CGTGACTGGT	ACCATCGAAC	TGCCGGAAGG	CGTAGAGATG	GTAATGCCGG	750
35	GCGACAACAT	CAAATGGTT	GTTACCCTGA	TCCACCCGAT	CGCGATGGAC	800
	GACGGTCTGC	GTTTCGCA				818

## 40 2) INFORMATION FOR SEQ ID NO: 174

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 806 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

45

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Shigella flexneri*  
 (B) STRAIN: ATCC 12022

50

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 174

55

	CCTGGTAGTT	GCTGCGACTG	ACGGCCCGAT	GCCGCAGACT	CGTGAGCACA	50
	TCCTGCTGGG	TCGTCAGGTA	GGCGTTCCGT	ACATCATCGT	GTTCTCTGAA	100
	AAATGCGACA	TGGTTGATGA	CGAAGAGCTG	CTGGAAGTGG	TTGAAATGGA	150
	AGTTCGTGAA	CTTCTGTCTC	AGTACGACTT	CCGGGCGAC	GACACTCCGA	200
60	TCGTTCTGTT	TTCTGCTCTG	AAAGCGCTGG	AAGGCGACGC	AGAGTGGGAA	250

```

GCGAAAATCC TGGAACTGGC TGGCTTCCTG GATTCTTACA TTCCGGAACC      300
AGAGCGTGCG ATTGACAAGC CGTTCCTGCT GCCGATCGAA GACGTATTCT      350
CCATCTCCGG TCGTGGTACC GTTGTTACCG GTCGTGTAGA ACGCGGTATC      400
ATCAAAGTTG GTGAAGAAGT TGAAATCGTT GGTATCAAAG AGACTCAGAA      450
5 GTCTACCTGT ACTGGCGTTG AAATGTTCCG CAAACTGCTG GACGAAGGCC      500
GTGCTGGTGA GAACGTAGGT GTTCTGCTGC GTGGTATCAA ACGTGAAGAA      550
ATCGAACGTG GTCAGGTACT GGCTAAGCCG GGCACCATCA AGCCGCACAC      600
CAAGTTCGAA TCTGAAGTGT ACATTCTGTC CAAAGATGAA GGCGGMCGTC      650
10 ATACTCCGTT CTTCAAAGGC TACCGTCCGC AGTTCTACTT CCGTACTACT      700
GACGTGACTG GTACCATCGA ACTGCCGGA GCGGTAGAGA TGGTAATGCC      750
GGGCGACAAC ATCAAAATGG TTGTTACCCT GATCCACCCG ATCGCGATGG      800
ACGACC                                             806

```

15

## 2) INFORMATION FOR SEQ ID NO: 175

## (i) SEQUENCE CHARACTERISTICS:

```

20 (A) LENGTH: 832 bases
    (B) TYPE: Nucleic acid
    (C) STRANDEDNESS: Double
    (D) TOPOLOGY: Linear

```

## (ii) MOLECULE TYPE: Genomic DNA

25

## (vi) ORIGINAL SOURCE:

```

    (A) ORGANISM: Shigella sonnei
    (B) STRAIN: ATCC 29930

```

30

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 175

```

CGGCGCGATC CTGGTAGTTG CTGCGACTGA CGGCCCGATG CCGCAGACTC      50
GTGAGCACAT CCTGCTGGGT CGTCAGGTAG GCGTTCCGTA CATCATCGTG      100
TTCCTGAACA AATGCGACAT GGTGTGATGAC GAAGAGCTGC TGGAAGTGGT      150
35 TGAAATGGAA GTTCGTGAAC TTCTGTCTCA GTACGACTTC CCGGGCGACG      200
ACACTCCGAT CGTTCGTGGT TCTGCTCTGA AAGCGCTGGA AGGCGACGCA      250
GAGTGGGAAG CGAAAATCCT GGAAGTGGCT GGCTTCCTGG ATTCTTACAT      300
TCCGGAACCA GAGCGTGCGA TTGACAAGCC GTTCCTGCTG CCGATCGAAG      350
ACGTATTCTC CATCTCCGGT CGTGGTACCG TTGTTACCGG TCGTGTAGAA      400
40 CGCGGTATCA TCAAAGTTGG TGAAGAAGTT GAAATCGTTG GTATCAAAGA      450
GACTCAGAAG TCTACCTGTA CTGGCGTTGA AATGTTCCGC AAAGTCTGG      500
ACGAAGGCCG TGCTGGTGAG AACGTAGGTG TTCTGCTGCG TGGTATCAAA      550
CGTGAAGAAA TCGAACGTGG TCAGGTACTG GCTAAGCCGG GCACCATCAA      600
GCCGCACACC AAGTTCGAAT CTGAAGTGTA CATTCTGTCC AAAGATGAAG      650
45 GCGGYCGTCA TACTCCGTTT TTCAAAGGCT ACCGTCCGCA GTTCTACTTC      700
CGTACTACTG ACGTGACTGG TACCATCGAA CTGCCGGAAG GCGTAGAGAT      750
GGTAATGCCG GGCGACAACA TCAAATGGT TGTTACCCTG ATCCACCCGA      800
TCGCGATGGA CGACGGTCTG CGTTTCGCAA TC                               832

```

50

## 2) INFORMATION FOR SEQ ID NO: 176

## (i) SEQUENCE CHARACTERISTICS:

```

55 (A) LENGTH: 716 bases
    (B) TYPE: Nucleic acid
    (C) STRANDEDNESS: Double
    (D) TOPOLOGY: Linear

```

## (ii) MOLECULE TYPE: Genomic DNA

106

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Staphylococcus aureus*

(B) STRAIN: ATCC 13301

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 176

5  
 10  
 15  
 20  
 25  
 30  
 35  
 40  
 45  
 50  
 55  
 60  
 65  
 70  
 75  
 80  
 85  
 90  
 95  
 100  
 105  
 110  
 115  
 120  
 125  
 130  
 135  
 140  
 145  
 150  
 155  
 160  
 165  
 170  
 175  
 180  
 185  
 190  
 195  
 200  
 205  
 210  
 215  
 220  
 225  
 230  
 235  
 240  
 245  
 250  
 255  
 260  
 265  
 270  
 275  
 280  
 285  
 290  
 295  
 300  
 305  
 310  
 315  
 320  
 325  
 330  
 335  
 340  
 345  
 350  
 355  
 360  
 365  
 370  
 375  
 380  
 385  
 390  
 395  
 400  
 405  
 410  
 415  
 420  
 425  
 430  
 435  
 440  
 445  
 450  
 455  
 460  
 465  
 470  
 475  
 480  
 485  
 490  
 495  
 500  
 505  
 510  
 515  
 520  
 525  
 530  
 535  
 540  
 545  
 550  
 555  
 560  
 565  
 570  
 575  
 580  
 585  
 590  
 595  
 600  
 605  
 610  
 615  
 620  
 625  
 630  
 635  
 640  
 645  
 650  
 655  
 660  
 665  
 670  
 675  
 680  
 685  
 690  
 695  
 700  
 705  
 710  
 715  
 720  
 725  
 730  
 735  
 740  
 745  
 750  
 755  
 760  
 765  
 770  
 775  
 780  
 785  
 790  
 795  
 800  
 805  
 810  
 815  
 820  
 825  
 830  
 835  
 840  
 845  
 850  
 855  
 860  
 865  
 870  
 875  
 880  
 885  
 890  
 895  
 900  
 905  
 910  
 915  
 920  
 925  
 930  
 935  
 940  
 945  
 950  
 955  
 960  
 965  
 970  
 975  
 980  
 985  
 990  
 995  
 1000

## 2) INFORMATION FOR SEQ ID NO: 177

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 719 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Staphylococcus aureus*

(B) STRAIN: ATCC 29247

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 177

40  
 45  
 50  
 55  
 60  
 65  
 70  
 75  
 80  
 85  
 90  
 95  
 100  
 105  
 110  
 115  
 120  
 125  
 130  
 135  
 140  
 145  
 150  
 155  
 160  
 165  
 170  
 175  
 180  
 185  
 190  
 195  
 200  
 205  
 210  
 215  
 220  
 225  
 230  
 235  
 240  
 245  
 250  
 255  
 260  
 265  
 270  
 275  
 280  
 285  
 290  
 295  
 300  
 305  
 310  
 315  
 320  
 325  
 330  
 335  
 340  
 345  
 350  
 355  
 360  
 365  
 370  
 375  
 380  
 385  
 390  
 395  
 400  
 405  
 410  
 415  
 420  
 425  
 430  
 435  
 440  
 445  
 450  
 455  
 460  
 465  
 470  
 475  
 480  
 485  
 490  
 495  
 500  
 505  
 510  
 515  
 520  
 525  
 530  
 535  
 540  
 545  
 550  
 555  
 560  
 565  
 570  
 575  
 580  
 585  
 590  
 595  
 600  
 605  
 610  
 615  
 620  
 625  
 630  
 635  
 640  
 645  
 650  
 655  
 660  
 665  
 670  
 675  
 680  
 685  
 690  
 695  
 700  
 705  
 710  
 715  
 720  
 725  
 730  
 735  
 740  
 745  
 750  
 755  
 760  
 765  
 770  
 775  
 780  
 785  
 790  
 795  
 800  
 805  
 810  
 815  
 820  
 825  
 830  
 835  
 840  
 845  
 850  
 855  
 860  
 865  
 870  
 875  
 880  
 885  
 890  
 895  
 900  
 905  
 910  
 915  
 920  
 925  
 930  
 935  
 940  
 945  
 950  
 955  
 960  
 965  
 970  
 975  
 980  
 985  
 990  
 995  
 1000

## 2) INFORMATION FOR SEQ ID NO: 178

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 625 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus aureus*  
 (B) STRAIN: ATCC 33591

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 178

```

15 GTGAACACAT TCTTTTATCA CGTAACGTTG GTGTACCAGC ATTAGTAGTA      50
   TTCTTAAACA AAGTTGACAT GGTTGACGAT GAAGAATTAT TAGAATTAGT      100
   AGAAATGGAA GTTCGTGACT TATTAAGCGA ATATGACTTC CCAGGTGACG      150
   ATGTACCTGT AATCGCTGGT TCAGCATTAA AAGCTTTAGA AGGCGATGCT      200
20 CAATACGAAG AAAAAATCTT AGAATTAATG GAAGCTGTAG ATACTTACAT      250
   TCCAAC TCCA GAACGTGATT CTGACAAACC ATTCATGATG CCAGTTGAGG      300
   ACGTATTCTC AATCACTGGT CGTGGTACTG TTGCTACAGG CCGTGTTGAA      350
   CGTGGTCAAA TCAAAGTTGG TGAAGAAGTT GAAATCATCG GTTTACATGA      400
   CACATCTAAA ACAACTGTTA CAGGTGTTGA AATGTTCCGT AAATTATTAG      450
25 ACTACGCTGA AGCTGGTGAC AACATTGGTG CATTATTACG TGGTGTTGCT      500
   CGTGAAGACG TACAACGTGG TCAAGTATTA GCTGCTCCTG GTTCAATTAC      550
   ACCACATACT GAATTCAAAG CAGAAGTATA CGTATTATCA AAAGACGAAG      600
   GTGGACGTCA CACTCCATTC TTCTC                                     625

```

## 2) INFORMATION FOR SEQ ID NO: 179

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 704 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus aureus*  
 (B) STRAIN: ATCC 43300

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 179

```

   GTTGGTGTAC CAGCATTAGT AGTATTCTTA AACAAAGTTG ACATGGTTGA      50
   CGATGAAGAA TTATTAGAAT TAGTAGAAAT GGAAGTTCGT GACTTATTAA      100
50 GCGAATATGA CTTCCCAGGT GACGATGTAC CTGTAATCGC TGGTTCAGCA      150
   TTAAAAGCTT TAGAAGGCGA TGCTCAATAC GAAGAAAAAA TCTTAGAATT      200
   AATGGAAGCT GTAGATACTT ACATTCCAAC TCCAGAACGT GATTCTGACA      250
   AACCATTTCAT GATGCCAGTT GAGGACGTAT TCTCAATCAC TGGTCGTGGT      300
   ACTGTTGCTA CAGGCCGTGT TGAACGTGGT CAAATCAAAG TTGGTGAAGA      350
55 AGTTGAAATC ATCGGTTTAC ATGACACATC TAAAACAAC TTTACAGGTG      400
   TTGAAATGTT CCGTAAATTA TTAGACTACG CTGAAGCTGG TGACAACATT      450
   GGTGCATTAT TACGTGGTGT TGCTCGTGAA GACGTACAAC GTGGTCAAGT      500
   ATTAGCTGCT CCTGGTTCAA TTACACCACA TACTGAATTC AAAGCAGAAG      550
   TATACGTATT ATCAAAAGAC GAAGGTGGAC GTCACACTCC ATTCTTCTCA      600
60 AACTATCGTC CACAATTCTA TTTCCGTACT ACTGACGTAA CTGGTGTGTG      650

```

TCACCTTACCA GAAGGTACTG AAATGGTAAT GCCTGGTGAT AACGTTGAAA 700  
 TGAC 704

5

## 2) INFORMATION FOR SEQ ID NO: 180

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 730 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus aureus* subsp. *aureus*  
 (B) STRAIN: ATCC 6538

## 20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 180

GTGAACACAT TCTTTTATCA CGTAACGTTG GTGTACCAGC ATTAGTAGTA 50  
 TTCTTAAACA AAGTTGACAT GGTGACGAT GAAGAATTAT TAGAATTAGT 100  
 AGAAATGGAA GTTCGTGACT TATTAAGCGA ATATGACTTC CCAGGTGACG 150  
 25 ATGTACCTGT AATCGCTGGT TCAGCATTAA AAGCTTTAGA AGGCGATGCT 200  
 CAATACGAAG AAAAAATCTT AGAATTAATG GAAGCTGTAG ATACTTACAT 250  
 TCCAACCTCA GAACGTGATT CTGACAAACC ATTCATGATG CCAGTTGAGG 300  
 ACGTATTCTC AATCACTGGT CGTGGTACTG TTGCTACAGG CCGTGTTGAA 350  
 CGTGGTCAAA TCAAAGTTGG TGAAGAAGTT GAAATCATCG GTTTACATGA 400  
 30 CACATCTAAA ACAACTGTGA CAGGTGTTGA AATGTTCCGT AAATTATTAG 450  
 ACTACGCTGA AGCTGGTGAC AACATTGGTG CATTATTACG TGGTGTTGCT 500  
 CGTGAAGACG TACAACGTGG TCAAGTATTA GCTGCTCCTG GTTCAATTAC 550  
 ACCACATACT GAATTCAAAG CAGAAGTATA CGTATTATCA AAAGACGAAG 600  
 GTGGACGTCA CACTCCATTC TTCTCAAAC ATCGTCCACA ATTCTATTTT 650  
 35 CGTACTACTG ACGTAACTGG TGTTGTTCAC TTACCAGAAG GTACTGAAAT 700  
 GGTAATGCCT GGTGATAACG TTGAAATGAC 730

## 40 2) INFORMATION FOR SEQ ID NO: 181

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 834 bases  
 (B) TYPE: Nucleic acid  
 45 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus auricularis*  
 (B) STRAIN: ATCC 33753

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 181

CGGTGCGATC TTAGTTGTAT CTGCAGCTGA TGGTCCAATG CCACAAACTC 50  
 GTGAACACAT CTTATTATCA CGTAACGTTG GTGTACCAGC ATTAGTTGTA 100  
 TTCTTAAACA AAGTTGACCA AGTTGACGAC GAAGAATTAT TAGAATTAGT 150  
 AGAAATGGAA GTTCGTGACT TATTAAGCGA ATACGACTAC CCAGGTGACG 200  
 60 ATGTACCTGT AATCTCTGGT TCTGCGTTGA AAGCATTAGA AGGCGACAAA 250

```

GAATACGAAC  AAAAAATCTT  AGACTTAATG  CAACAAGTTG  ACGATTACAT  300
TCCAACCTCCA  GAACGTGACT  CTGATAAACC  ATTCATGATG  CCAGTTGAAG  350
ACGTATTCTC  AATCACTGGT  CGTGGTACTG  TTGCAACAGG  CCGTGTGAA  400
CGTGGTCAAA  TCAAAGTCGG  TGAAGAAGTT  GAAATCATCG  GTATGAAAGA  450
5  CGGTTTCAAA  AAAACAACAG  TTAAGTGGT  AGAAATGTTC  CGTAAATTAT  500
TAGACTACGC  TGAAGCTGGT  GACAACATCG  GTGCTTTATT  ACGTGGTATT  550
TCACGTGAAG  AAGTACAACG  TGGTCAAGTT  TTAGCTGCTC  CTGGTTCAAT  600
TACACCACAC  ACTAAATTCA  CTGCAGAAAG  TTACGTATTA  TCTAAAGATG  650
AAGGTGGACG  TCACACTCCA  TTCTTCTCTA  ACTACCGTCC  ACAATTCTAT  700
10  TTCCGTACTA  CTGACGTAAC  AGGTGTTGTT  ACTTTACCAG  AAGGTACAGA  750
AATGGTAATG  CCTGGCGATA  ACGTTAAAAT  GGAAGTTGAA  TTAATTTCTC  800
CAATCGCTAT  CGAAGACGGT  ACTCGTTTCT  CAAT  834

```

15

## 2) INFORMATION FOR SEQ ID NO: 182

## (i) SEQUENCE CHARACTERISTICS:

```

20  (A) LENGTH: 835 bases
      (B) TYPE: Nucleic acid
      (C) STRANDEDNESS: Double
      (D) TOPOLOGY: Linear

```

## (ii) MOLECULE TYPE: Genomic DNA

25

## (vi) ORIGINAL SOURCE:

```

      (A) ORGANISM: Staphylococcus capitis subsp. capitis
      (B) STRAIN: ATCC 27840

```

30

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 182

```

CGGCGGTATC  TTAGTAGTAT  CTGCTGCTGA  CGGTCCAATG  CCACAAACTC  50
GTGAACACAT  CTTATTATCA  CGTAACGTTG  GTGTACCAGC  ATTAGTTGTA  100
TTCTTAAACA  AAGTTGACAT  GGTAGACGAC  GAAGAATTAT  TAGAATTAGT  150
35  TGAAATGGAA  GTTCGTGACT  TATTAAGCGA  ATATGACTTC  CCAGGTGATG  200
ATGTACCTGT  AATCGCTGGT  TCAGCATTA  AAGCTTTAGA  AGGCGATGCT  250
CAATACGAAG  AAAAAATCTT  AGAATTAATG  CAAGCAGTTG  ATGATTACAT  300
TCCAACCTCCA  GAACGTGATT  CTGACAAACC  ATTCATGATG  CCAGTTGAGG  350
ACGTATTCTC  AATCACTGGT  CGTGGTACTG  TTGCTACAGG  CCGTGTGAA  400
40  CGTGTCAAA  TCAAAGTTGG  TGAAGAAGTT  GAAATCATCG  GTATCCACGA  450
AACTTCTAAA  ACAACTGTTA  CTGGTGTAGA  AATGTTCCGT  AAATTATTAG  500
ACTACGCTGA  AGCTGGTGAC  AACATCGGTG  CTTTATTACG  TGGTGTGCT  550
CGTGAAGACG  TACAACGTGG  TCAAGTATTA  GCTGCTCCTG  GTTCAATCAC  600
ACCACACACT  AAATTCAAAG  CGGAAGTTTA  CGTTTTATCT  AAAGACGAAG  650
45  GTGGACGTCA  CACTCCATTC  TTCAGTAACT  ACCGCCCACA  ATTCTATTTT  700
CGTACTACTG  ACGTAACTGG  TGTGTGTTAA  TTACCAGAAG  GTAATGAAAT  750
GGTTATGCCT  GGCGACAACG  TTGAAATGAC  AGTTGAATTA  ATCGCTCCTA  800
TCGCTATTGA  AGACGGTACT  CGTTTCTCAA  TCGGA  835

```

50

## 2) INFORMATION FOR SEQ ID NO: 183

## (i) SEQUENCE CHARACTERISTICS:

```

55  (A) LENGTH: 804 bases
      (B) TYPE: Nucleic acid
      (C) STRANDEDNESS: Double
      (D) TOPOLOGY: Linear

```

## (ii) MOLECULE TYPE: Genomic DNA

110

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Macrococcus caseolyticus*  
 (B) STRAIN: ATCC 13548

5

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 183

	GTATCTTAGT	AGTATCTGCT	GCTGACGGTC	CAATGCCACA	AACTCGTGAA	50
	CACATCCTTT	TATCACGTAA	CGTTGGTGTA	CCAGCATTAG	TAGTATTCTT	100
10	GAACAAAGTT	GACATGGTTG	ACGATGAAGA	ATTATTAGAA	TTAGTTGAAA	150
	TGGAAGTTCG	TGACTTATTA	TCTGAATATG	ACTTCCCTGG	TGACGATGTA	200
	CCTGTAATCG	CTGGATCTGC	TTTAAAAGCA	TTAGAAGGCG	TTGAAGAATA	250
	CGAAGACAAA	ATCATTGAAT	TAATGGACGC	AGTTGATGAG	TACATCCCAA	300
	CTCCAGAACG	TGATTCTGAC	AAACCATTCA	TGATGCCAGT	TGAGGACGTA	350
15	TTCTCAATCA	CTGGTCGTGG	TACAGTTGCA	ACTGGACGTG	TTGAGCGTGG	400
	ACAAGTTAAA	GTTGGTGAAG	AAGTTGAAAT	CATTGGTTTA	ACTGAAGAAC	450
	CAGCAAAAAC	TACAGTTACA	GGTGTAGAAA	TGTTCCGTAA	ATTATTAGAT	500
	TACGCTGAAG	CTGGAGATAA	CATCGGTGCT	TTATTACGTG	GTGTTTCTCG	550
	TGAAGACGTA	CAACGTGGAC	AAGTATTAGC	TAAACCAGGT	TCAATTACTC	600
20	CACATACTAA	ATTCAAAGCT	GAAGTTTACG	TATTATCTAA	AGAAGAAGGT	650
	GGACGTCATA	CTCCATTCTT	CACTAACTAC	CGCCCTCAGT	TCTACTTCCG	700
	TACAACTGAC	GTAAGTGGTG	TAGTTAACTT	ACCAGAAGGT	ACTGAAATGG	750
	TAATGCCTGG	AGATAACATC	GAAATGAACG	TTGAATTAAT	TTCTCCAATC	800
	GCGA					804

25

## 2) INFORMATION FOR SEQ ID NO: 184

## 30 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 832 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

35

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus cohnii*  
 (B) STRAIN: DSM 20260

40

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 184

	CGGAGCTATC	TTAGTAGTAT	CTGCTGCTGA	TGGCCCAATG	CCACAAACTC	50
45	GTGAACATAT	CCTTTTATCA	CGTAACGTTG	TGTTTCCAGC	ATTAGTTGTA	100
	TTCTTAAACA	AAGTTGACAT	GGTTGACGAT	GAAGAATTAT	TAGAATTAGT	150
	AGAAATGGAA	GTTCGTGACT	TATTAAGCGA	ATATGACTTC	CCAGGTGACG	200
	ATGTACCTGT	AATCTCTGGT	TCAGCATTA	AAGCTCTTGA	AGGCGACGCT	250
	GACTATGAGC	AAAAAATCTT	AGACTTAATG	CAAGCTGTTG	ATGACTTCAT	300
50	TCCAACACCA	GAACGTGATT	CTGACAAACC	ATTCATGATG	CCAGTTGAGG	350
	ACGTATTCTC	AATCACTGGT	CGTGGTACTG	TTGCTACAGG	GCGTGTGAA	400
	CGTGGTCAAA	TCAAAGTCGG	TGAAGAAGTT	GAAATCATCG	GTATGCAAGA	450
	AGATTCAAGC	AAAACAACCTG	TTACTGGTGT	AGAAATGTTC	CGTAAATTAT	500
	TAGACTACGC	TGAAGCTGGT	GACAACATTG	GTGCGTTATT	ACGTGGTGT	550
55	GCACGTGAAG	ACATCCAACG	TGGTCAAGTT	TTAGCTGCTC	CTGGTTCAAT	600
	TACACCACAC	ACAAACTTTA	AAGCGGAAGT	TTACGTTTTA	TCAAAAGATG	650
	AAGGTGGCCG	TCATACGCCA	TTCTTCAGTA	ACTATCGCCC	ACAATTCTAT	700
	TTCCGTACTA	CTGACGTAAC	AGGTGTTGTT	ACTTTACCAG	AAGGTACTGA	750
	AATGGTTATG	CCTGGCGACA	ACGTAGAAAT	GGAAGTTGAA	CTAATTCTC	800
50	CAATCGCTAT	CGAAGACGGT	ACACGTTTCT	CT		832



## 2) INFORMATION FOR SEQ ID NO: 185

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 699 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus epidermidis*  
 (B) STRAIN: CSG 269

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 185

20	ATCTGCTGCT	GACGGTCCAA	TGCCACAAAC	TCGTGAACAC	ATCTTATTAT	50
	CACGTAACGT	TGGTGTACCA	GCATTAGTTG	TATTCTTAAA	CAAAGTTGAC	100
	ATGGTAGACG	ACGAAGAATT	ATTAGAATTA	GTTGAAATGG	AAGTTCGTGA	150
	CTTATTAAGC	GAATATGACT	TCCCAGGTGA	CGATGTACCT	GTAATCGCTG	200
	GTTCTGCATT	AAAAGCATT	GAAGGCGATG	CTGAATACGA	ACAAAAAATC	250
25	TTAGACTTAA	TGCAAGCAGT	TGATGATTAC	ATTCCAACCTC	CAGAACGTGA	300
	TTCTGACAAA	CCATTCATGA	TGCCAGTTGA	GGACGTATTC	TCAATCACTG	350
	GTCGTGGTAC	TGTTGCTACA	GGCCGTGTTG	AACGTGGTCA	AATCAAAGTT	400
	GGTGAAGAAG	TTGAAATCAT	CGGTATGCAC	GAAACTTCTA	AAACAACCTGT	450
	TACTGGTGTA	GAAATGTTCC	GTAAATTATT	AGACTACGCT	GAAGCTGGTG	500
30	ACAACATCGG	TGCTTTATTA	CGTGGTGTG	CACGTGAAGA	CGTACAACGT	550
	GGTCAAGTAT	TAGCTGCTCC	TGGTTCTATT	ACACCACACA	CAAAATTCAA	600
	AGCTGAAGTA	TACGTATTAT	CTAAAGATGA	AGGTGGACGT	CACACTCCAT	650
	TCTTCACTAA	CTATCGCCCA	CAATTCTATT	TCCGTACTAC	TGACGTAAC	699

## 2) INFORMATION FOR SEQ ID NO: 186

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 829 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus haemolyticus*  
 (B) STRAIN: ATCC 29970

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 186

	CGGCGGTATC	TTAGTAGTAT	CTGCTGCTGA	CGGTCCAATG	CCACAAACTC	50
	GTGAACACAT	TCTTTTATCA	CGTAACGTTG	GTGTACCAGC	ATTAGTAGTA	100
55	TTCTTAAATA	AAGTTGACAT	GGTTGACGAT	GAAGAATTAT	TAGAATTAGT	150
	TGAAATGGAA	GTACGTGACT	TATTATCTGA	ATACGACTTC	CCAGGTGACG	200
	ATGTACCTGT	AATCGCTGGT	TCAGCATTAA	AAGCTTTAGA	AGGCGATGCT	250
	CAATACGAAG	AAAAAATCTT	AGAATTAATG	CAAGCAGTTG	ATGACTACAT	300
	TCCAACCTCA	GAACGTGATT	CTGACAAACC	ATTCATGATG	CCAGTTGAGG	350
60	ACGTATTCTC	AATCACTGGT	CGTGGTACTG	TTGCTACAGG	CCGTGTTGAA	400

CGTGGGCAAA TCAAAGTTGG TGAAGAAGTT GAAATCATTG ~~GYATCCATGA~~ 450  
 CACTTCTAAA ACAACTGTTA CTGGTGTAGA AATGTTCCGT AAATTATTAG 500  
 ACTACGCTGA AGCTGGTGAC AACATCGGTG CATTATTACG TGGTGTGCT 550  
 CGTGAAGACG TACAACGTGG TCAAGTATTA GCTGCTCCAG GTTCAATCAC 600  
 5 ACCTCACACA AAATTTAAAG CAGACGTATA CGTTTTATCT AAAGACGAAG 650  
 GTGGACGTCA CACTCCATTC TTCACAAACT ATCGTCCACA ATTCTATTTT 700  
 CGTACTACTG ACGTAACTGG TGTGTTAAC TTACCAGAAG GTACTGAAAT 750  
 GGTATGCTT GGCACAAACG TTGAAATGAC AGTAGAATTA ATCGCTCCTA 800  
 TCGCGATTGA AGACGGTACT CGTTTCTCA 829  
 10

## 2) INFORMATION FOR SEQ ID NO: 187

15 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 705 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear  
 20 (ii) MOLECULE TYPE: Genomic DNA  
 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: *Staphylococcus warneri*  
 25 (B) STRAIN: CSG 123

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 187

CACAACTCG TGAACACATT CTTTTATCAC GTAACGTTGG TGTACCAGCT 50  
 30 TTAGTTGTAT TCTTAAACAA AGTTGATATG GTAGACGACG AAGAATTATT 100  
 AGAATTAGTA GAAATGGAAG TTCGTGACTT ATTATCTGAA TATGACTTCC 150  
 CAGGTGACGA CGTACCTGTA ATCGCTGGTT CAGCATTAAA AGCTTTAGAA 200  
 GGCACGAAA AATACGAAGA AAAAATCTTA GAATTAATGC AAGCAGTTGA 250  
 TGACTACATT CCAACTCCAG AACGTGATTC TGACAAACCA TTCATGATGC 300  
 35 CAGTTGAGGA CGTATTCTCA ATCACTGGTC GTGGTACTGT TGCTACAGGC 350  
 CGTGTTGAAC GTGGTCAAAT CAAAGTTGGT GAAGAAGTTG AAATCATCGG 400  
 TTTACATGAC ACTTCTAAA CAACTGTTAC TGGTGTAGAA ATGTTCCGTA 450  
 AGTTATTAGA CTACGCTGAA GCTGGTGACA ACATCGGTGC TTTATTACGT 500  
 GGTGTTGCTC GTGAAGACGT ACAACGTGGT CAAGTATTAG CTGCTCCTGG 550  
 40 TTCAATTACA CCACATACAA AATTCAAAGC GGAAGTTTAC GTTTTATCTA 600  
 AAGACGAAGG TGGACGTCAC ACTCCATTCT TCAGTAACTA CCGCCACAA 650  
 TTCTATTTCC GTACTACTGA CGTAACTGGC GTTGTTCAT TACCAGAAGG 700  
 TACTG 705  
 45

## 2) INFORMATION FOR SEQ ID NO: 188

50 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 678 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear  
 55 (ii) MOLECULE TYPE: Genomic DNA  
 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: *Staphylococcus haemolyticus*  
 (B) STRAIN: CSG 23  
 60

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 188:

```

      TTTTATCACG TAACGTTGGT GTACCAGCAT TAGTAGTATT CTTAAACAAA      50
      GTTGACATGG TTGACGATGA AGAATTATTA GAATTAGTTG AAATGGAAGT      100
5     ACGTGACTTA TTATCTGAAT ACGACTTCCC AGGTGACGAC GTACCTGTAA      150
      TCGCTGGTTC AGCTTTAAAA GCTTTAGAAG GCGATGCTCA ATACGAAGAA      200
      AAAATCTTAG AATTAATGCA AGCAGTTGAT GATTACATTC CAACTCCAGA      250
      ACGTGACTCT GATAAACCAT TCATGATGCC AGTTGAGGAC GTATTCTCAA      300
      TCACTGGTTCG TGGTACTGTT GCTACAGGTC GTGTTGAACG TGGTCAAATC      350
10    AAAGTTGGTG AAGAAGTTGA AATTATTGGT ATCAAAGAAA CTTCTAAAAC      400
      AACTGTTACT GGTGTAGAAA TGTTCCGTAA ATTATTAGAC TACGCTGAAG      450
      CTGGTGACAA CATCGGTGCT TTATTACGTG GTGTTGCTCG TGAAGATGTA      500
      CAACGTGGTC AAGTATTAGC TGCTCCAGGT TCAATTACAC CTCACACAAA      550
      ATTCAAAGCA GACGTATACG TTTTATCAAA AGATGAAGGT GGACGTCATA      600
15    CTCCATTCTT CACTAACTAT CGTCCACAAT TCTATTTCCG TACTACTGAC      650
      GTAACGGTG TTGTAACTT ACCAGAAG      678

```

## 20 2) INFORMATION FOR SEQ ID NO: 189

## (i) SEQUENCE CHARACTERISTICS:

```

      (A) LENGTH: 668 bases
      (B) TYPE: Nucleic acid
25    (C) STRANDEDNESS: Double
      (D) TOPOLOGY: Linear

```

## (ii) MOLECULE TYPE: Genomic DNA

## 30 (vi) ORIGINAL SOURCE:

```

      (A) ORGANISM: Staphylococcus haemolyticus
      (B) STRAIN: CSG 33

```

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 189

```

35    ACCAGCATTG TAGTATTCT TAAATAAAGT TGACATGGTT GACGATGAAG      50
      AATTATTAGA ATTAGTTGAA ATGGAAGTAC GTGACTTATT ATCTGAATAC      100
      GACTTCCCAG GTGACGATGT ACCTGTAATC GCTGGTTCAG CATTAAAAGC      150
      TTTAGAAGGC GATGCTCAAT ACGAAGAAAA AATCTTAGAA TTAATGCAAG      200
40    CAGTTGATGA CTACATTCCA ACTCCAGAAC GTGATTCTGA CAAACCATTTC      250
      ATGATGCCAG TTGAGGACGT ATTCTCAATC ACTGGTCGTG GTACTGTTGC      300
      TACAGGCCGT GTTGAACGTG GTCAAATCAA AGTTGGTGAA GAAGTTGAAA      350
      TCATTGGTAT CCATGACACT TCTAAAACAA CTGTTACTGG TGTAGAAATG      400
      TTCCGTAAAT TATTAGACTA CGCTGAAGCT GGTGACAACA TCGGTGCATT      450
45    ATTACGTGGT GTTGCTCGTG AAGACGTACA ACGTGGTCAA GTATTAGCTG      500
      CTCCAGGTTT AATCACACCT CACACAAAAT TTAAAGCAGA CGTATACGTT      550
      TTATCTAAAG ACGAAGGTGG ACGTCACACT CCATTCTTCA CAACTATCG      600
      TCCACAATTTC TATTTCGTA CTACTGACGT AACTGGTGTT GTTAACTTAC      650
50    CAGAAGGTAC TGAAATGG      668

```

## 2) INFORMATION FOR SEQ ID NO: 190

## (i) SEQUENCE CHARACTERISTICS:

```

      (A) LENGTH: 593 bases
      (B) TYPE: Nucleic acid
50    (C) STRANDEDNESS: Double
      (D) TOPOLOGY: Linear

```

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 5 (A) ORGANISM: *Staphylococcus haemolyticus*  
 (B) STRAIN: CSG 8

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 190

```

10 AAAGTTGACA TGGTTGACGA TGAAGAATTA TTAGAATTAG TTGAAATGGA      50
   AGTACGTGAC TTATTATCTG AATACGACTT CCCAGGTGAC GATGTACCTG      100
   TAATCGCTGG TTCAGCATT AAGGCTTTAG AAGGCGATGC TCAATACGAA      150
   GAAAAAATCT TAGAATTAAT GCAAGCAGTT GATGATTACA TTCCAACCTCC      200
   AGAACGTGAT TCTGACAAAC CATTGATGAT GCCAGTTGAG GACGTATTCT      250
   CAATCACTGG TCGTGGTACT GTTGCTACAG GCCGTGTTGA ACGTGGTCAA      300
15 ATCAAAGTTG GTGAAGAAGT TGAAATCATT GGTATCCATG ACACCTTCTAA      350
   AACAACTGTT ACTGGTGTAG AAATGTTCCG TAAATTATTA GACTACGCTG      400
   AAGCTGGTGA CAACATTGGT GCATTATTAC GTGGTGTGTC TCGTGAAGAC      450
   GTACAACGTG GTCAAGTATT AGCTGCTCCA GGTTC AATCA CACCTCACAC      500
   AAAATTTAAA GCAGACGTAT ACGTTTTATC TAAAGACGAA GGTGGACGTC      550
20 ACACTCCATT CTTCAAAAC TATCGTCCAC AATTCTATTT CCG              593

```

2) INFORMATION FOR SEQ ID NO: 191

25

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 828 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 30 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 35 (A) ORGANISM: *Staphylococcus hominis* subsp. *hominis*  
 (B) STRAIN: ATCC 27844

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 191

```

40 CGGCGCTATC TTAGTAGTAT CTGCTGCTGA TGGTCCAATG CCACAAACTC      50
   GTGAACACAT TCTTTTATCA CGTAACGTTG GTGTACCAGC ATTAGTAGTA      100
   TTCTTAAACA AAGTTGACAT GGTTGACGAT GAAGAATTAT TAGAATTAGT      150
   TGAAATGGAA GTACGTGACT TATTATCTGA ATACGACTTC CCAGGTGACG      200
   ACGTACCTGT AATCGCTGGT TCAGCTTTAA AAGCTTTAGA AGGCGATGCT      250
45 CAATACGAAG AAAAAATCTT AGAATTAATG CAAGCAGTTG ATGATTATAT      300
   TCCAACTCCA GAACGTGACT CTGATAAACC ATTCATGATG CCAGTTGAGG      350
   ACGTATTCTC AATCACTGGT CGTGCTACTG TTGCTACAGG CCGTGTTGAA      400
   CGTGGTCAAA TCAAAGTTGG TGAAGAAGTT GAAATTATTG GTATCAAAGA      450
   AACTTCTAAA ACAACTGTTA CTGGTGTAGA AATGTTCCGT AAATTATTAG      500
50 ACTACGCTGA AGCTGGTGAC AACATCGGTG CTTTATTACG TGGTGTGCT      550
   CGTGAAGATG TACAACGTGG TCAAGTATTA GCTGCTCCAG GTTCAATTAC      600
   ACCTCACACA AAATTCAAAG CAGACGTATA CGTTTTATCA AAAGATGAAG      650
   GTGGACGTCA TACTCCATTC TTCTCTAACT ATCGTCCACA ATTCTATTTC      700
   CGTACTACTG ACGTAACTGG TGTGTTAATC TTACCAGAAG GTACTGAAAT      750
55 GGTAATGCCT GGTGACAACG TTGAAATGAC AGTAGAATTA ATCGCTCCTA      800
   TCGCGATTGA AGACGGTACT CGTTTCTC              828

```

60 2) INFORMATION FOR SEQ ID NO: 192

## (i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 620 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- 10 (A) ORGANISM: *Staphylococcus warneri*  
 (B) STRAIN: ATCC 35982

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 192

15 ATGGTCCAAT GCCACAACT CGTGAACACA TTCTTTTATC ACGTAACGTT 50  
 GGTGTACCAG CTTTAGTTGT ATTCTTAAAC AAAGTTGATA TGGTAGACGA 100  
 CGAAGAATTA TTAGAATTAG TAGAAATGGA AGTTCGTGAC TTATTATCTG 150  
 AATATGACTT CCCAGGTGAC GACGTACCTG TAATCGCTGG TTCAGCATT 200  
 20 AAAGCTTTAG AAGGCGACGA AAAATACGAA GAAAAAATCT TAGAATTAAT 250  
 GCAAGCAGTT GATGACTACA TTCCAACCTC AGAACGTGAT TCTGACAAAC 300  
 CATTCATGAT GCCAGTTGAG GACGTATTCT CAATCACTGG TCGTGGTACT 350  
 GTTGCTACAG GCCGTGTTGA ACGTGGTCAA ATCAAAGTTG GTGAAGAAGT 400  
 TGAAATCATC GGTTTACATG ACACTTCTAA AACAACTGTT ACTGGTGTAG 450  
 25 AAATGTTCCG TAAGTTATTA GACTACGCTG AAGCTGGTGA CAACATCGGT 500  
 GCTTTATTAC GTGGTGTTGC TCGTGAAGAC GTACAACGTG GTCAAGTATT 550  
 AGCTGCTCCT GGTTC AATTA CACCACATAC AAAATTCAAA GCGGAAGTTT 600  
 ACGTTTTATC TAAAGACGAA 620

30

## 2) INFORMATION FOR SEQ ID NO: 193

## (i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 692 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- 40 (A) ORGANISM: *Staphylococcus hominis*  
 (B) STRAIN: CSG 170

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 193

CCAGCATTAG TAGTATTCTT AAACAAAGTT GACATGGTTG ACGATGAAGA 50  
 ATTATTAGAA TTAGTTGAAA TGGAAGTACG TGACTTATTA TCTGAATACG 100  
 50 ACTTCCAGG TGACGACGTA CCTGTAATCG CTGGTTCAGC TTTAAAAGCT 150  
 TTAGAAGGCG ATGCTCAATA CGAAGAAAAA ATCTTAGAAT TAATGCAAGC 200  
 AGTTGATGAT TATATTCCAA CTCCAGAACG TGACTCTGAT AAACCATTCA 250  
 TGATGCCAGT TGAGGACGTA TTCTCAATCA CTGGTCGTGG TACTGTTGCT 300  
 ACAGGCCGTG TTGAACGTGG TCAAATCAAA GTTGGTGAAG AAGTTGAAAT 350  
 55 TATTGGTATC AAAGAACTT CTAAAACAAC TGTTACTGGT GTAGAAATGT 400  
 TCCGTAAATT ATTAGACTAC GCTGAAGCTG GTGACAACAT CCGTGCTTTA 450  
 TTACGTGGTG TTGCTCGTGA AGATGTACAA CGTGGTCAAG TATTAGCTGC 500  
 TCCAGGTTCA ATTACACCTC ACACAAAATT CAAAGCAGAC GTATACGTTT 550  
 TATCAAAAGA TGAAGGTGGA CGTCATACTC CATTCTTCTC TAACTATCGT 600  
 60 CCACAATTCT ATTTCCGTAC TACTGACGTA ACTGGTGTG TTAACCTACC 650

AGAAGGTACT GAAATGGTAA TGCCTGGTGA CAACGTTGAA AT '

5 2) INFORMATION FOR SEQ ID NO: 194

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 684 bases  
 (B) TYPE: Nucleic acid  
 10 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

15 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus hominis*  
 (B) STRAIN: CSG 36

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 194

20 CATTCCTTTTA TCACGTAACG TTGGTGTACC AGCATTAGTA GTATTCTTAA 50  
 ACAAAGTTGA CATGGTTGAC GATGAAGAAT TATTAGAATT AGTTGAAATG 100  
 GAAGTACGTG ACTTATTATC TGAATACGAC TTCCCAGGTG ACGACGTACC 150  
 TGTAATCGCT GGTTCAGCTT TAAAAGCTTT AGAAGGCGAT GCTCAATACG 200  
 25 AAGAAAAAAT CTTAGAATTA ATGCAAGCAG TTGATGATTA TATTCCAAC T 250  
 CCAGAACGTG ACTCTGATAA ACCATTTCATG ATGCCAGTTG AGGACGTATT 300  
 CTCAATCACT GGTCTGTTGTA CTGTTGCTAC AGGCCGTGTT GAACGTGGTC 350  
 AAATCAAAGT TGGTGAAGAA GTTGAAATTA TTGGTATCAA AGAACTTCT 400  
 AAAACAAC T TACTGGTGT AGAAATGTTT CGTAAATTAT TAGACTACGC 450  
 30 TGAAGCTGGT GACAACATCG GTGCTTTATT ACGTGGTGTT GCTCGTGAAG 500  
 ATGTACAACG TGGTCAAGTA TTAGCTGCTC CAGGTTCAAT TACACCTCAC 550  
 ACAAATTC AAGCAGACGT ATACGTTTTA TCAAAAGATG AAGGTGGACG 600  
 TCATACTCCA TTCTTCTCTA ACTATCGTCC ACAATTCTAT TTCCGTACTA 650  
 CTGACGTAAC TGGTGTGTT AACTTACCAG AAGG 684  
 35

2) INFORMATION FOR SEQ ID NO: 195

40 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 685 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 45 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus hominis*  
 50 (B) STRAIN: CSG 6

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 195

55 ACCAGCATTG TAGTATTCT TAAACAAAGT TGACATGGTT GACGATGAAG 50  
 AATTATTAGA ATTAGTTGAA ATGGAAGTAC GTGACTTATT ATCTGAATAC 100  
 GACTTCCCAG GTGACGACGT ACCTGTAATC GCTGGTTCAG CTTTAAAGC 150  
 TTTAGAAGGC GATGCTCAAT ACGAAGAAAA AATCTTAGAA TTAATGCAAG 200  
 CAGTTGATGA TTACATTCCA ACTCCAGAAC GTGACTCTGA TAAACCATTC 250  
 ATGATGCCAG TTGAGGACGT ATTCTCAATC ACTGGTCGTG GTACTGTTGC 300  
 60 TACAGGCCGT GTTGAACGTG GTCAAATCAA AGTTGGTGAA GAAGTTGAAA 350

TTATTGGTAT CAAAGAACT TCTAAAACAA CTGTTACTGG TGTAGAAATG 400  
 TTCCGTAAAT TATTAGACTA CGCTGAAGCT GGTGACAACA TCGGTGCTTT 450  
 ATTACGTGGT GTTGCTCGTG AAGATGTACA ACGTGGTCAA GTATTAGCTG 500  
 CTCCAGGTTC AATTACACCT CACACAAAAT TCAAAGCAGA CGTATACGTT 550  
 5 TTATCAAAAG ATGAAGGTGG ACGTCATACT CCATTCTTCA CTAAGTATCG 600  
 TCCACAATTC TATTTCCGTA CTACTGACGT AACTGGTGTG GTTAACTTAC 650  
 CAGAAGGTAC TGAAATGGTA ATGCCTGGCG ACAAC 685

10

## 2) INFORMATION FOR SEQ ID NO: 196

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 611 bases  
 15 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

20

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus hominis*  
 (B) STRAIN: CSG 62

25

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 196

GACTTATTAT CTGAATACGA CTTCCCAGGT GACGACGTAC CTGTAATCGC 50  
 TGGTTCAGCT TTAAAAGCTT TAGAAGGCGA TGCTCAATAC GAAGAAAAAA 100  
 TCTTAGAATT AATGCAAGCA GTTGATGATT ACATTCCAAC TCCAGAACGT 150  
 30 GACTCTGATA AACCATTCTAT GATGCCAGTT GAGGACGTAT TCTCAATCAC 200  
 TGGTCGTGGT ACTGTTGCTA CAGGCCGTGT TGAACGTGGT CAAATCAAAG 250  
 TTGGTGAAGA AGTTGAAATT ATTGGTATCA AAGATACTTC TAAAACAACT 300  
 GTTACTGGTG TAGAAATGTT CCGTAAATTA TTAGACTACG CTGAAGCTGG 350  
 TGACAACATC GGTGCTTTAT TACGTGGTGT TGCTCGTGAA GATGTACAAC 400  
 35 GTGGTCAAGT ATTAGCTGCT CCAGGTTCAA TCACACCTCA CACAAAATTC 450  
 AAAGCAGACG TATATGTTTT ATCAAAAGAT GAAGGTGGAC GTCATACTCC 500  
 ATTCTTCACT AACTATCGTC CACAATTCTA TTCCGTACT ACTGACGTAA 550  
 CTGGTGTTGT TAACTTACCA GAAGGTACTG AAATGGTAAT GCCTGGCGAC 600  
 AACGTTGAAA T 611

40

## 2) INFORMATION FOR SEQ ID NO: 197

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 828 bases  
 45 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

50

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus lugdunensis*  
 55 (B) STRAIN: ATCC 43809

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 197

CGGCGGTATC TTAGTAGTTT CTGCTGCAGA TGGTCCAATG CCACAACTC 50  
 50 GTGAACACAT TCTTTTATCA CGTAACGTTG GTGTGCCAGC ATTAGTAGTA 100

```

TTCTTAAACA AAGTTGACAT GGTGACGAT GAAGAATTAT TAGAATTAGT 150
AGAAATGGAA GTTCGTGATT TATTAAGTGA ATATGACTTC CCAGGTGACG 200
ATGTGCCTGT AATCGCTGGT TCAGCATTAA AAGCTTTAGA AGGCGACGAA 250
AAATACGAAG CTAAAATCTT AGAATTAATG GATGCAGTTG ATAAGTACAT 300
5 TCCAACCTCA GAACGTGACT CTGACAAACC ATTCATGATG CCAGTTGAGG 350
ACGTATTCTC AATCACTGGT CGTGGTACTG TTGCTACAGG CCGTGTTGAA 400
CGTGGTCAAA TCAAAGTCGG TGAAGAAGTT GAAATTATTG GTATCCACGA 450
TACTACTAAA ACAACTGTTA CTGGTGTAGA AATGTTCCGT AAATTATTAG 500
ACTACGCTGA AGCTGGTGAC AACATCGGTG CGTTATTACG TGGTGTGCT 550
10 CGTGAAGATG TACAACGTGG ACAAGTATTA GCTGCTCCAG GTTCAATTAC 600
ACCTCACACT AAATTTAAAG CTGACGTATA TGTTTTATCT AAAGATGAAG 650
GTGGACGTCA TACACCATTG TTCTCAAACCT ACCGCCACCA ATTCTATTTC 700
CGTACTACAG ACGTAACTGG TGTGTGTTAA TTACCAGAAG GTACAGAAAT 750
GGTTATGCCT GGCGACAACG TTGAAATGAC AGTTGAATTA ATCGCTCCAA 800
15 TCGCTATCGA AGACGGAACCT CGTTTCTC 828

```

## 2) INFORMATION FOR SEQ ID NO: 198

20

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 690 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 25 (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- 30 (A) ORGANISM: *Staphylococcus saprophyticus*  
 (B) STRAIN: ATCC 35552

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 198

```

35 AGTAGTATCT GCTGCTGATG GCCCAATGCC ACAAACCTCGT GAACACATTC 50
TTTTATCACG TAACGTTGGT GTTCCAGCAT TAGTTGTATT CTTAAACAAA 100
GTTGACATGG TTAGCGATGA AGAATTATTA GAATTAGTAG AAATGGAAGT 150
TCGTGACTTA TTAAGCGAAT ATGACTTCCC AGGTGACGAT GTACCTGTAA 200
TCTCTGGTTC TGCATTAAAA GCTTTAGAAG GCGACGCTGA CTATGAGCAA 250
40 AAAATCTTAG ACTTAATGCA AGCTGTTGAT GACTTCATTC CAACACCAGA 300
ACGTGATTCT GACAAACCAT TCATGATGCC AGTTGAGGAC GTATTCTCAA 350
TCACTGGTCG TGGTACTGTT GCTACAGGCC GTGTTGAACG TGGTCAAATC 400
AAAGTCGGTG AAGAAATCGA AATCATCGGT ATGCAAGAAG AATCAAGCAA 450
AACAACCTGTT ACTGGTGTAG AAATGTTCCG TAAATTATTA GACTACGCTG 500
45 AAGCTGGTGA CAACATTGGT GCATTATTAC GTGGTGT TTC ACGTGATGAC 550
GTACAACGTG GTCAAGTTT AGCTGCTCCT GGTACTATTA CACCACATAC 600
AAAATTCAAA GCGGATGTTT ACGTTTATC TAAAGATGAA GGTGGTCGTC 650
ATACACCATT CTTACTAAC TACCGCCAC AATTCTATTT 690

```

50

## 2) INFORMATION FOR SEQ ID NO: 199

## (i) SEQUENCE CHARACTERISTICS:

- 55 (A) LENGTH: 723 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

119



## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus saprophyticus*  
 (B) STRAIN: CSG 83

5

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 199

	GCATTAGTTG	TATTCTTAAA	CAAAGTTGAC	ATGGTTGACG	ATGAAGAATT	50
	ATTAGAATTA	GTAGAAATGG	AAGTTCGTGA	TTTATTAAGC	GAATATGACT	100
10	TCCCAGGTGA	CGATGTACCT	GTAATCTCTG	GTTCTGCATT	AAAAGCTTTA	150
	GAAGGCGACG	CTGACTATGA	GCAAAAATC	TTAGACTTAA	TGCAAGCTGT	200
	TGATGACTTC	ATTCCAACAC	CAGAACGTGA	TTCTGACAAA	CCATTCATGA	250
	TGCCAGTTGA	GGACGTATTG	TCAATCACTG	GTCGTGGTAC	TGTTGCTACA	300
	GGCCGTGTTG	AACGTGGTCA	AATCAAAGTC	GGTGAAGAAA	TCGAAATCAT	350
15	CGGTATGCAA	GAAGAATCAA	GCAAAACAAC	TGTTACTGGT	GTAGAAATGT	400
	TCCGTAAATT	ATTAGACTAC	GCTGAAGCTG	GTGACAACAT	TGGTGCATTA	450
	TTACGTGGTG	TTTCACGTGA	TGACGTACAA	CGTGGTCAAG	TTTTAGCTGC	500
	TCCTGGTACT	ATTACACCAC	ATACAAAATT	CAAAGCGGAT	GTTTACGTTT	550
	TATCTAAAGA	TGAAGGTGGT	CGTCATACAC	CATTCTTCAC	TAACTACCGC	600
20	CCACAATTCT	ATTTCCGTAC	TACTGACGTA	ACTGGTGTG	TTAACTTACC	650
	AGAAGGTACT	GAAATGGTTA	TGCCTGGCGA	TAACGTTGAA	ATGGATGTTG	700
	AATTAATTTT	TCCAATCGCT	ATT			723

25

## 2) INFORMATION FOR SEQ ID NO: 200

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 697 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

35

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus saprophyticus*  
 (B) STRAIN: CSsa 18

40

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 200

	CGTTGGTGTT	CCAGCATTAG	TTGTATTCTT	AAACAAAGTT	GACATGGTTG	50
	ACGATGAAGA	ATTATTAGAA	TTAGTAGAAA	TGGAAGTTCG	TGACTTATTA	100
	AGCGAATATG	ACTTCCCAGG	TGACGATGTA	CCTGTAATCT	CTGGTTCTGC	150
45	ATTAAAAGCT	TTAGAAGGCG	ACGCTGACTA	TGAGCAAAAA	ATCTTAGACT	200
	TAATGCAAGC	TGTTGATGAC	TTCATTCCAA	CACCAGAACG	TGATTCTGAC	250
	AAACCATTC	TGATGCCAGT	TGAGGACGTA	TTCTCAATCA	CTGGTCGTGG	300
	TACTGTTGCT	ACAGGCCGTG	TTGAACGTGG	TCAAATCAAA	GTCGGTGAAG	350
	AAATCGAAAT	CATCGGTATG	CAAGAAGAAT	CAAGCAAAAC	AACTGTTACT	400
50	GGTGTAGAAA	TGTTCCGTAA	ATTATTAGAC	TACGCTGAAG	CTGGTGACAA	450
	CATTGGTGCA	TTATTACGTG	GTGTTTCACG	TGATGACGTA	CAACGTGGTC	500
	AAGTTTTAGC	TGCTCCTGGT	ACTATTACAC	CACATACAAA	ATTCAAAGCG	550
	GATGTTTACG	TTTTATCTAA	AGATGAAGGT	GGTCGTCATA	CACCATTCTT	600
	CACTAACTAC	CGCCCACAAT	TCTATTTCCG	TACTACTGAC	GTAACCTGGT	650
55	TTGTTAACTT	ACCAGAAGGT	ACTGAAATGG	TTATGCCTGG	CGATAAC	697

60

## 2) INFORMATION FOR SEQ ID NO: 201

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 835 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus sciuri* subsp. *sciuri*  
 (B) STRAIN: ATCC 29060

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 201

```

15  CGGCGGTATC TTAGTAGTAT CTGCTGCTGA CGGTCCAATG CCTCAAACCTC      50
    GTGAGCACAT TCTTTTATCA CGTAACGTAG GTGTTCTCTG ATTAGTAGTA      100
    TTCTTAAACA AAGTTGACAT GGTGACGAT  GAAGAATTAT TAGAATTAGT      150
    TGAAATGGAA GTTCGTGACT TATTATCTGA ATATGACTTC CCAGGCGACG      200
    ACGTTCCTGT AATTGCTGGT TCAGCATTAA AAGCATTAGA AGGCGACGAA      250
20  GCTTACGAAG ACAAATCAT  GGAATTAATG GATGCTGTTG ATACATTCTAT      300
    CCCAACTCCA GAACGTGACT CTGACAAACC ATTCATGATG CCAGTTGAGG      350
    ACGTATTCTC AATCACTGGT CGTGGTACTG TTGCTACAGG CCGTGTGAGG      400
    CGTGGTCAAA TCACTGTTGG TGAAGAAGTT GAAATCATCG GTTTAACTGA      450
    AGAATCTTCT AAAACAACCTG TAACTGGTGT TGAAATGTTC CGTAAATTAT      500
25  TAGACTTCGC TGAAGCTGGA GATAACATCG GTGCATTATT ACGTGGTGTG      550
    GCTCGTGAAG ACGTTAACCG TGGTCAAGTA TTAGCTAAAC CAGGTTCAAT      600
    CACACCTCAC ACTAAATTCA AAGCTGAAGT TTATGTATTA TCTAAAGACG      650
    AAGGTGGACG TCATACTCCA TTCTTCACAA ACTACCGCCC ACAATTCTAT      700
    TTCCGTTACT CTGACGTAAC TGGTGTAGTT AACTTACCAG AAGGTACTGA      750
30  AATGGTTATG CCTGGCGACA ACGTTGAAAT GGACGTTGAA TTAATTTTAC      800
    CAATCGCTAT TGAAGACGGT ATCGTTTCTC AATCA                      835
  
```

## 35 2) INFORMATION FOR SEQ ID NO: 202

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 831 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus warneri*  
 (B) STRAIN: ATCC 27836

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 202

```

50  CGGCGGTATC TTAGTTGTAT CTGCAGCTGA TGGTCCAATG CCACAAACTC      50
    GTGAACACAT TCTTTTATCA CGTAACGTTG GTGTACCAGC TTAGTTGTAT      100
    TTCTTAAACA AAGTTGATAT GGTAGACGAC GAAGAATTAT TAGAATTAGT      150
    AGAAATGGAA GTTCGTGACT TATTATCTGA ATATGACTTC CCAGGTGACG      200
55  ACGTACCTGT AATCGCTGGT TCAGCATTAA AAGCTTTAGA AGGCGACGAA      250
    AAATACGAAG AAAAAATCTT AGAATTAATG CAAGCAGTTG ATGACTACAT      300
    TCCAACTCCA GAACGTGATT CTGACAAACC ATTCATGATG CCAGTTGAGG      350
    ACGTATTCTC AATCACTGGT CGTGGTACTG TTGCTACAGG CCGTGTGAGG      400
    CGTGGTCAAA TCAAAGTTGG TGAAGAAGTT GAAATCATCG GTTTACATGA      450
60  CACTTCTAAA ACAACTGTTA CTGGTGTAGA AATGTTCCGT AAGTTATTAG      500
  
```

	ACTACGCTGA	AGCTGGTGAC	AACATCGGTG	CTTTATTACG	TGGTGTGCT	550
	CGTGAAGACG	TACAACGTGG	TCAAGTATTA	GCTGCTCCTG	GTTCAATTAC	600
	ACCACATACA	AAATTCAAAG	CGGAAGTTTA	CGTTTTATCT	AAAGACGAAG	650
	GTGGACGTCA	CACTCCATTC	TTCAGTAACT	ACCGCCCACA	ATTCTATTTT	700
5	CGTACTACTG	ACGTAACCTGG	CGTTGTTCAA	TTACCAGAAG	GTACTGAAAT	750
	GGTTATGCCT	GGTGATAACG	TTGAAATGAC	AGTAGAATTA	ATCGCTCCTA	800
	TCGCGATTGA	AGACGGTACT	CGTTTCTCAA	C		831

10

## 2) INFORMATION FOR SEQ ID NO: 203

## (i) SEQUENCE CHARACTERISTICS:

15

- (A) LENGTH: 829 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

20

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus warneri*
- (B) STRAIN: CSG 50

25

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 203

	CGGCGGTATC	TTAGTTGTAT	CTGCAGCTGA	TGGTCCAATG	CCACAAACTC	50
	GTGAACACAT	TCTTTTATCA	CGTAACGTTG	GTGTACCAGC	TTTAGTTGTA	100
	TTCTTAAACA	AAGTTGATAT	GGTAGACGAC	GAAGAATTAT	TAGAATTAGT	150
30	AGAAATGGAA	GTTTCGTGACT	TATTATCTGA	ATATGACTTC	CCAGGTGACG	200
	ACGTACCTGT	AATCGCTGGT	TACAGCATTAA	AAGCTTTAGA	AGGCGACGAA	250
	AAATACGAAG	AAAAAATCTT	AGAATTAATG	CAAGCAGTTG	ATGACTACAT	300
	TCCAACCTCCA	GAACGTGATT	CTGACAAACC	ATTCATGATG	CCAGTTGAGG	350
	ACGTATTCTC	AATCACTGGT	CGTGGTACTG	TTGCTACAGG	CCGTGTTGAA	400
35	CGTGGTCAAA	TCAAAGTTGG	TGAAGAAGTT	GAAATCATCG	GTTTACATGA	450
	CACTTCTAAA	ACAACGTGTTA	CTGGTGTAGA	AATGTTCCGT	AAGTTATTAG	500
	ACTACGCTGA	AGCTGGTGAC	AACATCGGTG	CTTTATTACG	TGGTGTGCT	550
	CGTGAAGACG	TACAACGTGG	TCAAGTATTA	GCTGCTCCTG	GTTCAATTAC	600
	ACCACATACA	AAATTCAAAG	CGGAAGTTTA	CGTTTTATCT	AAAGACGAAG	650
40	GTGGACGTCA	CACTCCATTC	TTCAGTAACT	ACCGCCCACA	ATTCTATTTT	700
	CGTACTACTG	ACGTAACCTGG	CGTTGTTCAA	TTACCAGAAG	GTACTGAAAT	750
	GGTTATGCCT	GGTGATAACG	TTGAAATGAC	AGTAGAATTA	ATCGCTCCTA	800
	TCGCGATTGA	AGACGGTACT	CGTTTCTCA			829

45

## 2) INFORMATION FOR SEQ ID NO: 204

## (i) SEQUENCE CHARACTERISTICS:

50

- (A) LENGTH: 839 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

55

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Bifidobacterium longum*
- (B) STRAIN: ATCC 15707

60

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 204

```

TGGCGCTATC CTCGTTGTGG CCGCCACCGA CGGCCCGATG GCCCAGACTC      50
GCGAGCACGT GCTGCTCGCC CGTCAGGTG GCGTTCCGAA GATCCTCGTC      100
5  GCCCTGAACA AGTGCGACAT GGTCGACGAT GAAGAGCTCA TCGAGCTCGT      150
   CGAAGAAGAG GTCCGCGACC TCCTCGACGA GAACGGCTTC GACCGTGACT      200
   GCCCGGTCAT CCACACCTCC GCTTACGGTG CTCTGCACGA CGACGCTCCG      250
   GACCACGAGA AGTGGGTCCA GTCCGTTAAG GACCTCATGG ACGCTGTCTGA      300
   CGACTACATC CCGACCCCGG TTCACGACCT GGACAAGCCG TTCCTGATGC      350
10  CGATCGAGGA CGTCTTCACC ATCTCCGGCC GTGGTACCGT TGTCACCGGT      400
   CGTGTCGAGC GTGGCCAGCT GGCCGTCAAC ACCCCGGTCG AGATCGTTGG      450
   TATCCGTCCG ACCCAGCAGA CCACCGTCAC CTCCATCGAG ACCTTCCACA      500
   AGACCATGGA CGCCTGCGAG GCTGGCGACA ACACCGGTCT GCTTCTGCGT      550
   GTTCTCGGCC GTGACGATGT CGAGCGTGGC CAGGTTGTGG CCAAGCCGGG      600
15  CTCCGTCAACC CCGCACACCA AGTTCGAGGG CGAAGTCTAC GTGCTGACCA      650
   AGGACGAAGG CGGCCGTCAC TCGCCGTTCT TCTCCAATA CCGTCCGCAG      700
   TTCTACTTCC GCACCACCGA CGTCACCGGC GTCATCGAGC TGCCGGAAGG      750
   CGTCGAGATG GTTCAGCCGG GCGACCACGC TACCTTCACC GTTGAGCTGA      800
   TTCAGCCCAT CGCTATGGAG GAAGGCCTGA CCTTCGCTG      839
20

```

## 2) INFORMATION FOR SEQ ID NO: 205

```

25  (i) SEQUENCE CHARACTERISTICS:
      (A) LENGTH: 754 bases
      (B) TYPE: Nucleic acid
      (C) STRANDEDNESS: Double
      (D) TOPOLOGY: Linear
30

```

```

(ii) MOLECULE TYPE: Genomic DNA

```

```

(vi) ORIGINAL SOURCE:

```

```

35  (A) ORGANISM: Stenotrophomonas maltophilia
      (B) STRAIN: CDC F3338

```

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 205

```

CGGCGCGATC CTGGTGTGCT CGGCCGCTGA CGGCCCGATG CCGCAGACCC      50
40  GTGAGCACAT CCTGCTGTCG CGCCAGGTCG GCGTGCCGTA CATCGTCGTG      100
   TTCCTGAACA AGGCCGACAT GGTCGACGAC GCCGAGCTGC TCGAGCTGGT      150
   CGAGATGGAA GTGCGCGAAC TGCTGAGCAA GTACGAGTTC CCGGGCGACG      200
   ACACCCCGAT CATCGCCGGT TCGGCCCGCC TGGCGCTGGA AGGCGACCAG      250
   AGCGACATCG GCGTGCCGGC CATCCTGAAG CTGGTCGACG CGCTGGACAG      300
15  CTGGATTCCG GAGCCGGAGC GTGCGATCGA CAAGCCGTTT CTGATGCCCG      350
   TGGAAGACGT GTTCTCGATC TCGGGCCGCG GCACCGTGGT GACCGGTCGT      400
   ATCGAGCGCG GCGTGATCAA GGTGCGCGAC GAAATCGAAA TCGTCGGCAT      450
   CCGTCCGGTG CAGAAGACCA CCGTGACCGG CGTTGAAATG TTCCGCAAGC      500
   TGCTGGACCA GGGTCAGGCA GGCACAAACG CTGGCCTGCT GCTGCGCGGC      550
50  ACCAAGCGTG ATGACGTCGA GCGTGCCAG GTGCTGGCCA AGCCGGGCAC      600
   GATCAAGCCG CACACCAAGT TCGAAGGCGA AGTGTACGTC CTGTCGAAGG      650
   ACGAGGGCGG CCGCCACACC CCGTTCTTCA ACGGCTACCG TCCGCAGTTC      700
   TACTTCCGCA CCACCGACAT CACCGGCGCC GCTGCACTGC CGGAAGGCGT      750
   CGAA
55

```

## 2) INFORMATION FOR SEQ ID NO: 206

```

50  (i) SEQUENCE CHARACTERISTICS:

```

(A) LENGTH: 835 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

5

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

10

(A) ORGANISM: *Streptococcus acidominimus*  
 (B) STRAIN: ATCC 51726

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 206

15	TGGTGCTATC	CTTGTAGTAG	CTTCAACTGA	CGGACCAATG	CCACAAACTC	50
	GTGAGCACAT	CCTTCTTTCA	CGTCAAGTTG	GTGTTAAAAA	CCTTATCGTT	100
	TTCATGAACA	AAGTTGACCT	TGTTGATGAT	GAAGAATTGC	TTGAATTGGT	150
	TGAAATGGAA	ATCCGTGACC	TTCTTTTCAGA	ATACGATTTC	CCAGGTGATG	200
	ATCTTCCAGT	TGTTCAAGGT	TCAGCTCTTA	AAGCGCTTGA	AGGTGATTCA	250
	GCACAAGAAG	ATGTTATCAT	GGAATTGATG	TCAATCGTTG	ACACATACAT	300
20	TCCAGAACCA	GAACGTGATA	CTGACAAACC	ATTGCTTCTT	CCAGTCGAGG	350
	ATGTATTCTC	AATCACTGGA	CGTGGTACTG	TTGCTTCAGG	ACGTATCGAC	400
	CGTGGTACTG	TTAAAGTTAA	TGACGAAGTT	GAAATCGTTG	GTATCAAAGA	450
	CGAAATCTCT	AAAGCAGTTG	TTACTGGTGT	TGAAATGTTT	CGTAAACAAC	500
	TTGACGAAGG	TCTTGCTGGA	GATAACGTTG	GTGTTCTTCT	TCGTGGTGTA	550
25	CAACGTGATG	AAATCGAACG	TGGTCAAGTT	CTTGCTAAAC	CAGGTTCAAT	600
	CAACCCACAC	ACTAAATTCA	AAGGTGAAGT	TTACGTTCTT	TCTAAAGAAG	650
	AAGGTGGACG	TCACACTCCA	TTCTTCGATA	ACTACCGTCC	TCAGTTCTAC	700
	TTCCGTACAA	CTGACGTAAC	TGGTTCAATC	AAATTGCCAG	AAGGTACTGA	750
	AATGGTAATG	CCTGGTGATA	ACGTAACAT	CGAAGTTGAG	TTGATCCACC	800
30	CAATCGCCGT	TGAACAAGGT	ACTACTTTCT	CTATC		835

2) INFORMATION FOR SEQ ID NO: 207

35

(i) SEQUENCE CHARACTERISTICS:

40

(A) LENGTH: 819 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

45

(A) ORGANISM: *Streptococcus agalactiae*  
 (B) STRAIN: ATCC 12403

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 207

50	CTATCCTTGT	AGTTGCTTCA	ACTGATGGAC	CAATGCCACA	AACTCGTGAG	50
	CACATCCTTC	TTTCACGTCA	AGTTGGTGTG	AAACACCTTA	TCGTATTTCAT	100
	GAACAAAGTT	GACCTTGTTG	ATGATGAAGA	ATTGCTTGAA	TTGGTTGAAA	150
	TGGAAATTCT	TGACCTTCTT	TCAGAATACG	ACTTCCCAGG	TGATGACCTT	200
	CCAGTTATCC	AAGGTTTCAGC	TCTTAAAGCA	CTTGAAGGCG	ACGAAAAATA	250
55	CGAAGACATC	ATCATGGAAT	TGATGAGCAC	TGTTGATGAG	TACATTCCAG	300
	AACCAGAACG	TGATACTGAC	AAACCTTTAC	TTCTTCCAGT	TGAAGATGTA	350
	TTCTCAATCA	CTGGACGTGG	TACAGTTGCT	TCAGGACGTA	TCGACCGTGG	400
	TACTGTTTCG	GTCAACGACG	AAGTTGAAAT	CGTTGGTATT	AAAGAAGATA	450
	TCCAAAAAGC	AGTTGTTACT	GGTGTTGAAA	TGTTCCGTAA	ACAACTTGAC	500
50	GAAGGTCTTG	CAGGGGACAA	CGTTGGTGTG	CTTCTTCGTG	GTGTTCAACG	550

TGATGAAATC GAACGTGGTC AAGTTCCTGC TAAACCAGGT TCAATCAACC 600  
 CACACACTAA ATTTAAAGGT GAAGTTTACA TCCTTTCTAA AGAAGAAGGT 650  
 GGACGTCATA CTCCATTCTT CAACAACACTAC CGTCCACAAT TCTACTTCCG 700  
 TACAACAGGAC GTAACAGGTT CAATCGAACT TCCAGCAGGA ACAGAAATGG 750  
 5 TTATGCCTGG TGATAACGTT ACTATCGAAG TTGAATTGAT TCACCCAATC 800  
 GCCGTAGAAC AAGGTACTA 819

10 2) INFORMATION FOR SEQ ID NO: 208

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 819 bases  
 (B) TYPE: Nucleic acid  
 15 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

20 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus agalactiae*  
 (B) STRAIN: ATCC 12973

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 208

25 CTATCCTTGT AGTTGCTTCA ACTGATGGAC CAATGCCACA AACTCGTGAG 50  
 CACATCCTTC TTTCACGTCA AGTTGGTGTT AAACACCTTA TCGTATTCAT 100  
 GAACAAAGTT GACCTTGTTG ATGATGAAGA ATTGCTTGAA TTGGTTGAAA 150  
 TGGAAATTCC TGACCTTCTT TCAGAATACG ACTTCCCAGG TGATGACCTT 200  
 30 CCAGTTATCC AAGGTTTCAGC TCTTAAAGCA CTTGAAGGCG ATGAAAATA 250  
 CGAAGACATC ATCATGGAAT TGATGAGCAC TGTTGATGAG TACATTCCAG 300  
 AACCAGAACG TGATACTGAC AAACCTTTAC TTCTTCCAGT CGAAGATGTA 350  
 TTCTCAATCA CTGGACGTGG TACAGTTGCT TCAGGACGTA TCGACCGTGG 400  
 TACTGTTCGT GTCAACGACG AAGTTGAAAT CGTTGGTATT AAAGAAGATA 450  
 35 TCCAAAAGC AGTTGTTACT GGTGTTGAAA TGTTCCGTAA ACAACTTGAC 500  
 GAAGGTCTTG CAGGGGACAA CGTTGGTGTT CTTCTTCGTG GTGTTCAACG 550  
 TGATGAAATC GAACGTGGTC AAGTTCCTGC TAAACCAGGT TCAATCAACC 600  
 CACACACTAA ATTTAAAGGT GAAGTTTACA TCCTTTCTAA AGAAGAAGGT 650  
 GGACGTCATA CTCCATTCTT CAACAACACTAC CGTCCACAAT TCTACTTCCG 700  
 40 TACAACAGGAC GTAACAGGTT CAATCGAACT TCCAGCAGGA ACAGAAATGG 750  
 TTATGCCTGG TGATAACGTT ACTATCGAAG TTGAATTGAT TCACCCAATC 800  
 GCCGTAGAAC AAGGTACTA 819

45 2) INFORMATION FOR SEQ ID NO: 209

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 822 bases  
 50 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

55

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus agalactiae*  
 (B) STRAIN: ATCC 13813

60 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 209

```

AGCTATCCTT GTAGTTGCTT CAACTGATGG ACCAATGCCA CAAACTCGTG      50
AGCACATCCT TCTTTCACGT CAAGTTGGTG TTAAACACCT TATCGTATTC      100
ATGAACAAAG TTGACCTTGT TGATGATGAA GAATTGCTTG AATTGGTTGA      150
5  AATGGAAATT CGTGACCTTC TTTCAGAATA CGACTTCCCA GGTGATGACC      200
TTCCAGTTAT CCAAGGTTCA GCTCTTAAAG CACTTGAAGG CGATGAAAAA      250
TACGAAGACA TCATCATGGA ATTGATGAGC ACTGTTGATG AGTACATTCC      300
AGAACCAGAA CGTGATACTG ACAAACCTTT ACTTCTTCCA GTCGAAGATG      350
TATTCTCAAT CACTGGACGT GGTACAGTTG CTTCAGGACG TATCGACCGT      400
10 GGTACTGTTT GTGTCAACGA CGAAGTTGAA ATCGTTGGTA TTAAAGAAGA      450
TATCCAAAAA GCAGTTGTTA CTGGTGTGTA AATGTTCCGT AAACAACCTG      500
ACGAAGGTCT TGCAGGGGAC AACGTTGGTG TTCTTCTTCG TGGTGTTCAG      550
CGTGATGAAA TCGAACGTGG TCAAGTTCTT GCTAAACCAG GTTCAATCAA      600
CCCACACACT AAATTTAAAG GTGAAGTTTA CATCCTTTCT AAAGAAGAAG      650
15 GTGGACGTCA TACTCCATTC TTCAACAACT ACCGTCCACA ATTCTACTTC      700
CGTACAACCTG ACGTAACAGG TTCAATCGAA CTTCCAGCAG GAACAGAAAT      750
GGTTATGCCT GGTGATAACG TTACTATCGA AGTTGAATTG ATTCACCCAA      800
TCGCCGTAGA ACAAGGTACT AC                                     822

```

20

## 2) INFORMATION FOR SEQ ID NO: 210

```

25 (i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 825 bases
    (B) TYPE: Nucleic acid
    (C) STRANDEDNESS: Double
    (D) TOPOLOGY: Linear

```

30 (ii) MOLECULE TYPE: Genomic DNA

```

(vi) ORIGINAL SOURCE:
    (A) ORGANISM: Streptococcus agalactiae
    (B) STRAIN: CDCss-1073

```

35

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 210

```

CGGAGCTATC CTTGTAGTTG CTTCAACTGA TGGACCAATG CCACAAACTC      50
GTGAGCACAT CCTTCTTTCA CGTCAAGTTG GTGTAAACA CCTTATCGTA      100
40 TTCATGAACA AAGTTGACCT TGTTGATGAT GAAGAATTGC TTGAATTGGT      150
TGAAATGGAA ATTCGTGACC TTCTTTCAGA ATACGACTTC CCAGGTGATG      200
ACCTTCCAGT TATCCAAGGT TCAGCTCTTA AAGCACTTGA AGGCGACGAA      250
AAATACGAAG ACATCATCAT GGAATTGATG AGCACTGTTG ATGAGTACAT      300
TCCAGAACCA GAACGTGATA CTGACAAACC TTTACTTCTT CCAGTTGAAG      350
45 ATGTATTCTC AATCACTGGA CGTGGTACAG TTGCTTCAGG ACGTATCGAC      400
CGTGGTACTG TTCGTGTCAA CGACGAAGTT GAAATCGTTG GTATTAAAGA      450
AGATATCCAA AAAGCAGTTG TTAAGTGGTG TGAAATGTTT CGTAAACAAC      500
TTGACGAAGG TCTTGCAGGG GACAACGTTG GTGTTCTTCT TCGTGGTGTT      550
CAACGTGATG AAATCGAACG TGGTCAAGTT CTTGCTAAAC CAGGTTCAAT      600
50 CAACCCACAC ACTAAATTTA AAGGTGAAGT TTACATCCTT TCTAAAGAAG      650
AAGGTGGACG TCATACTCCA TTCTTCAACA ACTACCGTCC ACAATTCTAC      700
TTCCGTACAA CTGACGTAAC AGGTTCAATC GAACTTCCAG CAGGAACAGA      750
AATGGTTATG CCTGGTGATA ACGTTACTAT CGAAGTTGAA TTGATTCACC      800
CAATCGCCGT AGAACAAGGT ACTAC                                     825

```

55

## 2) INFORMATION FOR SEQ ID NO: 211

60 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 826 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

5

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus anginosus*  
 (B) STRAIN: ATCC 33397

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 211

15	GGAGCTATCC	TTGTAGTAGC	TTCAACTGAC	GGACCAATGC	CTCAAACCTCG	50
	TGAACACATC	CTTCTTTCAC	GCCAAGTAGG	TGTTAAATAC	CTTATCGTCT	100
	TCATGAATAA	AGTTGACTTG	GTTGACGATG	AAGAATTGCT	TGAATTGGTT	150
	GAAATGGAAA	TCCGTGACCT	TCTTTCAGAA	TACGATTTCC	CAGGTGATGA	200
	AATCCCAGTT	ATCCAAGGTT	CAGCTCTTAA	AGCTCTTGAA	GGTGATGAAA	250
	AATATGAAGA	CATCATCATG	GAATTGATGG	ATACTGTTGA	TGAATACATT	300
20	CCAGAACCAG	AACGTGACAC	TGACAAACCA	TTGCTTCTTC	CAGTTGAAGA	350
	TGTATTCTCA	ATTACTGGAC	GTGGTACTGT	TGCTTCAGGA	CGTATCGACC	400
	GTGGTACTGT	TAAAGTCAAC	GACGAAGTTG	AAATCGTTGG	TATCCGTGAT	450
	GAAATCCAAA	AAGCAGTTGT	TACTGGTGTT	GAAATGTTCC	GTAAACAATT	500
	GGACGAAGGT	CTTGCTGGAG	ATAACGTAGG	GGTTCCTTCT	CGTGGTATCC	550
25	AACGTGACGA	AATCGAACGT	GGACAAGTTC	TTGCTAAACC	AGGTTCAATT	600
	CATCCACACA	CTAAATTCAA	AGGTGAAGTT	TACATCCTTA	CTAAAGAAGA	650
	AGGTGGACGT	CATACTCCAT	TCTTCAACAA	CTACCGTCCT	CAATTCTACT	700
	TCCGTACTAC	AGACGTTACA	GGTTCAATCG	AACTTCCTGC	AGGTACTGAA	750
	ATGGTAATGC	CTGGTGATAA	CGTAACAATC	GACGTTGAAT	TGATCCACCC	800
30	AATTGCCGTA	GAACAAGGAA	CTACAT			826

2) INFORMATION FOR SEQ ID NO: 212

35

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 827 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

40

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus bovis*  
 (B) STRAIN: ATCC 33317

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 212

50	TGGTGCTATC	CTTGTAGTAG	CTTCTACAGA	TGGTCCAATG	CCACAAACAC	50
	GTGAACACAT	CCTTCTTTCA	CGTCAAGTTG	GTGTAAACA	CCTTATCGTC	100
	TTCATGAACA	AAGTTGACCT	TGTTGATGAC	GAAGAATTGC	TTGAATTGGT	150
	TGAAATGGAA	ATCCGTGACC	TTCTTTCAGA	ATATGATTTC	CCAGGTGATG	200
	AAATCCCTGT	AATCCAAGGT	TCAGCTCTTA	AAGCCCTTGA	AGGTGACACT	250
55	CACTACGAAG	ACATCATCAT	GGAATTGATG	AACACTGTAG	ATGAATACAT	300
	TCCAGAACCA	AAACGTGATA	CTGACAAACC	ATTGCTTCTT	CCAGTCGAAG	350
	ACGTATTCTC	AATCACTGGT	CGTGGTACTG	TAGCATCAGG	ACGTATCGAC	400
	CGTGGTACTG	TTAAAGTCAA	CGACGAAGTT	GAAATCGTTG	GTATCCGTGA	450
	CGACATCCAA	AAAGCTGTTG	TTACTGGTGT	TGAAATGTTC	CGTAAACAAC	500
50	TTGATGAAGG	TATCGCAGGG	GATAACGTTG	GTGTTCTTCT	TCGTGGTATC	550



```

CAACGTGATG AAATCGAACG TGGTCAAGTT CTTGCTAAAC CAGGTTCAAT 600
CCACCCACAC ACTAAATTCA AAGGTGAAGT TTACATCCTT ACTAAAGAAG 650
AAGGTGGACG TCACACTCCA TTCTTCAACA ACTACCGTCC TCAATTCTAC 700
TTCCGTACAA CTGACGTTAC AGGTTCAATC GAACTTCCAG CAGGTACTGA 750
5 AATGGTAATG CCTGGTGATA ACGTTACTAT CGACGTTGAA TTGATTCACC 800
CAATCGCCGT TGAACAAGGT ACTACAT 827

```

10 2) INFORMATION FOR SEQ ID NO: 213

(i) SEQUENCE CHARACTERISTICS:

```

15 (A) LENGTH: 821 bases
    (B) TYPE: Nucleic acid
    (C) STRANDEDNESS: Double
    (D) TOPOLOGY: Linear

```

(ii) MOLECULE TYPE: Genomic DNA

20 (vi) ORIGINAL SOURCE:

```

    (A) ORGANISM: Streptococcus anginosus (deposited as
        Streptococcus constellatus)
    (B) STRAIN: ATCC 27823

```

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 213

```

GCTATCCTCG TAGTAGCTTC AACTGATGGA CCAATGCCTC AAACTCGTGA 50
ACATATCCTT CTTTCACGTC AAGTAGGTGT TAAATACCTT ATCGTCTTCA 100
TGAACAAAGT TGACTTGGTT GACGATGAAG AATTGCTTGA ATTGGTTGAA 150
30 ATGGAAATCC GTGACCTTCT TTCAGAATAC GATTTCCTCAG GTGATGAAAT 200
CCGAGTTATC CAAGGTTTCAG CTCTTAAAGC TCTTGAAGGT GATGAAAAAT 250
ATGAAGACAT CATCATGGAA TTGATGGATA CTGTTGATGA ATACATTCCA 300
GAACCAGAAC GTGACACTGA CAAACCACTT CTTCTTCCAG TCGAAGATGT 350
ATTCTCAATC ACTGGACGTG GTACTGTTGC TTCAGGACGT ATCGACCGTG 400
35 GTACTGTTAA AGTCAATGAT GAAGTTGAAA TTGTTGGTAT TCGTGACGAA 450
ATCCAAAAAG CAGTTGTTAC TGGTGTGAA ATGTTCCGTA AACAATTGGA 500
CGAAGGTCTT GCTGGAGATA ACGTAGGGGT TCTTCTTCGT GGTATCCAAC 550
GTGACGAAAT CGAACGTGGA CAAGTTCTTG CTAAACCAGG TTCAATTCAT 600
CCACACACTA AATTCAAAGG TGAAGTTTAC ATCCTTACTA AAGAAGAAGG 650
40 TGGACGTCAT ACTCCATTCT TCAACAATA CCGTCCTCAA TTCTACTTCC 700
GTACTACAGA CGTTACAGGT TCAATCGAAC TTCCTGCAGG TACTGAAATG 750
GTAATGCCTG GTGATAACGT AACAATTGAT GTTGAGTTGA TCCACCCAAT 800
TGCCGTAGAA CAAGGAACTA C 821

```

45

2) INFORMATION FOR SEQ ID NO: 214

(i) SEQUENCE CHARACTERISTICS:

```

50 (A) LENGTH: 821 bases
    (B) TYPE: Nucleic acid
    (C) STRANDEDNESS: Double
    (D) TOPOLOGY: Linear

```

55 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

```

    (A) ORGANISM: Streptococcus cricetus
    (B) STRAIN: ATCC 19642

```

60

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 214

```

5   GCTATCCTTG TAGTAGCTTC TACAGACGGA CCAATGCCAC AAAC TCGTGA      50
    ACACATCTTG CTTTCACGCC AAGTTGGTGT TAAGAGCCTT ATCGTCTTCA      100
    TGAACAAGGT TGACTTGGTT GACGATGAAG AATTGCTTGA ATTGGTTGAA      150
    ATGGAAATCC GTGATCTTCT TTCAGAATAC GATTTCCCAG GTGATGATAT      200
    CCCTGTTGTT CAAGGTTTCAG CTCTTAAAGC CCTTGAAGGT GATACAGCTG      250
    CCGAAGACAA GATCATGGAA TTGATGGACA TCGTTGATGA CTACATTCCA      300
    GAACCAAAAC GTGATACTGA TAAGCCATTG CTTCTTCCAG TCGAAGACGT      350
10  ATTCTCAATC ACTGGACGTG GTACTGTTGC TTCAGGACGT ATCGACCGTG      400
    GTACTGTTAA GGTCAATGAC GAAGTTGAAA TCGTTGGTAT CAAGGACGAA      450
    ATCCAAAAGG CGGTTGTTAC CGGAGTTGAA ATGTTCCGTA AACAAATTGGA      500
    TGAAGGTCTT GCAGGGGATA ACGTTGGTGT GCTTCTTCGT GGTATCCAAC      550
    GTGATGAAAT CGAACGTGGT CAAGTATTGG CTGCACCTGG TTCAATCCAT      600
15  CCACACACTA AATTCAAGGG TGAAGTTTAC ATCCTTTCTA AAGATGAAGG      650
    TGGACGTCAC ACTCCATTCT TCAACAATA CCGTCCACAG TTCTACTTCC      700
    GTACAACTGA CGTAACTGGT TCAATCGAAT TGCCAGCAGG TACTGAAATG      750
    GTTATGCCTG GTGATAACGT TACTATCGAC GTTGAATTGA TCCACCCAAT      800
    CGCTGTTGAA AAAGGTACTA C                                821
20

```

## 2) INFORMATION FOR SEQ ID NO: 215

## 25 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 821 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

## 30 (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus cristatus*  
 35 (B) STRAIN: ATCC 51100

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 215

```

40  TATCCTTGTA GTAGCTTCAA CTGACGGACC AATGCCACAA ACTCGTGAGC      50
    ACATCCTTCT TTCACGTCAG GTTGGTGTTA AACACCTTAT CGTCTTCATG      100
    AACAAGATCG ACTTGGTTGA TGACGAAGAA TTGCTTGAAT TGGTTGAAAT      150
    GGAAATCCGT GACCTCTTGT CAGAATACGA CTTCCCAGGT GACGATCTTC      200
    CAGTTATCCA AGGTTTCAGCT CTTAAAGCTC TTGAAGGTGA TACTAAGTAC      250
    GAAGACATCA TCATGGAATT GATGAACACT GTTGATGAGT ACATCCCAGA      300
45  ACCAGAACGT GATACTGACA AACCTCTTCT TCTTCCAGTC GAAGACGTAT      350
    TCTCAATCAC TGGTCGTGGT ACAGTTGCTT CAGGACGTAT CGACCGTGGT      400
    ACTGTTCGTG TCAACGATGA AATCGAAATC GTTGGTATCA AAGAAGAAAT      450
    CCAAAAAGCA GTTGTTACTG GTGTTGAAAT GTTCCGTAAA CAGCTTGACG      500
    AAGGTCTTGC AGGGGACAAC GTAGGTGTAC TTCTTCGTGG TATCCAACGT      550
50  GATGAAATCG AACGTGGTCA AGTTATCGCT AAACCAGGTT CAATCAACCC      600
    ACACACTAAA TTCAAGGGTG AAGTTTACAT CCTTACTAAA GAAGAAGGTG      650
    GACGTCACAC TCCATTCTTC AACAACTACC GTCCACAGTT CTACTTCCGT      700
    ACAACTGACG TTACAGGTTT AATCGAACTT CCAGCAGGTA CTGAAATGGT      750
    AATGCCTGGT GATAACGTAA CTATCGACGT TGAGTTGATC CACCCAATCG      800
55  CCGTTGAACA AGGTACTCCT T                                821

```

## 2) INFORMATION FOR SEQ ID NO: 216

60

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 792 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus downei*  
 (B) STRAIN: ATCC 33748

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 216

```

15  AGTAGCTTCT ACTGATGGAC CAATGCCACA AACTCGTGAA CACATCTTGC      50
    TTTCACGTCA GGTTGGTGTG AAGAACCTTA TCGTCTTCAT GAACAAGGTT      100
    GACTTG GTT AC GATGAAGA ATTGCTTGAA TTGGTTGAAA TGGAAATCCG      150
    TGACCTGCTT TCAGAATACG ATTTCCCAGG TGATGATATC CCTGTTGTTC      200
    AAGGTT CAGC TCTTAAGGCT CTTGAAGGTG ATACAGCTGC CGAAGACAAG      250
20  ATCATGGAAT TGATGGACAT CGTTGATGAC TACATTCCAG AACCAAAACG      300
    TGATACTGAT AAGCCTTTGC TTCTTCCAGT CGAAGATGTA TTCTCAATCA      350
    CTGGACGTGG TACTGTAGCT TCAGGACGTA TCGACCGTGG TACTGTTAAG      400
    GTCAACGACG AAGTTGAAAT CGTTGGTATC AAGGACGAAA TCCAAAAGC      450
    AGTTGTTACC GGAGTTGAAA TGTTCCGTAA ACAATTGGAC GAAGGTCTTG      500
25  CAGGGGATAA CGTTGGTGTG CTTCTTCGTG GTATCCAACG TGATGAAATC      550
    GAACGTGGTC AAGTGTTGGC TGC GCCTGGT TCGATT CACC CACACACTAA      600
    GTTTAAAGGT GAAGTTTACA TCCTTTCTAA AGAAGAAGGT GGACGTCATA      650
    CTCCATTCTT TAACA ACTAC CGTCCACAGT TCTACTTCCG TACA ACTGAC      700
    GTA ACTGGTT CAATCGAATT GCCAGCGGGT ACTGAAATGG TTATGCCTGG      750
30  TGATAACGTT ACTATCGACG TTGAATTGAT CCACCCAATT GC              792
  
```

## 2) INFORMATION FOR SEQ ID NO: 217

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 795 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus dysgalactiae*  
 (B) STRAIN: ATCC 43078

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 217

```

50  GTAGTTGCTT CAACAGACGG ACCAATGCCA CAAACTCGTG AGCACATCCT      50
    CCTTTCACGT CAGGTTGGTG TTAAACACCT TATCGTGTTT ATGAACAAAA      100
    TTGACCTTGT TGACGATGAA GAATTGCTTG AATTGGTTGA AATGGAAATC      150
    CGTGACCTTC TTTCAGAATA CGATTTCCTA GGTGATGACC TTCCAGTTAT      200
    CCAAGGTTCA GCTCTTAAAG CTCTTGAAGG CGACACTAAA TTTGAAGACA      250
55  TCATCATGGA ATTGATGGAT ACTGTTGATT CATAATTCC AGAACCAGAA      300
    CGTGACACTG ACAAACCATT GCTTCTTCCA GTCGAAGACG TATTCTCAAT      350
    CACAGGTCGT GGTACAGTTG CTT CAGGACG TATCGACCGT GGTACTGTTC      400
    GTGTCAACGA CGAAATCGAA ATCGTTGGTA TCAAAGAAGA AACTAAAAAA      450
    GCTGTTGTTA CTGGTGTTGA AATGTTCCGT AAACA ACTTG ACGAAGGTCT      500
50  TGCAGGAGAC AACGTAGGTA TCCTTCTTCG TGGTGTTCAA CGTGACGAAA      550
  
```

	TCGAACGTGG	TCAAGTTATT	GCTAAACCAG	GTTCAATCAA	CCCACACACT	600
	AAATTCAAAG	GTGAAGTATA	TATCCTTTCT	AAAGACGAAG	GTGGACGTCA	650
	CACTCCATT	TTCAACAAC	ATCGTCCACA	ATTCTACTTC	CGTACAACTG	700
	ACGTAACAGG	TTCAATCGAA	CTTCCAGCTG	GTACAGAAAT	GGTTATGCCT	750
5	GGTGATAACG	TGACAATCAA	CGTTGAGTTG	ATCCACCCAA	TCGCC	795

## 2) INFORMATION FOR SEQ ID NO: 218

10

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 828 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 15 (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- 20 (A) ORGANISM: *Streptococcus equi* subsp. *equi*  
 (B) STRAIN: ATCC 9528

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 218

25	CGGAGCTATC	CTTGTAAGTTG	CTTCAACTGA	CGGACCAATG	CCACAAACTC	50
	GTGAGCACAT	CCTTCTTTCA	CGTCAGGTTG	GTGTTAAGCA	CCTTATCGTG	100
	TTCATGAACA	AGGTTGACCT	TGTTGACGAT	GAAGAATTGC	TTGAGCTTGT	150
	TGAAATGGAA	ATTCGTGACC	TTCCTTCAGA	ATATGATTTC	CCAGGTGATG	200
	ACCTTCCAGT	TATCCAAGGT	TCAGCGCTTA	AGGCTCTTGA	AGGCGACAGC	250
30	AAATACGAAG	ATATCATCAT	GGAATTGATG	GATACTGTTG	ATTCATACAT	300
	TCCAGAACCA	GAACGTGACA	CAGACAAGCC	ATTGCTTCTT	CCAGTCGAGG	350
	ACGTATTCTC	AATCACTGGA	CGTGGTACTG	TTGCTTCAGG	ACGTATCGAC	400
	CGCGGTACTG	TTCGTGTTAA	CGACGAAATC	GAAATCGTTG	GTATCAGAGA	450
	CGAGATCAAA	AAAGCAGTTG	TTACTGGTGT	CGAAATGTTC	CGTAAACAGC	500
35	TTGACGAAGG	TCTTGCAGGG	GACAACGTTG	GTGTTCTTCT	TCGTGGTGTA	550
	CAACGTGATG	AAATCGAACG	TGGTCAAGTT	ATTGCTAAGC	CAGGTTCTAT	600
	CAACCCACAC	ACTAAATTTA	AAGGTGAAGT	ATATATCCTT	ACTAAAGAAG	650
	AAGGTGGACG	TCACACACCA	TTCTTCAACA	ACTATCGTCC	ACAATTCTAC	700
	TTCCGTACTA	CTGACGTAAC	AGGTTCAATC	GAGCTTCCAG	CAGGTACAGA	750
40	AATGGTTATG	CCTGGTGATA	ACGTGACTAT	TGACGTTGAG	TTGATCCACC	800
	CAATCGCCGT	AGAACAAGGT	ACTACATT			828

## 45 2) INFORMATION FOR SEQ ID NO: 219

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 825 bases  
 (B) TYPE: Nucleic acid  
 50 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- 55 (A) ORGANISM: *Streptococcus ferus*  
 (B) STRAIN: ATCC 33477

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 219

60

```

CGGTGCAATC CTTGTAGTAG CTTCTACAGA TGGACCAATG CCACAAACTC      50
GTGAGCACAT CCTTCTTTCA CGTCAGGTAG GTGTAAACA CTTATCGTC      100
TTCATGAACA AAGTTGACTT GGTGACGAT GAAGAATTGC TTGAATTGGT      150
TGAAATGGAA ATCCGTGACC TGCTTTCAGA ATATGATTTC CCAGGTGATG      200
5 ACCTTCCAGT TATCCAAGGT TCAGCTCTTA AAGCGCTTGA AGGTGATACT      250
GCTCAAGAAG ATGTTATCAT GGAATTGATG AAAACCGTTG ATGAGTACAT      300
CCCAGAACCA GAACGTGATA CTGACAAACC ATTGCTTCTT CCAGTCGAAG      350
ATGTATTCTC AATCACAGGT CGTGGTACTG TAGCTTCAGG ACGTATCGAT      400
CGTGGTACTG TAAGAGTCAA CGATGAAGTT GAAATCGTTG GTATCAAAGA      450
10 CGAAATCACT AAAGCAGTTG TTACCGGTGT TGAAATGTTT CGTAAACAAT      500
TGGACGAAGG TCTTGCTGGT GATAACGTTG GTGTGCTTCT CCGTGGTGTG      550
CAACGTGATG AAATCGAACG TGGTCAAGTA TTGGCTAAAC CAGGTTCAAT      600
CAACCCACAC ACTAAATTTA AAGGTGAAGT TTACATCCTT ACTAAAGAAG      650
AAGGTGGACG TCATACACCA TTCTTCAACA ACTACCGTCC ACAGTTCTAC      700
15 TTCCGTACAA CTGACGTAAC TGGTTCAATC GAATTGCCAG CAGGTACTGA      750
AATGGTTATG CCTGGTGATA ACGTGACTAT CGACGTTGAA TTGATCCACC      800
CAATCGCCGT TGAACAAGGT ACTAC                                     825

```

20

## 2) INFORMATION FOR SEQ ID NO: 220

## (i) SEQUENCE CHARACTERISTICS:

```

25 (A) LENGTH: 826 bases
    (B) TYPE: Nucleic acid
    (C) STRANDEDNESS: Double
    (D) TOPOLOGY: Linear

```

## (ii) MOLECULE TYPE: Genomic DNA

30

## (vi) ORIGINAL SOURCE:

```

    (A) ORGANISM: Streptococcus gordonii
    (B) STRAIN: ATCC 10558

```

35

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 220

```

CGGAGCTATC CTTGTAGTAG CTTCAACTGA TGGTCCTATG CCACAAACTC      50
GTGAGCACAT CCTTCTCTCA CGCCAAGTTG GTGTAAACA CTTGATCGTG      100
TTCATGAACA AAGTTGACTT GGTGACGAT GAAGAATTGC TTGAGTTGGT      150
40 TGAAATGGAA ATCCGTGACC TCTTGTCAGA ATACGACTTC CCAGGTGACG      200
ATCTTCCAGT TATCCAAGGT TCAGCTCTTA AAGCTCTTGA AGGTGACTCT      250
AAATATGAAG ATATCATCAT GGAATTGATG AACACTGTTG ATGAGTACAT      300
CCCAGAACCA GAACGCGACA CTGACAAACC ATTGCTTCTT CCAGTCGAAG      350
ACGTATTCTC AATCACTGGA CGTGGTACAG TTGCTTCAGG ACGTATCGAC      400
45 CGTGGTATCG TTAAAGTCAA TGACGAAATC GAAATCGTTG GTATCAAAGA      450
AGAAATCCAA AAAGCAGTTG TTAAGTGGTGT TGAAATGTTT CGTAAACAGC      500
TTGACGAAGG TCTTGCAGGG GACAACGTTG GTGTGCTTCT TCGTGGTATC      550
CAACGTGATG AAATCGAACG TGGACAAGTT ATTGCTAAAC CAGGTTCAAT      600
CAACCCACAC ACTAAATTTA AAGGTGAAGT TTATATCCTT ACTAAAGAAG      650
50 AAGGTGGACG TCACACTCCA TTCTTCAACA ACTACCGTCC ACAGTTCTAC      700
TTCCGTACAA CTGACGTTAC AGGTTCAATC GAATTGCCAG CAGGTACTGA      750
AATGGTAATG CCTGGTGATA ACGTAACTAT CGACGTTGAG TTGATCCACC      800
CAATCGCCGT TGAACAAGGT ACTACT                                     826

```

55

## 2) INFORMATION FOR SEQ ID NO: 221

## (i) SEQUENCE CHARACTERISTICS:

```

50 (A) LENGTH: 799 bases

```

5 (ii) MOLECULE TYPE: Genomic DNA

(A) ORGANISM: *Streptococcus anginosus*  
(B) STRAIN: ATCC 27335

TGTAGTAGCT	TCAACTGACG	GACCAATGCC	TCAAACCTCGT	GAACATATCC	50
TTCTTTTCACG	TCAAGTAGGT	GTTAAATACC	TTATTGTCTT	CATGAACAAA	100
GTTGACTTGG	TTGACGATGA	AGAATTGCTT	GAATTGGTTG	AAATGGAAAT	150
CCGTGATCTT	CTTTCAGAAAT	ACGATTTCCT	AGGTGATGAT	ATTCCAGTAA	200
TCCAAGGTTC	AGCACTTAAA	GCTCTTGAAG	GTGATGAAAA	ATATGAAGAC	250
ATCATCATGG	AATTGATGAA	TACTGTTGAT	GAATATATTC	CAGAACCAGA	300
ACGTGATACT	GACAAACCAT	TGCTTCTTCC	AGTCGAAGAT	GTATTCTCAA	350
TCACTGGACG	TGGTACTGTT	GCTTCAGGAC	GTATCGACCG	TGGTACTGTT	400
AAAGTCAACG	ATGAAGTTGA	AATCGTTGGT	ATCCGCGAGG	AAATCCAAAA	450
AGCAGTTGTT	ACTGGTGTGG	AAATGTTCCG	TAAACAATTG	GACGAAGGTC	500
TTGCTGGAGA	TAACGTAGGG	GTTCTTCTTC	GTGGTATCCA	ACGTGACGAA	550
ATTGAACGTG	GACAAGTTCT	TGCTAAACCA	GGTTCAATTC	ATCCACACAC	600
TAAATTCAAA	GGTGAAGTTT	ACATCCTTAC	TAAAGAAGAA	GGTGGACGTC	650
ATACTCCATT	CTTCAACAAC	TACCGTCCTC	AATTCTACTT	CCGTACTACA	700
GACGTTACAG	GTTCAATCGA	ACTTCCTGCA	GGTACTGAAA	TGGTAATGCC	750
TGGTGATAAC	GTAACAATTG	ATGTTGAGTT	GATCCACCCA	ATTGCCGTA	799

(i) SEQUENCE CHARACTERISTICS:

(ii) MOLECULE TYPE: Genomic DNA

(A) ORGANISM: *Streptococcus macacae*  
(B) STRAIN: ATCC 35911

TGGTGCTATT	CTTGTAGTAG	CTTCAACTGA	CGGTCCAATG	CCTCAAACGC	50
GTGAACATAT	CCTTCTTTCA	CGCCAAGTAG	GTGTTAAAAA	CCTTATTGTT	100
TTCATGAATA	AAGTTGACTT	AGTTGATGAT	GAAGAATTGC	TTGAATTGGT	150
TGAAATGGAA	ATCCGTGATC	TTCTTACAGA	ATATGATTTC	CCAGGCGATG	200
AACTTCCAGT	TATCCAAGGT	TCAGCACTTA	AAGCTCTTGA	AGGTGATACT	250
AAGTACGAAG	ATATTATCAT	GGAATTGTTG	GATACTGTAG	ATGATTACAT	300
CCCAGAACCA	CAACGTGATA	CTGACAAGCC	ATTGCTTCTT	CCAGTCGAAG	350
ATGTTTTCTC	TATTACTGGA	CGTGGTACTG	TTGCTTCAGG	ACGTATTGAC	400
CGTGGTACTG	TTAAGGTTAA	TGATGAAGTT	GAAATCGTTG	GTATTCGTGA	450
CGATATTCAA	AAAGCAGTTG	TTACTGGTGT	TGAAATGTTT	CGTAAACAGC	500
TTGACGAAGG	TCTTGCTGGT	GATAACGTCG	GTGCTCTTCT	TCGTGGTATC	550
CAACGTGATG	AAATTGAACG	CGGTCAAGTT	CTTGCTAAAC	CAGGATCAAT	600
TCATCCACAT	ACTAAATTCA	AAGGTGAAGT	TTATATTCTT	ACTAAAGAAG	650

AAGGTGGACG	TCATACTCCA	TTCTTTAACA	ACTACCGTCC	ACAGTTCTAC	700
TTCCGTACAA	CTGATGTAAC	TGGTTCAATT	GATTTGCCAG	CAGGTACTGA	750
AATGGTTATG	CCTGGTGATA	ATGTTACGAT	TGATGTTGAA	CTGATCCACC	800
CAATCGCTGT	TGAACAAGGT	ACAAC			825

5

## 2) INFORMATION FOR SEQ ID NO: 223

## 10 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 822 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

15

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus gordonii* (deposited as *Streptococcus mitis*)
- (B) STRAIN: ATCC 33399

20

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 223

25	CTATCCTTGT	AGTAGCTTCA	ACTGACGGAC	CAATGCCACA	AACTCGTGAG	50
	CACATCCTTC	TTTCACGTCA	GGTTGGTGTT	AAACACCTTA	TCGTCTTCAT	100
	GAACAAAGTT	GACTTGGTTG	ACGACGAAGA	ATTGCTTGAA	TTGGTTGAAA	150
	TGGAAATCCG	TGACCTATTG	TCAGAATACG	ACTTCCCAGG	TGACGATCTT	200
	CCAGTTATCC	AAGGTTTCAGC	TCTTAAAGCC	CTTGAAGGTG	ACACTAAATA	250
30	CGAAGACATC	GTTATGGAAT	TGATGAACAC	AGTTGATGAG	TACATCCCAG	300
	AACCAGAACG	TGACACTGAC	AAACCATTCG	TTCTTCCAGT	CGAAGACGTA	350
	TTCTCAATCA	CTGGTCGTGG	TACAGTTGCT	TCAGGACGTA	TCGACCGTGG	400
	TATCGTTAAA	GTCAACGACG	AAATCGAAAT	CGTTGGTATC	AAAGAAGAAA	450
	CTCAAAAAGC	AGTTGTTACT	GGTGTGAAA	TGTTCCGTAA	ACAACCTGAC	500
35	GAAGGTCTTG	CCGGAGATAA	TGTAGGTGTC	CTTCTTCGTG	GTGTTCAACG	550
	TGATGAAATC	GAACGTGGAC	AAGTTATTGC	TAAACCAGGT	TCAATCAACC	600
	CACACACTAA	ATTCAAAGGT	GAAGTTTACA	TCCTTACTAA	AGAAGAAGGT	650
	GGACGTCACA	CTCCATTCTT	CAACAACACTAC	CGTCCACAAT	TCTACTTCCG	700
	TACTACTGAC	GTTACAGGTT	CAATCGAACT	TCCAGCAGGT	ACTGAAATGG	750
40	TAATGCCTGG	TGATAACGTG	ACAATCGACG	TTGAGTTGAT	CCACCCAATC	800
	GCCGTAGAAC	AAGGTACTAC	AT			822

## 45 2) INFORMATION FOR SEQ ID NO: 224

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 827 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

50

## (ii) MOLECULE TYPE: Genomic DNA

## 55 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus mutans*
- (B) STRAIN: ATCC 25175

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 224

50

	CCCTGGTGCT	ATCCTTGTAG	TAGCTTCAAC	TGATGGACCA	ATGCCACAAA	50
	CTCGTGAACA	CATTCTTCTT	TCACGTCAAG	TTGGTGTTAA	ATACCTCATT	100
	GTCTTCATGA	ATAAAGTTGA	TTTGGTTGAC	GATGAAGAAT	TGCTTGAATT	150
	GGTTGAAATG	GAAATCCGTG	ATCTTCTTTC	AGAATATGAT	TTCCCAGGTG	200
5	ATGATATTCC	AGTTATTCAA	GGTTCAGCTC	TTAAAGCTCT	TGAAGGCGAT	250
	ACTGCTCAAG	AAGATATCAT	CATGGAATTA	ATGCATACTG	TTGATGACTA	300
	CATTCCAGAT	CCAGAACGTG	ATACTGACAA	GCCGCTCCTT	CTTCCAGTCG	350
	AAGATGTTTT	CTCAATCACT	GGTCGTGGTA	CTGTTGCTTC	AGGACGTATT	400
	GATCGTGGTA	CTGTTAAAGT	TAACGATGAA	GTTGAAATCG	TTGGTATCCG	450
10	TGATGACATT	CAAAAAGCTG	TTGTTACTGG	TGTTGAAATG	TTCCGTAAAC	500
	AATTGGATGA	AGGTATTGCA	GGGGATAATG	TTGGTGTCTT	CCTTCGTGGT	550
	ATCCAACGTG	ATGAAATCGA	ACGTGGTCAA	GTTCTTGCTA	AACCAGGTTT	600
	AATTCACCCA	CATACATAAT	TCAAAGGTGA	AGTTTATATC	CTTACTAAAG	650
	AGGAAGGTGG	ACGTCATACA	CCATTCTTCA	ATAACTATCG	TCCACAATTC	700
15	TACTTCCGTA	CAACTGACGT	AACTGGTTCA	ATTGAGTTGC	CAGCAGGTAC	750
	TGAAATGGTT	ATGCCTGGTG	ATAACGTTAC	TATTGACGTT	GAATTGATCC	800
	ATCCAATCGC	TGTTGAACAA	GGTACTA			827

20

## 2) INFORMATION FOR SEQ ID NO: 225

## (i) SEQUENCE CHARACTERISTICS:

	(A)	LENGTH: 824 bases
25	(B)	TYPE: Nucleic acid
	(C)	STRANDEDNESS: Double
	(D)	TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

30

## (vi) ORIGINAL SOURCE:

	(A)	ORGANISM: <i>Streptococcus parasanguinis</i>
	(B)	STRAIN: ATCC 15912

35

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 225

	AGCTATCCTT	GTAGTAGCTT	CAACTGACGG	ACCAATGCCA	CAAACACGTG	50
	AACACATCCT	TCTTTCACGT	CAGGTTGGTG	TTAAACACTT	GATCGTCTTC	100
	ATGAACAAAG	TTGACTTGGT	TGATGATGAA	GAATTGCTTG	AATTGGTTGA	150
40	AATGGAAATC	CGTGACCTTC	TTTCAGAATA	CGATTTCCCA	GGTGATGACC	200
	TTCCAGTTAT	CCAAGGTTCA	GCTCTTAAAG	CTCTTGAAGG	TGACTCTAAA	250
	TATGAAGATA	TCATCATGGA	ATTGATGGAT	ACTGTTGATG	AGTACATCCC	300
	AGAACCAGAA	CGCGATACTG	ACAAACCATT	GCTTCTTCCA	GTCGAAGACG	350
	TATTCTCAAT	CACTGGACGT	GGTACAGTTG	CTTCAGGACG	TATCGACCGT	400
45	GGTGTGTTC	GTGTCAATGA	TGAAATCGAA	ATCGTTGGTA	TCAAAGAAGA	450
	AATCCAAAAA	GCA GTTGTTA	CTGGTGTTGA	AATGTTCCGT	AAACA ACTTG	500
	ACGAAGGTCT	TGCAGGGGAT	AACGTTGGTG	TGCTTCTTCG	TGGTATCCAA	550
	CGTGATGAAA	TCGAACGTGG	ACAAGTTATC	GCTAAACCAG	GTTCAATCAA	600
	CCCACACACT	AAATTCAAAG	GTGAAGTTTA	CATCCTTACT	AAAGAAGAAG	650
50	GTGGACGTCA	TACTCCATTC	TTCAACA ACT	ACCGTCCACA	GTTCTACTTC	700
	CGTACA ACTG	ACGTAACTGG	ATCTATCGAA	CTTCCACCAG	GA ACTGAAAT	750
	GGTAATGCCT	GGTGATAACG	TGACTATCGA	CGTTGAGTTG	ATCCACCCAA	800
	TCGCCGTTGA	ACAAGGTACT	ACAT			824

55

## 2) INFORMATION FOR SEQ ID NO: 226

## (i) SEQUENCE CHARACTERISTICS:

50	(A)	LENGTH: 824 bases
----	-----	-------------------



(B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

5 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus ratti*  
 (B) STRAIN: ATCC 19645

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 226

	TGGTGCTATC	CTTGTAGTAG	CTTCAACTGA	TGGACCAATG	CCGCAAACCTC	50
	GTGAACACAT	CTTGCTTTCA	CGTCAAGTTG	GTGTTAAATA	CCTTATCGTC	100
15	TTCATGAACA	AGGTTGACTT	GGTTGATGAT	GAAGAATTGC	TTGAATTGGT	150
	TGAAATGGAA	ATCCGTGATC	TTCTTTTCAGA	ATACGATTTC	CCAGGTGATG	200
	ACATTCCAGT	TATCCAAGGT	TCAGCCCTTA	AAGCTCTTGA	AGGTGACACT	250
	GAACAAGAAG	ATGTTATCAT	GGAATTGATG	AAAACAGTTG	ATGAGTACAT	300
	CCCAGATCCA	GAACGCGATA	CTGATAAGCC	ATTGCTTCTT	CCAGTCGAAG	350
20	ACGTGTTCTC	AATCACTGGA	CGTGGTACTG	TTGCATCAGG	ACGTATCGAC	400
	CGTGGTACTG	TTAAAGTCAA	TGACGAAGTT	GAAATCGTTG	GTATCCGTGA	450
	TGACATCCAA	AAAGCTGTTG	TTACTGGTGT	TGAAATGTTC	CGTAAACAGC	500
	TTGACGAAGG	TCTTGCTGGT	GATAACGTTG	GTGTAATTCT	TCGTGGTATC	550
	CAACGTGATG	AAATCGAACG	CGGTCAAGTT	CTTGCTAAAC	CAGGTTCAAT	600
25	TCATCCGCAT	ACTAAATTTA	AAGGTGAAGT	TTACATCCTT	ACTAAAGAAG	650
	AAGGCGGACG	TCACACTCCA	TTCTTCAACA	ACTACCGTCC	ACAGTTCTAC	700
	TTCCGTACAA	CTGACGTAAAC	TGGTTCAATC	GAATTGCCAG	CAGGTACTGA	750
	AATGGTTATG	CCTGGTGATA	ACGTGACTAT	CGACGTTGAA	TTGATCCACC	800
30	CAATCGCTGT	TGAACAAGGT	ACTA			824

2) INFORMATION FOR SEQ ID NO: 227

35 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 795 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

40

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus sanguinis*  
 45 (B) STRAIN: ATCC 10556

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 227

	TGTAGTAGCT	TCAACTGACG	GACCAATGCC	ACAAACTCGT	GAGCACATCT	50
50	TGCTTTCACG	TCAGGTTGGT	GTAAACACT	TGATCGTCTT	CATGAACAAA	100
	GTTGACTTGG	TTGACGATGA	AGAATTGCTT	GAATTGGTTG	AAATGGAAAT	150
	CCGTGACCTC	TTGTCAGAAAT	ACGACTTCCC	AGGTGACGAT	CTTCCAGTTA	200
	TCCAAGGTTT	AGCTCTTAAA	GCTCTTGAAG	GTGACTCTAA	ATATGAAGAC	250
	ATCATCATGG	AATTGATGGA	CACTGTTGAT	GAGTACATCC	CAGAACCAGA	300
55	ACGCGATACT	GACAAGCCAT	TGCTTCTTCC	AGTCGAAGAC	GTATTCTCAA	350
	TCACTGGTCG	TGGTACAGTT	GCTTCAGGAC	GTATCGACCG	TGGTATCGTT	400
	AAAGTCAACG	ACGAAATCGA	AATCGTTGGT	ATCAAAGAAG	AAATCCAAAA	450
	AGCAGTTGTT	ACTGGTGTTG	AAATGTTCCG	TAAACAGCTT	GACGAAGGTC	500
	TTGCAGGGGA	CAACGTAGGT	GTGCTTCTCC	GTGGTATCCA	ACGTGATGAA	550
50	ATCGAACGTG	GACAAGTTAT	CGCTAAACCA	GGTTCAATCA	ACCCACACAC	600

TAAATTCAAG	GGTGAAGTTT	ATATCCTTAC	TAAAGAAGAA	GGCGGACGTC	650
ACACTCCATT	CTTCAACAAC	TACCGTCCAC	AGTTCTACTT	CCGTACAAC	700
GACGTTACAG	GTTCAATCGA	ACTTCCAGCA	GGTACTGAAA	TGGTAATGCC	750
TGGTGATAAC	GTAACAATCG	ACGTTGAGTT	GATCCACCCA	ATCGC	795

5

## 2) INFORMATION FOR SEQ ID NO: 228

## 10 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 795 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

15

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus sobrinus*  
 (B) STRAIN: ATCC 33478

20

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 228

TGTAGTAGCT	TCTACTGACG	GACCAATGCC	ACAAACTCGT	GAACACATCT	50
25 TGCTTTTCACG	CCAAGTTGGT	GTTAAGAACC	TCATCGTCTT	CATGAACAAG	100
GTTGACTTGG	TTGATGATGA	AGAATTGCTT	GAATTGGTTG	AAATGGAAAT	150
CCGTGATCTT	CTTTCAGAA	ACGATTTC	AGGTGACGAC	ATTCTGTG	200
TTCAAGGTT	AGCTCTTAAG	GCTCTTGAAG	GTGATACAGC	TGCCGAAGAC	250
AAGATTATGG	AATTGATGGA	CATCGTTGAT	GATTACATTC	CAGAACCAAA	300
30 ACGCGATACT	GATAAGCCAT	TGCTTCTCCC	AGTCGAAGAC	GTATTCTCAA	350
TCACTGGTCG	TGGTACTGTT	GCTTCAGGAC	GTATTGACCG	TGGTACTGTT	400
AAGGTTAACG	ACGAAGTTGA	AATCGTTGGT	ATCCGTGACG	ATATCCAAAA	450
AGCAGTTGTT	ACTGGAGTTG	AAATGTTCCG	TAAGCAATTG	GACGAAGGTC	500
TTGCTGGAGA	TAACGTTGGT	GTGCTTCTTC	GTGGTATCCA	ACGTGATGAA	550
35 ATTGAACGTG	GTCAAGTATT	GGCTGCACCT	GGTTCAATCC	ACCCACACAC	600
TAAGTTCAAG	GGTGAAGTTT	ACATCCTTTC	TAAAGATGAA	GGTGGACGTC	650
ACACTCCATT	CTTCAACAAC	TACCGTCCAC	AGTTCTACTT	CCGTACAAC	700
GACGTAAC	GTTCAATCGA	ATTGCCAGCA	GGTACTGAAA	TGGTTATGCC	750
40 TGGTGATAAC	GTTACTATCG	ACGTTGAATT	GATCCACCCA	ATCGC	795

## 2) INFORMATION FOR SEQ ID NO: 229

## 45 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 797 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

50

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus suis*  
 (B) STRAIN: ATCC 43765

55

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 229

TGTAGTAGCT	TCAACTGACG	GTCCAATGCC	ACAAACTCGT	GAGCACATCC	50
50 TTCTTTTCACG	TCAGGTTGGT	GTTAAACACC	TTATCGTCTT	CATGAACAAA	100

	GTTGACTTGG	TTGACGATGA	AGAATTGCTT	GAGTTGGTTG	AAATGGAAAT	150
	CCGTGACCTT	CTTTCAGAAT	ACGATTTCCC	AGGTGATGAT	CTTCCAGTTA	200
	TCCAAGGTTT	AGCTCTTAAA	GCTCTTGAAG	GTGACTCTAA	GTACGAAGAC	250
	ATCGTTATGG	AATTGATGAA	CACTGTTGAT	GAGTACATTC	CAGAACCAGA	300
5	ACGCGACACT	GACAAACCAT	TGTTGCTTCC	AGTCGAGGAC	GTATTCTCAA	350
	TCACTGGTCG	TGGTACTGTA	GCTTCAGGAC	GTATCGACCG	TGGTACTGTT	400
	CGTGTCAACG	ACGAAATCGA	AATCGTTGGT	CTTCAAGAAG	AAAAATCTAA	450
	AGCAGTTGTT	ACTGGTGTTG	AAATGTTCCG	TAAACAACCT	GACGAAGGTC	500
	TTGCCGCGCA	TAACGTTGGT	GTGCTTCTTC	GTGGTGTACA	ACGTGATGAA	550
10	ATCGAACGTG	GTCAAGTTAT	CTCTAAACCA	GGTCTATCA	ACCCACACAC	600
	TAAATTCAA	GGTGAAGTTT	ACATCCTTAC	TAAAGAAGAA	GGTGGACGTC	650
	ACACTCCATT	CTTCGACAAC	TACCGTCCAC	AGTTCCTACT	CCGTACAAC	700
	GACGTAAC	GTTCAATCAA	ATTGCCAGAA	GGTACTGAAA	TGGTAATGCC	750
	TGGTGATAAC	GTTACTATCG	ACGTTGAATT	GATCCACCCA	ATCGCCG	797

## 2) INFORMATION FOR SEQ ID NO: 230

## 20 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 793 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

## 25 (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus uberis*  
 (B) STRAIN: ATCC 19436

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 230

	TTGTTGTTGC	ATCAACTGAT	GGACCAATGC	CACAAACTCG	TGAGCACATC	50
35	CTTCTTTTAC	GCCAAGTTGG	TGTTAAACAC	CTTATCGTTT	TCATGAACAA	100
	AATCGACCTT	GTTGACGATG	AAGAATTGCT	TGAATTAGTT	GAAATGGAAA	150
	TCCGTGACCT	TCTTTCAGAA	TACGATTTC	CAGGTGATGA	CCTACCAGTT	200
	ATCCAAGGTT	CAGCTCTTAA	AGCTCTTGAA	GGTGATTCTA	AATACGAAGA	250
	CATCATCATG	GAATTGATGA	AAACTGTTGA	TGAGTATATT	CCAGAACCAG	300
40	AACGTGATAC	AGACAAACCA	TTACTTCTTC	CAGTCGAAGA	CGTATTCTCA	350
	ATCAGAGGTC	GTGGTACTGT	AGCTTCAGGA	CGTATCGATC	GTGGTACTGT	400
	TCGTGTCAAC	GACGAAATTG	AAATCGTTGG	TATCAAAGAA	GAAACTAAAA	450
	AAGCAGTTGT	TACTGGTGTT	GAAATGTTCC	GTAAACAAC	TGACGAAGGT	500
	CTTGCAGGAG	ATAACGTAGG	TATCCTTCTT	CGTGGTGTTT	AACGTGACGA	550
45	AATCGAACGT	GGACAAGTTA	TTGCTAAACC	AGGTTCAATC	AACCCACACA	600
	CTAAATTCAA	AGGTGAAGTT	TACATCCTTT	CTAAAGATGA	AGGTGGACGT	650
	CATACTCCAT	TCTTCAACAA	CTACCGTCCT	CAATTCTATT	TCCGTACAAC	700
	TGACGTAACA	GGTTCAATCG	AACTCCAGC	TGGTACTGAA	ATGGTAATGC	750
	CTGGTGATAA	CGTGACAATC	AGCGTTGAGT	TGATCCACCC	AAT	793

## 2) INFORMATION FOR SEQ ID NO: 231

## 55 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 798 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus vestibularis*  
 5 (B) STRAIN: ATCC 49124

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 231

```

10 TTGTAGTAGC ATCTACTGAC GGACCAATGC CACAAACTCG TGAGCACATC      50
   CTTCTTTTCAC GTCAGGTTGG TGTAAACAC CTTATCGTCT TCATGAACAA      100
   AGTTGACTTG GTTGACGATG AAGAATTGCT TGAATTGGTT GAAATGGAAA      150
   TCCGTGACCT TCTTTCAGAA TACGATTTC CAGGTGATGA TATTCCAGTT      200
   ATCCAAGGTT CAGCTCTTAA AGCTCTTGAA GGTGATTCTA AATACGAAGA      250
   CATCATCATG GACTTGATGA ACACGTGTTGA CGAATACATT CCAGAACCAG      300
15 AACGTGACAC TGACAAACCA TTGTTGCTTC CAGTCGAAGA CGTATTCTCA      350
   ATCACTGGTC GTGGTACTGT TGCTTCAGGA CGTATCGACC GTGGTGTGTG      400
   TCGTGTTAAT GACGAAGTTG AAATCGTTGG TCTTAAAGAA GAAATCCAAA      450
   AAGCAGTTGT TACTGGTGTA GAAATGTTCC GTAAACAAC TACGAAGGT      500
   ATTGCCGGAG ATAACGTCGG TGTCCTTCTT CGTGGTATCC AACGTGATGA      550
20 AATTGAACGT GGTCAAGTAT TGGCTGCACC TGGTTCAATC AACCCACACA      600
   CTAAATTCAA AGGTGAAGTT TACATCCTTT CTAAAGAAGA AGGTGGACGT      650
   CACACTCCAT TCTTCAACAA CTACCGTCCA CAGTTCTACT TCCGTACAAC      700
   TGACGTAACA GGTTCATCG AACTTCCTGC AGGTACTGAA ATGGTTATGC      750
   CTGGTGATAA CGTGACTATC GACGTTGAGT TGATCCACCC AATCGCCG      798
25

```

2) INFORMATION FOR SEQ ID NO: 232

30 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 829 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

35 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Tatumella ptyseos*  
 40 (B) STRAIN: ATCC 33301

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 232

```

15 GGCGCTATCC TGGTTGTTGC TGCAACTGAC GGCCCTATGC CTCAGACCCG      50
   TGAGCACATC CTGCTGGGCC GCCAGGTAGG CGTTCCTTAC ATCATCGTGT      100
   TCCTGAACAA ATGTGACATG GTTGATGATG AAGAGCTGCT GGAAGTGGTA      150
   GAAATGGAAG TCCGTGACCT GCTGTCACAG TACGACTTCC CGGGTGACGA      200
   CACGCCAATC GTTCGCGGTT CAGCGCTGAA AGCACTGGAA GGTGAAGGCG      250
   AGTGGAAGA GAAGATTCTG GAGCTGGCTG GCTTCCTGGA TTCTTACATC      300
20 CCTGAGCCAG AGCGTGCTAT CGATCAGCCG TTCCTGCTGC CAATCGAAGA      350
   CGTATTCTCA ATCTCCGGTC GTGGTACAGT TGTTACCGGT CGTGTAGAGC      400
   GCGGGATCAT CAAAGTCGGT GAAGAAGTTG AGATCGTTGG TATCAAAGAT      450
   ACTGCGAAAT CAACCTGTAC CGGTGTTGAA ATGTTCCGTA AACTGCTGGA      500
   CCAGGGTCAG GCGGGTGAGA ACGTTGGTGT TCTGCTGCGT GGTATCAAGC      550
30 GTGAAGAGAT CGAACGTGGT CAGGTTCTGG CTAAACCAGG TTCAATCAA      600
   CCACACACCC AGTTCGAGTC AGAAGTTTAT ATTCTGTCTA AAGACGAAGG      650
   CGGCCGTCAT ACTCCGTTCT TCAAAGGCTA CCGTCCACAG TTCTACTTCC      700
   GTACAACCTGA CGTGACCGGA ACCATCGAAC TGCCGGAAGG CGTAGAGATG      750
   GTAATGCCTG GTGACAACAT CAAAATGGTT GTTACCCTGA TCCATCCAAT      800
40 CGCGATGGAC GATGGTCTGC GTTTCGCAA      829

```

## 2) INFORMATION FOR SEQ ID NO: 233

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 829 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Trabulsiella guamensis*  
 (B) STRAIN: ATCC 49490

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 233

20	GGCGCAATCC	TGGTAGTAGC	AGCGACTGAC	GGCCCGATGC	CGCAGACTCG	50
	TGAGCACATC	CTGCTGGGTC	GTCAGGTAGG	CGTTCCGTAC	ATCATCGTGT	100
	TCCTGAACAA	ATGCGACATG	GTTGATGACG	AAGAGCTGCT	GGAAGTGGTA	150
	GAGATGGAAG	TTCGTGAACT	GCTGTCTCAG	TACGATTTCC	CGGGCGATGA	200
	CACGCCGATC	GTACGTGGTT	CTGCTCTGAA	AGCGCTGGAA	GGCGACGCAG	250
25	AGTGGGAAGC	GAAAATCATC	GAAGTGGCAG	GTTTCCTGGA	TTCTTACATT	300
	CCGGAACCAG	AGCGTGCGAT	TGACAAGCCG	TTCCTGCTGC	CGATCGAAGA	350
	CGTATTCTCC	ATCTCTGGTC	GTGGTACCGT	TGTTACCGGT	CGTGTAGAGC	400
	GCGGTATCAT	CAAAGTGGGT	GAAGAAGTAG	AAATCGTTGG	TATCAAAGAG	450
	ACTGCGAAGT	CAACCTGTAC	TGGCGTAGAA	ATGTTCCGCA	AACTGCTGGA	500
30	CGAAGGCCGT	GCTGGTGAGA	ACGTAGGTGT	TCTGCTGCGT	GGTATCAAAC	550
	GTGAAGAAAT	CGAACGTGGT	CAGGTACTGG	CTAAGCCGGG	CACCATCAAC	600
	CCGCACACCA	AGTTCGAATC	TGAAGTGTAC	ATTCTGTCCA	AAGACGAAGG	650
	CGGCCGTCAC	ACTCCGTTCT	TCAAAGGCTA	CCGTCCGCAG	TTCTACTTCC	700
	GTACAACTGA	CGTGACTGGC	ACCATCGAAC	TGCCGGAAGG	CGTAGAGATG	750
35	GTAATGCCGG	GCGACAACAT	CAAAATGGTT	GTTACCCTGA	TCCACCCGAT	800
	CGCGATGGAC	GACGGTCTGC	GTTTCGCAA			829

## 2) INFORMATION FOR SEQ ID NO: 234

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 825 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Veillonella parvula*  
 (B) STRAIN: ATCC 10790

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 234

55	CGGCGCTATC	TTGGTTGTAT	CCGCAGCTGA	CGGCCCTATG	CCTCAAATCT	50
	GCGAACACAT	CTTGTTGGCT	CGCCAAGTTG	GTGTTCTTGC	AATCGTAGTA	100
	TTCTTGAACA	AAGCTGACAT	GGTTGACGAT	GAAGAATTGA	TCGAATTGGT	150
	AGAAATGGAA	GTTCGTGAAC	TTCTTTCTTC	CTACGAATTC	CCTGGCGACG	200
60	AAGTACCTAT	CGTTGTAGGT	TCCGCGTTGA	AAGCTTTGGA	AGGCGATGCT	250

	CAATATGTAG	CTAAAATTGA	CGAATTGATG	GACGCTGTAG	ACTCCTACAT	300
	CCCAACACCA	GTTTCGTGACA	CTGATAAACC	ATTCTTGATG	CCTGTGGAAG	350
	ATGTTTTTAC	AATCACTGGT	CGTGGTACAG	TAGCAACTGG	CCGTGTTGAA	400
	CGTGGTCAAG	TAAACGTTGG	TGATACTGTT	GAAGTAGTAG	GCTTGAAAGA	450
5	AAAAGCTGAA	CAATACGTAG	TAACAGGTCT	TGAAATGTTC	CGTAAAGTGT	500
	TGGATTCTGC	AGTAGCAGGT	GACAACGTAG	GTGCATTGCT	TCGTGGTGT	550
	GATCGTAAAG	ACATYGAACG	TGGTCAAGTA	TTGGCTAAAC	CAGGTTCCAT	600
	CAACCCACAY	ACAAAATTCA	AAGCAGAAGT	ATACGTATTG	ACTAAAGAAG	650
	AAGGTGGTCG	TCATACTCCA	TTCTTCTCCA	ACTACCGTCC	ACAATTCTAC	700
10	TTCCGTACAA	CAGACGTAAC	AGGTGTTGTA	AACCTTCCTG	AAGGTGTAGA	750
	AATGTGTATG	CCTGGCGATA	ACGTAACAAT	GGAAATCGAA	TTGATTACTC	800
	CAATCGCTAT	CGAAGAAGGT	CTTCG			825

15

## 2) INFORMATION FOR SEQ ID NO: 235

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 825 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

25

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Yersinia enterocolitica*  
 (B) STRAIN: ATCC 9610

30

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 235

	CGCTATCCTG	GTTGTTGCTG	CAACTGATGG	CCCAATGCCA	CAGACTCGTG	50
	AGCACATCCT	GTTGGGTCGT	CAGGTTGGTG	TTCCTTACAT	CATCGTATTC	100
	ATGAACAAAT	GTGACATGGT	TGACGATGAA	GAGCTGCTAG	AACTGGTAGA	150
35	AATGGAAGTG	CGCGATCTTC	TGTCTACCTA	CGATTTCCCA	GGCGATGATA	200
	CGCCAGTTGT	TCGTGGTTCC	GCGCTGAAAG	CATTGGAAGG	CGAACCTGAG	250
	TGGGAAGCAA	AAATTATCGA	ACTGGCTGGC	TACCTGGATT	CTTACATCCC	300
	AGAACCAGAG	CGTGCTATCG	ATAAGCCGTT	CCTGCTGCCA	ATCGAAGACG	350
	TATTCTCTAT	CTCTGGTCGT	GGTACTGTTG	TAACGGGTCG	TGTAGAGCGC	400
40	GGTATCGTTA	AAGTTGGTGA	AGAAGTCGAA	ATTGTTGGCC	TGAAAGATAC	450
	CGTTAAATCT	ACTTGTA CTG	GCGTTGAAAT	GTTCCGCAAA	CTGCTGGATG	500
	AAGGCCGTGC	AGGTGAGAAC	GTTGGTGTTT	TGCTGCGTGG	TATCAAGCGT	550
	GAAGATATCG	AACGTGGTCA	AGTTCTTGCT	AAACAGGTT	CGATTAAACC	600
	ACACACCAAA	TTTGAATCAG	AAGTTTATAT	TCTGAGCAAA	GATGAAGGTG	650
45	GTCGCCATAC	TCCGTTCTTC	AAAGGCTACC	GTCCTCAGTT	CTACTTCCGT	700
	ACAACTGATG	TAACCGGTAC	TATTGAACTG	CCAGAAGGCG	TTGAGATGGT	750
	GATGCCAGGT	GATAACATTC	AAATGATTGT	TAACCTGATT	GCTCCTATCG	800
	CAATGGATGA	CGGCTTGCGC	TTTGC			825

50

## 2) INFORMATION FOR SEQ ID NO: 236

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 828 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

60

## (ii) MOLECULE TYPE: Genomic DN A

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Yersinia frederiksenii*  
 (B) STRAIN: ATCC 33641

5

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 236

	GGCGCGATCC	TGGTTGTTGC	TGCCACTGAT	GGCCCGATGC	CACAGACTCG	50
	CGAGCACATT	CTGTTAGGGC	GTCAGGTGGG	TGTTCTTAC	ATCCTGGTCT	100
10	TCCTGAACAA	ATGTGACATG	GTTGACGACG	AAGAGCTGCT	GGAAGTGGTA	150
	GAAATGGAAG	TTCGTGAACT	TCTGTCTCAG	TACGATTTC	CTGGCGACGA	200
	CACTCCAGTT	ATCCGTGGTT	CTGCGCTGAA	AGCGCTGGAA	GGCGAAGCTG	250
	AGTGGGAAGC	AAAAATCATC	GAATTGGCTG	AGGCGCTGGA	TAGCTATATT	300
	CCACAGCCAG	AGCGTGCGAT	TGATAAACCA	TTCCTGCTGC	CAATCGAAGA	350
15	CGTATTCTCA	ATCTCTGGCC	GTGGTACTGT	TGTCACCGGT	CGTGTAGAGC	400
	GCGGTATCGT	TAAAGTCGGC	GAAGAAGTCG	AAATCGTTGG	TATCATTGAT	450
	ACCATCAAGA	CTACCTGTAC	TGGTGTGAA	ATGTTCCGCA	AATTGCTGGA	500
	CGAAGGCCGT	GCGGGTGAGA	ACGTTGGTGT	TCTGCTACGT	GGTACTAAAC	550
	GTGATGACGT	ACAACGTGGT	CAGGTATTGG	CAAAACCAGG	TTCTATCAAG	600
20	CCACACACCA	AATTTGAATC	AGAAGTTTAT	ATTCTGAGCA	AAGATGAAGG	650
	TGGTCGCCAT	ACTCCGTTCT	TCAAAGGTTA	TCGTCCTCAG	TTCTACTTCC	700
	GTACAACTGA	CGTGACCGGT	ACTATCGAAC	TGCCAGAAGG	CGTTGAGATG	750
	GTGATGCCAG	GTGATAACAT	TCAAATGATT	GTTAACCTGA	TTGCTCCTAT	800
25	CGCAATGGAT	GACGGTCTGC	GCTTTGCG			828

## 2) INFORMATION FOR SEQ ID NO: 237

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 813 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

35

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Yersinia intermedia*  
 (B) STRAIN: ATCC 29909

40

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 237

	CTTGGTTGTC	GCTGCAACTG	ATGGTCCTAT	GCCACAGACT	CGCGAGCACA	50
45	TCCTGCTAGG	TCGTCAGGTG	GGTGTTCCCT	ACATCCTGGT	CTTCCTGAAC	100
	AAGTGTGACA	TGGTTGACGA	TGAGGAGTTG	CTGGAATTGG	TAGAAATGGA	150
	AGTCCGCGAA	CTTCTGTCTC	AATATGATTT	CCCTGGCGAT	GATACTCCTG	200
	TTATCCGTGG	TTCAGCGCTG	AAGGCGTTGG	AAGGCGAGCC	TGAATGGGAA	250
	GCAAAAATTA	TCGAATTAGC	TGAGGCGCTG	GATAGTTATA	TTCCACAGCC	300
50	AGAGCGCGCG	ATTGATAGAC	CATTCTTGCT	GCCAATCGAA	GACGTATTCT	350
	CTATCTCAGG	TCGTGGTACA	GTCGTCACTG	GTCGTGTAGA	GCGTGGGATC	400
	GTTAAAGTTG	GCGAAGAAGT	TGAAATCGTT	GGTATTATCG	ATTCCATTAG	450
	AACAACATGT	ACTGGCGTTG	AAATGTTCCG	CAAATTGCTG	GACGAAGGCC	500
	GCGCGGGTGA	GAACGTTGGT	GTTCTACTGC	GTGGGACTAA	ACGTGATGAC	550
55	GTACAGCGTG	GTCAGGTATT	AGCTAAGCCA	GGTTCTATCA	AGCCACATAC	600
	TAAATTCGAA	TCCGAAGTTT	ATATTCTGAG	CAAAGATGAA	GGCGGGCGTC	650
	ACACGCCGTT	CTTCAAAGGC	TACCGTCCTC	AGTTCTACTT	CCGTACAACG	700
	GATGTAACCG	GTAATAATTGA	ATTGCCAGAC	GGCGTTGAGA	TGGTGATGCC	750
	AGGTGATAAC	ATTCAAATGA	TTGTAAACCT	GATTGCACCT	ATTGCGATGG	800
50	ATGATGGTCT	GCG				813

## 2) INFORMATION FOR SEQ ID NO: 238

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 829 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Yersinia pestis*  
 (B) STRAIN: KIM D27

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 238

20	GGAGCGATCT	TGGTTGTTGC	TGCAACCGAT	GGCCCTATGC	CGCAGACTCG	50
	TGAGCATATC	CTGCTGGGCC	GCCAGGTTGG	TGTCCCATAC	ATTATTGTCT	100
	TCCTGAACAA	ATGTGACATG	GTTGACGATG	AAGAGTTGCT	AGAGTTGGTT	150
	GAAATGGAGG	TTCGTGAGCT	TCTGTCTCAA	TACGATTTCC	CAGGCGACGA	200
	CACTCCAGTC	ATCCGTGGTT	CAGCGTTGAA	AGCCCTGGAA	GGTGACGCTG	250
25	AGTGGGAAGC	TAAAATTATC	GAGTTGGCAG	AAGCTCTGGA	TAGCTATATT	300
	CCGCAACCAG	AACGCGCTAT	TGATAGACCA	TTCCTATTGC	CAATTGAAGA	350
	CGTATTCTCT	ATTTCTGGTC	GTGGTACTGT	AGTTACTGGT	CGTGTAGAAC	400
	GTGGTATTGT	TAAGGTCGGC	GAAGAAGTTG	AAATCGTTGG	TATTATCGAT	450
	ACGATTAAAA	CAACTTGTAC	TGGCGTTGAA	ATGTTCCGCA	AGCTGCTGGA	500
30	TGAAGGCCGT	GCTGGTGAAA	ATGTTGGTGT	TCTGCTGCGT	GGTACTAAGC	550
	GTGACGATGT	TCAGCGTGGT	CAAGTACTGG	CGAAACCAGG	TTCTATCAAG	600
	CCACACACGA	AGTTTGAGTC	AGAAGTTTAT	ATTCTGAGCA	AAGATGAAGG	650
	CGGCCGTCAT	ACACCGTTCT	TCAAGGGCTA	CCGTCCTCAG	TTCTACTTCC	700
	GTACAACTGA	CGTGACCGGT	ACCATTGAGC	TGCCAGAAGG	CGTTGAAATG	750
35	GTCATGCCTG	GTGACAACGT	AAACATGGTT	GTAAACCTAA	TTGCTCCTAT	800
	CGCAATGGAT	GATGGTCTGC	GCTTCGCAA			829

## 2) INFORMATION FOR SEQ ID NO: 239

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 817 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Yersinia pseudotuberculosis*  
 (B) STRAIN: ATCC 29833

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 239

55	TGGAGCGATC	TTGGTTGTTG	CTGCAACCGA	TGGCCCTATG	CCGCAGACTC	50
	GTGAGCATAT	CCTGCTGGGC	CGCCAGGTTG	GTGTCCCATA	CATTATTGTC	100
	TTCCTGAACA	AATGTGACAT	GGTTGACGAT	GAAGAGTTGC	TAGAGTTGGT	150
	TGAAATGGAG	GTTCGTGAGC	TTCTGTCTCA	ATACGATTTC	CCAGGCGACG	200
50	ACACTCCAGT	CATCCGTGGT	TCAGCGTTGA	AAGCCCTGGA	AGGTGACGCT	250



	GAGTGGGAAG	CTAAAATTAT	CGAGTTGGCA	GAAGCTCTGG	ATAGCTATAT	300
	TCCGCAACCA	GAACGCGCTA	TTGATAGACC	ATTCCCTATTG	CCAATTGAAG	350
	ACGTATTCTC	TATTTCTGGT	CGTGGTACTG	TAGTTACTGG	TCGTGTAGAA	400
	CGCGGTATTG	TTAAGGTCGG	CGAAGAAGTT	GAAATCGTTG	GTATTATCGA	450
5	TACGATTAAA	ACAACCTGTA	CTGGCGTTGA	AATGTTCCGC	AAGCTGCTGG	500
	ATGAAGGCCG	TGCTGGTGAA	AATGTTGGTG	TTCTGCTGCG	TGGTACTAAG	550
	CGTGACGATG	TTCAGCGTGG	TCAAGTACTG	GCGAAACCAG	GTTCTATCAA	600
	GCCACACACG	AAGTTTGAGT	CAGAAGTTTA	TATTCTGAGC	AAAGATGAAG	650
	GCGGCCGTCA	TACACCGTTC	TTCAAGGGCT	ACCGTCCTCA	GTTCTACTTC	700
10	CGTACAAC TG	ACGTGACCGG	TACCATTGAG	CTGCCAGAAG	GCGTTGAAAT	750
	GGTCATGCCT	GGTGACAACG	TAAACATGGT	TGTTAACCTA	ATTGCTCCTA	800
	TCGCAATGGA	TGATGGT				817

15

## 2) INFORMATION FOR SEQ ID NO: 240

## (i) SEQUENCE CHARACTERISTICS:

- 20 (A) LENGTH: 829 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

25

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Yersinia rohdei*  
 (B) STRAIN: ATCC 43380

30

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 240

	TGGCGCGATC	CTGGTTGTTG	CTGCAACTGA	TGGCCCAATG	CCACAGACTC	50
	GCGAGCACAT	CCTGTTGGGT	CGTCAAGTGG	GTGTTCCCTTA	CATCTTAGTC	100
	TTCCTGAACA	AGTGTGACAT	GGTTGACGAC	GAAGAGTTGC	TGGAAGTGGT	150
35	TGAAATGGAA	GTTCGTGAGC	TTCTGTCTCA	ATACGATTTC	CCTGGCGATG	200
	AACTCCGGT	TATTCGTGGT	TCCGCGCTGA	AAGCGCTGGA	AGGCGAGGCC	250
	GAGTGGGAAG	CCAAAATTAT	TGAACCTGCT	GAAGCACTGG	ATAGCTACAT	300
	TCCACAGCCA	GAGCGCGCGA	TTGATAAACC	ATTCTTGCTG	CCAATCGAAG	350
	ACGTATTCTC	TATCTCAGGC	CGTGGAACAG	TTGTTACCGG	GCGTGTGAG	400
40	CGCGGTATCG	TCAGAGTGGG	CGAAGAAGTT	GAAATCGTGG	GTATCATCGA	450
	CACCATTAAA	ACCACTTGTA	CCGGTGTGTA	AATGTTCCGC	AACTGCTGG	500
	ACGAAGGCCG	TGCCGGTGAG	AACGTTGGTG	TTCTGCTGCG	CGGTACTAAA	550
	CGCGATGACG	TGCAACGTGG	TCAAGTGTG	GCTAAACCAG	GTTCTATTAA	600
	GCCGCATACC	AAATTTGAGT	CAGAAGTTTA	TATTCTGAGC	AAAGATGAAG	650
45	GTGGTCGTCA	TACTCCGTTT	TTCAAAGGTT	ACCGTCCACA	GTTCTACTTC	700
	CGTACAAC TG	ACGTGACCGG	TACCATCGAA	CTGCCAGACG	GTGTTGAGAT	750
	GGTGATGCCA	GGTGATAACA	TTCAAATGAT	TGTTAACCTG	ATTGCGCCTA	800
	TTGCAATGGA	TGACGGTCTA	CGATTTGCA			829

50

## 2) INFORMATION FOR SEQ ID NO: 241

## (i) SEQUENCE CHARACTERISTICS:

- 55 (A) LENGTH: 804 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

50

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Yokenella regensburgei*

(B) STRAIN: ATCC 35313

5

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 241

	TGGCGCGATC	CTGGTTGTTG	CTGCGACTGA	CGGCCCGATG	CCGCAGACTC	50
	GTGAGCACAT	CCTGCTGGGT	CGTCAGGTAG	GCGTTCCGTA	CATCATCGTG	100
10	TTCCTGAACA	AATGCGACAT	GGTTGATGAC	GAAGAGCTGC	TGGAAGCTGGT	150
	AGAAATGGAA	GTTTCGTGAAC	TTCTGTCTCA	GTACGATTTC	CCGGGCGACG	200
	ACACTCCGAT	CATCCGTGGT	TCTGCTCTGA	AAGCGCTGGA	AGGCGAAGCA	250
	GAGTGGGAAG	CTAAAATCGT	TGAGCTGGCT	GGCTTCCTGG	ATTCTTACAT	300
	CCCAGAACCA	GTTTCGTGCTA	TCGACCTGCC	GTTCTGCTG	CCGATCGAAG	350
15	ACGTATTCTC	CATCTCCGGT	CGTGGCACC	TTGTTACCGG	TCGTGTAGAG	400
	CGCGGTATCG	TTAAAGTTGG	CGAAGAAGTT	GAAATCGTTG	GTATCAAAGA	450
	GACTGCTAAG	TCTACCTGTA	CCGGCGTTGA	AATGTTCCGC	AAACTGCTGG	500
	ACGAAGGCCG	TGCTGGTGAG	AACGTTGGTG	TTCTGCTGCG	TGGTATCAAA	550
	CGTGAAGAAA	TCGAACGTGG	TCAGGTACTG	GCTAAGCCGG	GTTCCATCAA	600
20	GCCGCACACC	AAATTCGAAT	CTGAAGTTTA	TATCCTGTCC	AAAGACGAAG	650
	GCGGCCGTCA	TACTCCGTTT	TTCAAAGGCT	ACCGTCCGCA	GTTCTACTTC	700
	CGTACAACCTG	ACGTGACTGG	TACCATCGAA	CTGCCGGAAG	GCGTAGAGAT	750
	GGTAATGCCG	GGCGACAACA	TCAAATGGT	TGTTACCCTG	ATCCACCCGA	800
	TCGC					804

25

## 2) INFORMATION FOR SEQ ID NO: 242

## 30 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 849 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

35

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Achromobacter xylosoxidans* subsp. *denitrificans*

40

(B) STRAIN: ATCC 15173

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 242

45	TCAGTTCCCC	CGCGATCACA	TGCCCAAGAT	CTACGAAGCG	CTTACTCTGG	50
	CCGACGAGGG	TTCCTCGTTC	GCCGAAAAGG	GTCTGACGCT	GGAAGTGCAG	100
	CAACAGCTGG	GCGACGGCGT	GGTGC GTACC	ATCGCGCTGG	GCTCCAGCGA	150
	CGGCCTGCGC	CGCGGTATGA	AGGTCACCGG	TACGGGCGCG	CCGATCTCGG	200
	TGCCGGTTCG	CACCGGCACG	CTGGGCCGCA	TCATGGACGT	GCTGGGTTCG	250
50	CCCATCGACG	AAGCCGGCCC	GATCCAGCAC	GAAGAAAAGC	GTGGCATTCA	300
	CCAGCCGGCT	CCCCGTTTCG	ACGAACTGTC	GCCGTCGGTG	GAAGTGTCTG	350
	AAACCGGCAT	CAAGGTTATT	GACCTGGTCT	GCCCGTTCGC	CAAGGGCGGC	400
	AAGGTCGGCC	TGTTCTGGCG	CGCCGGCGTG	GGCAAGACCG	TCAACATGAT	450
	GGAAGTGCAT	AACAACATCG	CCAAGCAGCA	CAGCGGCTTG	TCGGTGTTCG	500
55	CCGGCGTGGG	CGAGCGTACC	CGCGAAGGCA	ACGACTTCTA	CCACGAAATG	550
	GAAGAGTCGA	ACGTTCTGGA	CAAGGTTGCG	ATGGTGTTCG	GTCAGATGAA	600
	CGAACCCCGG	GGCAACCGTC	TGCCGCTGGC	GCTGACCGGC	CTGACCATTG	650
	CCGAGAAGTT	CCGCGACGAA	GGCCGCGACA	TCCTGTTCTT	CGTGGACAAC	700
	ATCTACCGCT	ACACCTGGGC	CGGTACGGAA	GTGTCCGCGC	TGCTGGGCCG	750
50	TATGCCGTCG	GCAGTGGGCT	ACCAGCCAC	GCTGGCCGAA	GAAATGGGCA	800

AGCTGCAAGA GCGCATCACC TCGACCAAGA CCGGCTCGAT CACCTCGAT<sup>1</sup> 849

## 5 2) INFORMATION FOR SEQ ID NO: 243

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 787 bases  
 (B) TYPE: Nucleic acid  
 10 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

## 15 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Acinetobacter baumannii*  
 (B) STRAIN: ATCC 19606

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 243

20 TGAAACTACT TTAGAAGTTC AGCAACAACT TGGTGATGGT GTTGTTTCGTA 50  
 CCATCGCAAT GGGTTCTACA GAAGGTCTTA AACGTGGTCT TACTGTAACT 100  
 AGCACAAACG CACCGATCTC TGTTCCAGTT GGTACAGCCA CTCTTGGCCG 150  
 TATCATGGAC GTTTTAGGTC GTCCTATCGA TGAAGCAGGT CCTGTTGCGA 200  
 25 CTGAAGAACG TTTGCCGATT CACCGTCAAG CGCCTTCTTA TGCTGAACAA 250  
 GCAGCTTCTA CTGACCTTTT AGAAACTGGT ATTAAAGTCA TCGACTTACT 300  
 TTGCCCCGTTT GCGAAAGGTG GTAAAGTTGG TTTATTCCGT GGTGCTGGTG 350  
 TTGGTAAAC CGTTAACATG ATGGAATTGA TCAACAACAT CGCGAAAGCA 400  
 CACTCAGGTT TATCTGTGTT TGCTGGTGTT GGTGAGCGTA CTCGTGAAGG 450  
 30 TAATGACTTC TATCACGAAA TGAAAGATTC TAACGTTCTT GACAAAGTAG 500  
 CAATGGTCTA CGGTCAGATG AACGAGCCAC CAGGTAACCG TTTACGCGTA 550  
 GCGTTAACTG GTTTGACTAT GGCTGAATAC TTCCGTGATG AAAAAGACGA 600  
 AAACGGTAAA GGTCGTGACG TATTATTATT CGTCGACAAC ATCTACCGTT 650  
 ATACACTTGC AGGTACTGAA GTATCAGCAT TGTTAGGTCG TATGCCATCT 700  
 35 GCGGTAGGTT ACCAACCTAC ACTTGCAGAA GAAATGGGTG TTCTTCAAGA 750  
 GCGTATTACA TCTACTAAAT CTGGTTCGAT CACTTCG 787

## 40 2) INFORMATION FOR SEQ ID NO: 244

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 825 bases  
 (B) TYPE: Nucleic acid  
 45 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

## 50 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Acinetobacter lwoffii*  
 (B) STRAIN: CDCF 3697

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 244

55 GTTCCTAAGA TCTATGACGC TCTCCACGTT GATGGCACTG AAACCTACATT 50  
 AGAAGTTCAG CAACAACCTG GTGATGGCGT AGTTCGTACT ATTGCAATGG 100  
 GTTCTACTGA AGGCCTTAAG CGTGGTTTGA ACGTAACTAA CACTAACGCG 150  
 CCGATTTCTG TACCAGTAGG TACAGCGACT CTAGGTCGTA TCATGGACGT 200  
 50 TCTTGGTTCG CCAATCGACG AAGCTGGTCC AGTTGCGACT GAAGCGCGTT 250

	TGCCGATTCA	CCGTCAAGCA	CCTTCTTATG	CTGAACAAGC	AGCTTCTACT	300
	GACCTTTTAG	AAACTGGTAT	TAAAGTCATC	GACTTACTTT	GCCCGTTCGC	350
	TAAAGGTGGT	AAAGTTGGTC	TGTTCTGGTG	TGCCGGTGTT	GGTAAACTG	400
	TAAACATGAT	GGAGTTGATC	AACAACATCG	CTAAAGCGCA	CTCAGGTTTA	450
5	TCTGTATTCT	CTGGTGTTGG	TGAGCGTACT	CGTGAAGGTA	ATGACTTCTA	500
	TCACGAGATG	AAAGACTCAA	ACGTTCTAGA	CAAAGTAGCA	ATGGTCTACG	550
	GTCAGATGAA	CGAGCCACCG	GGTAACCGTT	TACGCGTAGC	GTTGACTGGT	600
	TTGACCATGG	CTGAGTACTT	CCGTGACGAG	AAAGACGAAA	ACGGCAAAGG	650
	CCGTGACGTA	CTATTGTTCT	TAGATAACAT	CTACCGTTAT	ACACTAGCAG	700
10	GTACTGAAGT	ATCAGCACTT	CTAGGTCGTA	TGCCGTCTGC	AGTAGGTTAC	750
	CAACCGACAC	TTGCAGAAGA	GATGGGTGTT	CTTCAAGAAC	GTATTACATC	800
	GACTAAGTCT	GGTTCGATTA	CGTCA			825

15

## 2) INFORMATION FOR SEQ ID NO: 245

## (i) SEQUENCE CHARACTERISTICS:

20

- (A) LENGTH: 837 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

25

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus saprophyticus*
- (B) STRAIN: CSG-197

30

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 245

	CAATGAAGTT	CCAGAAATTA	ACAATGCCTT	AGTCGTAGAC	GTTGAAAGAG	50
	ATGAAGGTAC	AGTATCTCTT	ACATTAGAAG	TGGCATTACA	ACTTGGCGAT	100
	GATGTCGTAC	GTACAATTGC	AATGGATTCT	ACTGATGGTG	TTAAACGTGG	150
35	TACAGAAGTT	CGAGATAGCG	GAGATAGCAT	CAGTGTTCCA	GTTGGTGATG	200
	CTACGTTAGG	ACGTGTGTTT	AATGTTCTTG	GTGATACAAT	TGACTTAGAC	250
	GAGAAGCTTG	ATACTTCTGT	CAAACGTGAT	CCAATTCATA	GAGAAGCACC	300
	TGCATTCGAT	CAATTATCAA	CAAAAGTTGA	AATCTTAGAA	ACAGGTATTA	350
	AAGTAATTGA	TTTACTTGCA	CCATATATTA	AAGGTGGTAA	AATCGGTTTA	400
40	TTCCGGTGGCG	CTGGTGTAGG	TAAAACAGTA	TTAATTCAAG	AATTAATTAA	450
	TAATATAGCT	CAAGAACATG	GTGGTATTTT	AGTATTTGCC	GGCGTAGGTG	500
	AACGTACGCG	TGAAGGTAAT	GACTTATACT	ACGAAATGAG	TGATAGTGGT	550
	GTTATTAAGA	AAACAGCTAT	GGTCTTCGGA	CAAATGAATG	AGCCACCTGG	600
	TGCGCGTATG	CGTGTTGCTT	TATCAGGCTT	ACAATGGCT	GAACACTTCC	650
45	GTGATGTACA	AGGACAAGAT	GTTTTACTAT	TTATTGATAA	CATATTCAGA	700
	TTTACGCAAG	CTGGTTCAGA	AGTATCAGCA	CTATTAGGTC	GTATGCCATC	750
	AGCCGTTGGT	TATCAACCTA	CCCTTGCTAC	TGAAATGGGT	CAATTACAAG	800
	AACGTATTAC	ATCAACAAC	AAAGGATCTG	TAACGTC		837

50

## 2) INFORMATION FOR SEQ ID NO: 246

## (i) SEQUENCE CHARACTERISTICS:

55

- (A) LENGTH: 851 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

60

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Alcaligenes faecalis*

(B) STRAIN: ATCC 15554

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 246

```

5      TTCCCCCGCG ACAGCATCCC TAAAGTCTAC GAAGCATTGA CGCTCGTTGA      50
      CGAAAGTTTCG GCTTTCGCAG AAAAAGGCCT GACTTTTGAA GTACAGCAAC      100
10     AATTGGGTGA CGGTGTAGTT CGCACCATCG CCATGGGTTC CAGCGACGGC      150
      CTGCGCCGCG GTATGGAAGT GGCCGGTTTCG GGCGCTCCCA TCTCCGTTCC      200
      CGTGGGTGTC GGCACCCTGG GTCGCATTAT GGACGTTCTG GGTCGCCCTA      250
      TTGACGAAGT CGGTCCTATT CAGTCCGACG AGCGTCGCGC CATTACCAG      300
      CCTGCGCCTA CTTTCGACGA ACTGTCGCCT TCCGTAGAGC TGCTGGAAAC      350
15     CGGTATTAAA GTGATTGACC TGGTTTGCCC GTTCGCCAAG GGTGGTAAGG      400
      TTGGTCTGTT CGGTGGTGCC GGTGTGGGCA AGACCGTGAA CATGCTGGAG      450
      CTGATCAACA ACATCGCCAA GGCACACAGC GGTCTGTCCG TGTTTGCCCG      500
      TGTGGGTGAG CGTACCCGTG AAGGTAACGA CTTCTACCAC GAAATGGCCG      550
      ATGCTGGCGT TATCCAGATG GACAACCTGA GCGAGTCCAA AGTGGCCATG      600
20     GTGTTCGGTC AGATGAACGA ACCTCCAGGC AACCGTCTGC GTGTGGCACT      650
      GTCCGGCCTG ACCATGGCCG AGAAGTTCCG TGACGAAGGC CGTGACATCC      700
      TGTTCCTTTGT GGACAACATC TACCGCTACA CGCTGGCCCG TACAGAAGTG      750
      TCCGCTCTGC TGGGTCGTAT GCCTTCCGCA GTGGGTTACC AGCCTACGCT      800
      GGCCGAGGAA ATGGGTAAGC TGCAAGAGCG CATTACCTCC ACCAAGACCG      850
25     G

```

## 2) INFORMATION FOR SEQ ID NO: 247

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 846 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Bacillus anthracis*

(B) STRAIN: 4229

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 247

```

15     GATGGCGGAA AGCTACCAGA AATCTACAAC GCCCTTACGG TAAAACAGAG      50
      CAACGAAAAC GGAACAAGCA TTAACCTAAC ATTTGAAGTT GCACTTCATT      100
      TAGGTGATGA CACAGTTCGT ACAGTTGCAA TGTCTTCCAC AGATGGACTT      150
      GTTCGTGGCA CAGAAGTAGA AGATACTGGT AAAGCAATCT CTGTACCAGT      200
      TGGTGATGCA ACACTTGGTC GTGTATTTAA CGTATTAGGT GATGCAATTG      250
20     ACTTAGATGG TGAGGTTCCT GCGGATGTAC GTCGTGATCC AATTCACCGT      300
      CAAGCACCTG CATTCTGAAGA ATTATCTACT AAAGTAGAAA TTCTTGAAAC      350
      TGGTATTAAA GTAGTAGACT TACTTGCTCC TTACATTAAG GGTGGTAAGA      400
      TCGGTCTATT CGGTGGTGCC GGTGTAGGTA AAACGGTATT AATTCAGGAA      450
      TTAATCAATA ACATCGCACA AGAACACGGT GGTATCTCTG TATTGCTGG      500
25     TGTAGGTGAG CGTACTCGTG AGGGTAATGA CTTATACCAC GAAATGAGCG      550
      ATTCTGGCGT AATTAAGAAA ACTGCGATGG TATTGCGACA AATGAACGAG      600
      CCACCTGGAG CACGTCAACG TGTTCGCTTA ACAGGTTTAA CAATGGCTGA      650
      GCATTTCGTG GATGAGCAAG GATGAGATGT ACTTCTGTTT ATCGATAATA      700
      TCTTCCGTTT CACGCAAGCA GGTTCCTGAAG TATCTGCCCT TCTTGGCCGT      750
30     ATGCCATCTG CGGTAGGTTA CCAACCAACA CTTGCAACAG AAATGGGTCA      800

```

ATTACAAGAG CGTATTACAT CTACAAATAA AGGGTCTATC ACGTCT

846

## 5 2) INFORMATION FOR SEQ ID NO: 248

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 810 bases  
(B) TYPE: Nucleic acid  
10 (C) STRANDEDNESS: Double  
(D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

## 15 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Bacillus cereus*  
(B) STRAIN: ATCC 14579

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 248

20 CCAGAAATCT ACAATGCCCT TACGGTAAAA CAAAGCAACG AAAACGGAAG 50  
CATGAACTTA ACATTTGAAG TTGCACTTCA TTTAGGTGAT GATACAGTTC 100  
GTACAGTTGC GATGTCTTCC ACAGATGGAC TTGTTTCGTGG CACAGAAGTA 150  
GAAGATACTG GTAAAGCAAT CTCTGTACCA GTTGGTGATG CAACACTTGG 200  
25 ACGTGTATTG AACGTATTAG GTGATGCAAT TGACTTAGAT GGTGAACTTC 250  
CTGCGGATGT ACACCGTGAT CCAATTACC GTCAAGCACC TGCATTGCGAA 300  
GAATTATCTA CTAAAGTAGA AATTCTTGAA ACTGGTATTA AAGTAGTAGA 350  
CTTACTTGCT CCTTACATTA AGGGTGGTAA GATCGGCCTA TTCGGTGCTG 400  
CCGGCGTAGG TAAACAGTA TTAATTCAGG AGTTAATCAA TAACATCGCA 450  
30 CAAGAGCACG GTGGTATCTC TGTATTCGCT GGTGTAGGTG AGCGTACTCG 500  
TGAGGGTAAT GACTTATACC ACGAAATGAG CGATTCTGGC GTAATCAAGA 550  
AAACTGCGAT GGTATTCGGA CAAATGAACG AGCCACCTGG AGCACGTCAA 600  
CGTGTTCGAT TAACAGGTTT AACAAATGGCT GAGCATTTCG GTGATGAGCA 650  
AGGACAAGAC GTACTTCTGT TCATCGATAA CATCTTCCGT TTCACGCAAG 700  
35 CGGGTTCTGA AGTATCTGCC CTTCTTGGTC GTATGCCATC TGCGGTAGGT 750  
TACCAACCAA CACTTGCAAC AGAAATGGGT CAATTACAAG AGCGTATTAC 800  
ATCTACAAAT 810

## 40 2) INFORMATION FOR SEQ ID NO: 249

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 944 bases  
45 (B) TYPE: Nucleic acid  
(C) STRANDEDNESS: Double  
(D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

## 50 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Bacteroides distasonis*  
(B) STRAIN: ATCC 8503

## 55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 249

CTTTGATTAT GGGACAGAAG AAACAGTAAC CCTCCCCCGT ATCCACGACG 50  
CCATGGAGAT TTCCCGCCCA AACGGAAAGA TCTTGATCGT CGAAGTTCAG 100  
CAACACATCG GGGAAAACAC CGTCCGTACC GTAGCGATGG ATACGACCGA 150  
50 CGGATTGAGA CGAGGCATGG AGGCCGTGTC ATACGGAATG CCCATCACCA 200

	TGCCGACCGG	CGACCAAGTC	AAAGGACGTT	TAATGAATGT	CACCGGCGAC	250
	CCTATCGATG	GCATGGCCCA	GCTTACTAAA	GACGGGGCTC	TTCCCATCCA	300
	TCGTGAGCCT	CCTAAATTCT	AGGATCTGAC	AACGACCCAA	GAGGTCTTGT	350
	ACACGGGTAT	TAAAGTAATC	GATTTATTGG	AACCTTACGC	CAAAGGAGGC	400
5	AAGATCGGAC	TTTTCGGAGG	AGCCGGAGTC	GGCAAAACGG	TATTGATCAT	450
	GGAATTGATC	AACAACATCG	CAAAGAAAAA	CAACGGATTC	TCCGTCTTCG	500
	CCGGTGTGGG	TGAACGTACA	CGTGAAGGAA	ATGACCTATT	GCGTGAAATG	550
	ATCCAATCCG	GTGTCATCCG	ATACGGCGAG	GAGTTTAAGA	AGAGTATGGA	600
	GGCAGGCAAC	TGGGACTTGT	CGAAGATCGA	TTACGATGAA	TTGGCTAAGT	650
10	CGCAGGCTAC	CTTGGTATTC	GGGCAGATGA	ACGAACCGCC	GGGCGCCCGC	700
	TCGTCCGTGG	CCTTATCCGG	TTTGACGATC	GCCGAATCCT	TCCGTGACAA	750
	AGCCTCTGAG	GGAGAAAGAA	AAGATATATT	ATTCTTCATC	GATAATATCT	800
	TCCGTTTCAC	CCAAGCCGGT	TCCGAGGTTT	CCGCCTTGCT	GGGGCGTATG	850
	CCTTCCGCCG	TAGGTTACCA	ACCGACATTG	GCCACGGAAA	TGGGAGCTAT	900
15	GCAAGAGCGT	ATCACTTCAA	CCAAGAAGGG	CTCCATCACC	TCCG	944

## 2) INFORMATION FOR SEQ ID NO: 250

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 939 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Bacteroides ovatus*  
 (B) STRAIN: ATCC 8483

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 250

35	TTGAGGGTAC	GGATGCAGAA	TTGGTGCTGC	CAAGCATCCA	CGACGCACTG	50
	GAGATAAAGA	GGCCAAACGG	CAAATACTG	GTTGTAGAAG	TTGAGCAACA	100
	TATCGGCGAA	AATACGGTGC	GTACCGTAGC	GATGGACAGT	ACTGACGGAC	150
	TTCAGAGAGG	CATGAAAGTG	TATCCCACCG	GAGGCCCGAT	CACGATGCCG	200
	ATTGGCGAAC	AGATTAAAGG	ACGACTGATG	AACGTAGTCG	GTGATTTCGAT	250
40	CGACGGTATG	AAAGGACTCG	ACCGCAAAGG	TGCATATTCC	ATTCATCGCG	300
	ACCCCCCTAA	GTTTGAGGAT	TTGACTACTG	TGCAAGAGGT	GCTCTTCACA	350
	GGTATCAAAG	TGATCGACCT	GCTCGAACCG	TATGCCAAAG	GTGGTAAAT	400
	CGGTTTGTTC	GGCGGTGCCG	GTGTAGGAAA	GACTGTATTG	ATTCAGGAAC	450
	TTATCAATAA	TATCGCCAAG	AAACATAATG	GATTCTCTGT	ATTTGCCGGA	500
45	GTAGGTGAAC	GTACCCGTGA	AGGTAACGAC	TTGCTGCGCG	AAATGATTGA	550
	ATCCGGTGTA	ATCCGTTACG	GCGAAGCATT	CAAAGAAGGA	ATGGAGAAAG	600
	GTCACTGGGA	TCTTTCGAAA	GTGGATTATA	ACGAAGTGGG	GAAATCGCAA	650
	GTGTCTCTGA	TTTTCGGTCA	GATGAACGAG	CCTCCGGGCG	CACGTGCCTC	700
	TGTGGCATTG	TCCGGACTGA	CGGTGGCGGA	ATCTTTCCGC	GACGCAGGAA	750
50	AAGAAGGTGA	GAAACGCGAT	ATTCTGTTCT	TTATTGATAA	TATCTTCCGT	800
	TTCACGCAAG	CAGGTTTACA	AGTGTCCGCC	CTTTTGGGAC	GTATGCCCTC	850
	CGCTGTTGGT	TACCAGCCCA	CGTTGGCTAC	GGAAATGGGT	GCGATGCAGG	900
	AACGTATCAC	GTCTACCCGC	AAAGGTTCTA	TCACCTCCG		939

## 2) INFORMATION FOR SEQ ID NO: 251

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 833 bases

(B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

5 (ii) MOLECULE TYPE: DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Leclercia adecarboxylata*

(B) STRAIN: ATCC 23216

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 251

	CGAATTCCT	CAGGATGCCG	TACCGCGCGT	GTACGATGCT	CTTGAGGTTC	50
	AGAATGGTAA	TGAGAGCCTG	GTGCTGGAAG	TTCAGCAGCA	GCTCGGCGGC	100
15	GGTATTGTGC	GTACCATCGC	CATGGGTTCT	TCCGACGGTC	TGCGTCGTGG	150
	TCTGGAAGTT	AAAGACCTCG	AGCACCCAAT	CGAAGTACCA	GTAGGTAAAG	200
	CAACCCTGGG	CCGTATCATG	AACGTCCTGG	GTCAGCCGAT	CGACATGAAA	250
	GGCGACATCG	GCGAAGAAGA	GCGTTGGGCT	ATCCACCGTT	CAGCACCTTC	300
	CTATGAAGAG	CTGTCCAGCT	CTCAGGAACT	GCTGGAAACC	GGCATCAAAG	350
20	TTATCGACCT	GATGTGTCCG	TTCGCGAAGG	GCGGTAAAGT	TGGTCTGTTC	400
	GGCGGTGCGG	GTGTAGGTAA	AACCGTAAAC	ATGATGGAGC	TGATCCGTAA	450
	CATCGCGATC	GAGCACTCCG	GTTACTCCGT	GTTTGCAGGC	GTGGGTGAGC	500
	GTACTCGTGA	GGGTAACGAC	TTCTACCACG	AAATGACCGA	CTCCAACGTT	550
	CTGGACAAAG	TATCCCTGGT	TTACGGCCAG	ATGAACGAGC	CACCAGGAAA	600
25	CCGTCTGCGC	GTTGCGCTGA	CCGGCCTGAC	CATGGCTGAG	AAGTTCCGTG	650
	ACGAAGGTGC	TGACGTACTG	CTGTTTCGTTG	ACAACATCTA	CCGTTACACC	700
	CTGGCCGGTA	CGGAAGTATC	CGCACTGCTG	GGTCGTATGC	CATCAGCAGT	750
	AGGCTACCAG	CCGACCCTGG	CGGAAGAGAT	GGGTGTTCTG	CAGGAACGTA	800
30	TCACCTCTAC	CAAACCCGGT	TCTATCACCT	CCG		833

## 2) INFORMATION FOR SEQ ID NO: 252

35 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 819 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

40

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Stenotrophomonas maltophilia*

45

(B) STRAIN: CDC F3338

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 252

	GTGTACGACG	CACTGAAGGT	GGAAAACACC	GAGATCACCC	TCGAAGTCCA	50
50	GCAGCAGCTG	GGCGACGGCG	TGGTGCGTAC	CATCGCCCTC	GGTTCCACCG	100
	ACGGCCTGAA	GCGCAACCTG	GTTGCCGTCA	ACACCGGCCG	TGGCATCTCG	150
	GTGCCGCTCG	GCGCCGGCAC	CCTGGGCCGC	ATCATGGACG	TGCTGGGCCG	200
	TCCGATCGAC	GAAGCCGGCC	CGGTCGCTGC	CAGCGACAAC	TGGGAAATCC	250
	ACCGCGCTGC	GCCGTCGTAT	GAAGACCAGT	CCCCGGCCAC	CGAGCTGCTG	300
55	GAAACCGGCA	TCAAGGTCAT	CGACCTGATG	TGCCCCGTTG	CCAAGGGCGG	350
	CAAGGTCGGC	CTGTTCGGCG	GCGCCGGCGT	CGGCAAGACC	GTCAACATGA	400
	TGGAAGTATG	CAACAACATC	GCCAAGGCGC	ACAGCGGCCT	GTCCGTGTTC	450
	GCCGGCGTGG	GTGAGCGTAC	CCGTGAGGGC	AACGACTTCT	ACCACGAGAT	500
	GAAGGACTCC	AACGTCCTGG	ACAAGGTGGC	GATGGTGTAC	GGCCAGATGA	550
60	ACGAGCCGCC	GGGCAACCGT	CTGCGCGTCG	CCCTGACCGG	CCTGACCATG	600



	GCCGAGTACT	TCCGCGATGA	GAAGGACGAA	AACGGCAAGG	GCAAGGACGT	650
	CCTGCTGTTT	GTCGACAACA	TCTACCGCTA	CACCCTGGCC	GGTACCGAAG	700
	TGTCGGCACT	GCTGGGCGCG	ATGCCGTCCG	CGGTGGGTTA	CCAGCCGACC	750
	CTGGCCGAGG	AAATGGGCGT	CCTGCAGGAG	CGCATCACCT	CGACCAAGAA	800
5	TGGTTCGATC	ACCTCGATC				819

## 2) INFORMATION FOR SEQ ID NO: 253

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 864 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Bartonella henselae*  
 (B) STRAIN: ATCC 49882

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 253

25	AGTTTGAAGG	CCCTTTGCCA	AATATTCTCA	ATGCATTAGA	AACAGATAAT	50
	TTGGGCAATC	GGCTAGTTTT	AGAAGTTGCT	CAGCATTTGG	GTGAAAATAC	100
	CGTGCGTACC	ATTGCCATGG	ATACTACCGA	TGGTCTTGTC	CGTGGTCAAA	150
	AAGTTTTTTGA	TACAGGAACA	CAGATCAGTG	TTCCCGTGGG	AGAAGCAACA	200
	CTTGGTCGTA	TTATGAATGT	GATTGGAGAG	CCGGTTGATA	ATGTTGGCCC	250
30	AATTGCTACA	AGCAAAACCC	GTTCCATTCA	CCAAGAGGCT	CCTGAATATG	300
	TGGAGCAATC	AACCGCATCA	GAAATCCTTG	TGACTGGTAT	TAAAGTCGTT	350
	GATCTGTTAG	CTCCTTATTC	TAAAGGGGGG	AAGGTTGGTT	TGTTTGGAGG	400
	TGCCGGTGTT	GGTAAAACCG	TTCTCATTAT	GGAGCTTATC	AACAATATTG	450
	CAAAGGCGCA	TGGTGGCTAT	TCAGTGTTTG	CCGGTGTTGG	TGAACGTACA	500
35	CGTGAGGGAA	ATGATCTTTA	TTATGAAATG	ATCGAAAGCC	GTGTGAATGT	550
	GAATCCAAAA	GACAACAATG	GTTCAACAGA	AGGATCAAAA	TGTGCACTCG	600
	TTTATGGGCA	AATGAATGAA	CCACCAGGGG	CGCGTGACAG	TGTGGCTCTT	650
	TCAGGATTGA	CCATTGCAGA	AAGTTTCCGT	GATGAGGGAC	AAGATGTTTT	700
	GTTCTTCGTA	GATAATATTT	TCCGTTTTAC	GCAAGCAGGC	GCTGAAGTGT	750
40	CAGCTCTTTT	AGGGCGTATT	CCTTCTGCTG	TAGGGTATCA	GCCAACTTTG	800
	GCAACTGATA	TGGGGGCTTT	GCAAGAGCGT	ATTACCAGTA	CAAGAACAGG	850
	CTCTATTACC	TCTG				864

## 2) INFORMATION FOR SEQ ID NO: 254

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 866 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Bifidobacterium adolescentis*  
 (B) STRAIN: ATCC 15703

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 254

	TTCCCGGTGG	GCCACCTGCC	CGACATTTAC	AATGCACTTA	CCGTTGAACT	50
	GKCCAACACC	GGYGTCCACG	AASAGGGCGA	GACCACCAAG	AAGATCACCC	100
	TTGMMGGTTGA	ACAGCATCTT	GGCGATTCCA	CCGTGCGTAC	CGTCGCTCTG	150
5	AAGCCGACTG	ACGGCCTTGT	GCGTGCGGCC	ACCGTGTATG	ACACCGGCGG	200
	CCCGATCTCT	GTGCCGGTTG	GCGATGTCAC	CAAGGGCCAC	GTATTCGACG	250
	TGTCCGGCAA	CATCCTCAAC	AAGAAGGCCG	ACGAGACCGT	TAAGGTTACC	300
	GAACGTTGGT	CTATCCACCG	TAACCCGCCG	GCATTTCGACC	AGCTGGAGTC	350
	CAAGACCCAG	ATGTTTCGAAA	CCGGTATCAA	GGTCATCGAT	TTGCTGACCC	400
10	CGTATGTGCA	GGGCGGCAAG	ATCGGTCTGT	TCGGCGGCGC	AGGCGTCGGC	450
	AAGACCGTGC	TGATCCAGGA	AATGATTTCAG	CGTGTGGCTC	AGAACCACGG	500
	CGGTGTGTCC	GTGTTTCGCAG	GCGTCGGCGA	GCGTACCCGT	GAGGGTAACG	550
	ATCTGATCGG	CGAAATGGAC	GAAGCCGGCG	TGCTCGAGAA	GACCGCACTG	600
	GTCTTCGGCC	AGATGGATGA	GCAGCCGGGT	ACCCGTCTGC	GCGTGCCGCT	650
15	GACCGCACTG	ACCATGGCAG	AGTACTTCCG	TGACGTACAG	AATCAGGACG	700
	TGCTGCTGTT	CATCGATAAC	ATCTTCCGTT	TCACCCAGGC	TGGTTCCGAG	750
	GTGTCCACCC	TGCTCGGCCG	TATGCCGTCC	GCAGTGGGCT	ACCAGCCGAA	800
	CCTGGCCGAT	GAGATGGGCG	CGCTGCAGGA	GCGAATCACT	TCGACCCGTG	850
20	GACACTCCAT	CACCTC				866

## 2) INFORMATION FOR SEQ ID NO: 255

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 842 bases
  - (B) TYPE: Nucleic acid
  - (C) STRANDEDNESS: Double
  - (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Brucella abortus*
- (B) STRAIN: S2308

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 255

	AAGGCCAGCT	GCCGCTGATC	CTGAACGCGC	TTGAAGTGGA	CAATCAGGGC	50
40	CATCGTCTGG	TTCTCGAAGT	TGCCCAGCAC	CTCGGCGAAG	ACACCGTGCG	100
	CACCATCGCC	ATGGACGCGA	CCGAAGGTCT	CGTTCGCGGT	CAGGAAGCAC	150
	GCGACACTGG	CGAACCGATC	ATGGTGCCGG	TCGGCGTCTGA	AACGCTTGGC	200
	CGCATCATGA	ACGTCATCGG	CGAGCCGGTT	GACGAAGCAG	GCCCCATCAA	250
	GACCAAGGCA	ACCCGCGCCA	TCCACCAGAA	CGCGCCGGAA	TATATCGAAC	300
45	AGTCGACCGA	AGCCGAAATT	CTGGTCACGG	GCATCAAGGT	CGTCGACCTT	350
	CTGGCGCCTT	ACGCCAAGGG	CGCAAGATC	GGCCTCTTCG	GCGGTGCAGG	400
	CGTCGGCAAG	ACCGTTCTCA	TCATGGAAGT	CATCAACAAC	GTCGCCAAGG	450
	CGCACGGCGG	TTATTCCGTG	TTCGCAGGCG	TCGGTGAGCG	TACCCGTGAG	500
	GGCAACGACC	TTTACCACGA	AATGATCGAG	TCGGGCGTGA	ACAAGCTCGG	550
50	CGGCGGCGAA	GGCTCCAAGG	CAGCCCTCGT	TTACGGCCAG	ATGAACGAAC	600
	CCCCGGGTGC	CCGCGCCCGC	GTTGCCCTTT	CCGGTCTGAC	GGTTGCTGAA	650
	AACTTCCGTG	ACCAGGGCCA	GGACGTTCTG	TTCTTTCGTG	ACAACATCTT	700
	CCGCTTCACG	CAGGCAGGTT	CGGAAGTGTC	GGCTCTTCTC	GGCCGTATTC	750
	CTTCCGCTGT	GGGTTATCAG	CCGACGCTGG	CAACCGACAT	GGGCGCCATG	800
55	CAGGAACGCA	TCACCACGAC	GACCAAGGGT	TCGATCACCT	CG	842

## 2) INFORMATION FOR SEQ ID NO: 256

60

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 833 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Cedecea davisae*  
 (B) STRAIN: ATCC 33431

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 256

15	CGAGTTCCT	CAGGACGGCG	TACCGCGCGT	TKATGATGCG	CTTGAAGTAC	50
	AAAATAACAG	CGAGCAGCTG	GTGCTGGAAG	TTCAGCAGCA	GCTCGGCGGC	100
	GGTATCGTGC	GTACCATCGC	TATGGGTTC	TCCGACGGTC	TGCGTCGTGG	150
	TCTGGAAGTT	AAAGACCTCG	AGCACCCGAT	CGAAGTCCCG	GTAGGTAAAG	200
	CGACCCTTGG	CCGTATCATG	AACGTGCTGG	GTCAGCCGAT	CGACATGAAA	250
20	GGCGATATCG	GCGAAGAAGA	CCGTTGGGCT	ATTCACCGCG	CTGCACCTTC	300
	CTATGAAGAG	CTGTCCAGCT	CTCAGGAACT	GCTGGAAACC	GGCATCAAAG	350
	TAATCGACCT	TATCTGTCCG	TTGCTAAGG	GCGGTAAAGT	AGGTCTGTTC	400
	GGTGGTGCGG	GCGTGGGTAA	AACCGTAAAC	ATGATGGAGC	TTATCCGTAA	450
	CATCGCGATC	GAGCACTCCG	GCTACTCCGT	GTTTGCGGGC	GTGGGTGAGC	500
25	GTAATCGTGA	GGGTAACGAC	TTCTATCACG	AAATGACCGA	CTCCAACGTT	550
	CTGGACAAAG	TTGCCCTGGT	TTACGGCCAG	ATGAACGAGC	CACCGGGTAA	600
	CCGTCTGCGC	GTAGCGCTGA	CCGGTCTGAC	CATCGCGGAG	AAATTCCGTG	650
	ACGAAGGTCG	TGACGTTCTG	CTGTTCTGTTG	ATAACATCTA	CCGTTACACC	700
	CTGGCCGGTA	CTGAAGTATC	CGCGCTGCTG	GGTCGTATGC	CTTCTGCGGT	750
30	AGGTTACCAG	CCAATCTGG	CGGAAGAGAT	GGGTGTTCTT	CAGGAGCGTA	800
	TTACCTCCAC	CAAGACCGGT	TCCATCACCT	CCG		833

## 35 2) INFORMATION FOR SEQ ID NO: 257

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 829 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Cedecea lapagei*  
 (B) STRAIN: ATCC 33432

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 257

50	TTCCCTCAGG	ACGGCGTACC	GCGCGTATAT	GACGCGCTTG	AGGTACAGAA	50
	TAACAGCGAG	AAGCTGGTGC	TGGAAGTTCA	GCAGCAGCTC	GGCGGCGGTA	100
	TCGTACGTAC	CATCGCAATG	GGTTCCTCCG	ACGGTCTGCG	TCGTGGTCTG	150
	GAAGTGAAAG	ACCTCGAGCA	CCCGATCGAA	GTCCCAGGTAG	GTAAAGCGAC	200
55	TCTGGGTCTG	ATCATGAACG	TGCTGGGTCA	GCCAATTGAT	ATGAAAGGCG	250
	ACATCGGCGA	AGAAGATCGT	TGGGCGATTC	ACCGCGCAGC	ACCTTCCTAT	300
	GAAGACTGT	CCAGCTCTCA	GGAAGTCTG	GAAACCGGCA	TCAAAGTTAT	350
	CGACCTGATT	TGTCCTTCG	CTAAGGGCGG	TAAAGTTGGT	CTGTTCCGGT	400
	GTGCGGGCGT	AGGTAAACCC	GTAACATGTA	TGGAGCTGAT	CCGTAACATC	450
50	GCGATCGAGC	ACTCCGGTTA	CTCCGTGTTT	GCAGGCGTGG	GTGAGCGTAC	500

TCGTGAGGGT	AACGACTTCT	ACCACGAGAT	GACCGACTCC	AACGTTCTGG	550
ACAAAGTTGC	ACTGGTTTAC	GGCCAGATGA	ACGAGCCGCC	AGGTAACCGT	600
CTGCGCGTAG	CGCTGACCGG	TCTGACCATC	GCGGAGAAAT	TCCGTGACGA	650
AGGCCGTGAC	GTTCTGCTGT	TCGTGCGATAA	CATCTATCGT	TATACCCTGG	700
5 CCGGTACAGA	AGTTTCTGCA	CTGCTGGGTC	GTATGCCATC	TGCGGTAGGT	750
TATCAGCCTA	CTCTGGCAGA	AGAGATGGGT	GTTCTTCAGG	AGCGTATTAC	800
CTCCACCAAG	ACCGGTTCCA	TCACTTCCG			829

10

## 2) INFORMATION FOR SEQ ID NO: 258

## (i) SEQUENCE CHARACTERISTICS:

- 15 (A) LENGTH: 830 bases  
(B) TYPE: Nucleic acid  
(C) STRANDEDNESS: Double  
(D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

20

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Cedecea neteri*  
(B) STRAIN: ATCC 33855

25

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 258

TCCCTCAGGA	CGGCGTACCG	CGCGTTTATG	ACGCGCTTGA	GGTACAGAAC	50
AACAATGAGA	AGCTGGTGCT	GGAAGTTCAG	CAGCAGCTCG	GCGGCGGTAT	100
CGTGCGTACC	ATCGCAATGG	GTTCTTCCGA	CGGTCTGCGT	CGTGGTCTGG	150
30 TAGTAACAGA	CCTCGAGCAC	CCGATCGAAG	TCCCGGTAGG	TAAAGCGACC	200
CTTGGCCGTA	TCATGAACGT	GCTGGGTCAG	CCGATCGACA	TGAAAGGCGA	250
CATCGGCGAA	GAAGACCGTT	GGGCGATTCA	CCGCGCAGCA	CCTTCCTACG	300
AAGAGCTGTC	CAGCTCTCAG	GAATTGCTGG	AAACCGGCAT	CAAAGTTATC	350
GACCTGATTT	GTCCGTTTCG	TAAGGGCGGT	AAAGTAGGTC	TGTTTCGGTGG	400
35 TGCGGGCGTA	GGTAAAACCG	TAAACATGAT	GGAGCTGATC	CGTAACATTG	450
CGATCGAGCA	CTCCGTTTAT	TCCGTGTTTG	CGGGCGTGGG	TGAGCGTACT	500
CGTGAGGGTA	ACGACTTCTA	CCACGAAATG	ACCGACTCCA	ACGTTCTGGA	550
TAAAGTAGCA	CTGGTTTACG	GCCAGATGAA	CGAGCCACCA	GGTAACCGTC	600
TGCGCGTAGC	GCTGACCGGT	CTGACCATCG	CGGAAAAATT	CCGTGACGAA	650
40 GGCCGCGACG	TTTTGCTGTT	CGTTGATAAC	ATCTACCGTT	ATACCCTGGC	700
CGGTACCGAA	GTATCTGCAC	TGCTGGGTCG	TATGCCTTCT	GCGGTAGGTT	750
ATCAGCCAAC	TCTGGCAGAA	GAGATGGGTG	TTCTTCAGGA	GCGTATTACC	800
TCCACCAAGA	CCGGTTCTAT	CACCTCCGTA			830

45

## 2) INFORMATION FOR SEQ ID NO: 259

## (i) SEQUENCE CHARACTERISTICS:

- 50 (A) LENGTH: 931 bases  
(B) TYPE: Nucleic acid  
(C) STRANDEDNESS: Double  
(D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

55

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Chryseobacterium meningosepticum*  
(B) STRAIN: CDC B7681

50

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 259

	TTTCAGGAAG	TAGAGGAACT	ACCAAACATT	TATGACGCAC	TTGAAGTTGT	50
	CAGAGAAGGC	CAGAAAGGTC	TGATCTTAGA	AGTTGAACAA	CACATCGGTG	100
5	AGGATACAGT	GAGATGTATC	GCTATGGATG	CAACAGACGG	ACTTCAAAGA	150
	GGACAATCTG	TAATAGGACA	TGGAAGACAA	ATTACTATGC	CTATTGGTGA	200
	AGAAGTAAAT	GGTAGATTGT	TCAACGTGGT	AGGAGATGCT	ATCGACGGAC	250
	TTCAGGAATT	ATCTAAAGAC	AATGGTTTGC	CAATCCACAG	AGAAGCACCT	300
	AAATTCGATC	AGTTATCAAC	TTCTGCTGAA	GTACTATATA	CAGGTATCAA	350
10	AGTAATCGAC	CTTATCGAGC	CTTATGCAAA	AGGTGGTAAA	ATTGGTTTGT	400
	TCGGTGGTGC	TGGTGTAGGT	AAAACAGTAT	TGATCCAGGA	ATTGATTAAAT	450
	AACATTGCTA	AAGGACACGG	TGGTCTTTCT	GTATTCGCAG	GAGTAGGTGA	500
	GAGAACAAGA	GAAGGAAATG	ACCTTCTTCG	TGAGATGTTA	GAGTCTGGTA	550
	TTATTAAATA	TGGTGACGAA	TTCATGCATT	CTATGGAGAA	CGGTGGATGG	600
15	GATCTTTCTA	AAGTTGACAG	TGAGTTGATG	AAAGAGTCTA	AAGCTGCTTT	650
	CGTTTTTCGGA	CAGATGAACG	AGCCACCAGG	TGCAAGAGCA	CGTGTAGCCC	700
	TTTCTGGTCT	TACTTTAGCT	GAATACTACC	GTGATGGTGG	CGAAAGCGGA	750
	CAAGGTAGAG	ACGTTCTTTT	CTTCGTAGAC	AACATCTTCC	GTTTTACACA	800
	GGCTGGTTCT	GAGGTGTCTG	CACTTCTAGG	TCGTATGCCT	TCAGCGGTAG	850
20	GTTACCAACC	AACTCTAGCT	TCTGAGATGG	GTGCAATGCA	GGAGAGAATT	900
	ACTTCAACTA	AAAACGGATC	TATTACATCT	G		931

## 25 2) INFORMATION FOR SEQ ID NO:260

## (i) SEQUENCE CHARACTERISTICS:

- |    |     |                      |
|----|-----|----------------------|
|    | (A) | LENGTH: 726 bases    |
|    | (B) | TYPE: Nucleic acid   |
| 30 | (C) | STRANDEDNESS: Double |
|    | (D) | TOPOLOGY: Linear     |

## (ii) MOLECULE TYPE: Genomic DNA

## 35 (vi) ORIGINAL SOURCE:

- |  |     |   |
|--|-----|---|
|  | (A) | ORGANISM: <i>Citrobacter amalonaticus</i> |
|  | (B) | STRAIN: ATCC 25405                        |

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 260

40	GTATCGTACG	TACCATCGCA	ATGGGTTCTT	CCGACGGTCT	GCGTCGTGGT	50
	CTGGAAGTCA	AAGACCTCGA	GCACCCGATC	GAAGTCCCGG	TAGGTAAAGC	100
	AACCCTGGGT	CGTATCATGA	ACGTCCTGGG	TCACCCGATC	GACATGAAAG	150
	GCGATATCGG	TGAAGAAGAG	CGTTGGGCTA	TCCACCGCGC	AGCACCGTCC	200
45	TATGAAGAGC	TGTCCAGCTC	TCAGGAACTG	CTGGAAACCG	GTATCAAAGT	250
	TATCGACCTG	ATGTGTCCGT	TCGCGAASGG	CGGTAAAGTG	GGTCTGTTCC	300
	GTGGTGCGGG	TGTAGGTAAA	ACCGTAAACA	TGATGGAGCT	TATCCGTAAC	350
	ATCGCGATCG	AGCACTCCGG	TTACTCCGTG	TTTGCGGGCG	TAGGTGAACG	400
	TACTCGTGAG	GGTAACGACT	TCTACCACGA	AATGACCGAC	TCCAACGTTC	450
50	TGGATAAAGT	ATCCCTGGTA	TATGGCCAGA	TGAACGAGCC	GCCGGGAAAC	500
	CGTCTGCGCG	TTGCACTGAC	CGGTCTGACC	ATGGCAGAGA	AATTCCGTGA	550
	CGAAGGTCGT	GACGTACTGC	TGTTCGTCGA	TAACATCTAT	CGTTACACCC	600
	TGGCCGGTAC	GGAAGTTTCC	GCACTGCTGG	GTCGTATGCC	ATCAGCGGTA	650
	GGTTACCAGC	CGACCCCTGG	GGAAGAGATG	GGTGTTCCTG	AGGAACGTAT	700
55	CACTTCTACC	AAAACCGGTT	CTATCA			726

## 2) INFORMATION FOR SEQ ID NO: 261

50

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 812 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Citrobacter braakii*  
 (B) STRAIN: ATCC 43162

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 261

```

15  GCCGTACCGC GCGTGTACGA TGCTCTTGAG GTTATGAATG GTAAAGAGAG      50
    CCTGGTGCTG GAAGTTCAGC AGCAGCTCGG CGGCGGTATC GTACGTACCA      100
    TCGCCATGGG TTCTTCCGAC GGTCTGCGTC GTGGTCTGGA AGTTAAAGAT      150
    CTCGAGCACC CGATCGAAGT CCCGGTAGGT AAAGCAACTC TGGGTCGTAT      200
    CATGAACGTC CTGGGTCACC CGATCGACAT GAAAGGCGAT ATCGGTGAAG      250
20  AAGAGCGTTG GGCTATCCAC CGCGCGGCAC CTTCTATGA AGAGCTGTCC      300
    AGCTCTCAGG AACTGCTGGA AACCGGCATC AAAGTTATCG ACCTGATGTG      350
    TCCGTTTCGT AAGGGCGGTA AAGTTGGTCT GTTCGGTGGT GCGGGTGTAG      400
    GTAAAACCGT AAACATGATG GAGCTGATCC GTAACATCGC GATCGAACAC      450
    TCCGGTTACT CCGTGTTTGC GGGCGTGGGT GAACGTACTC GTGAGGGTAA      500
25  CGACTTCTAC CACGAAATGA CCGACTCCAA CGTTCCTGGAT AAAGTATCCC      550
    TGGTATATGG CCAGATGAAC GAGCCGCCCG GAAACCGTCT GCGCGTTGCT      600
    CTGACCGGTC TGACCATGGC AGAGAAGTTC CGTGACGAAG GTCGTGACGT      650
    TCTGCTGTTT GTTGATAACA TCTATCGTTA CACCCTGGCC GGTACAGAAG      700
    TATCCGCTCT GCTGGGTCGT ATGCCATCAG CCGTAGGCTA CCAGCCGACC      750
30  CTGGCGGAAG AGATGGGTGT TCTTCAGGAA CGTATCACCT CTACCAAAC      800
    CGGTTCTATC AC                                     812
  
```

## 35 2) INFORMATION FOR SEQ ID NO: 262

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 811 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Citrobacter koseri*  
 (B) STRAIN: ATCC 27156

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 262

```

50  GCGCGTGTA GACGCCCTTG AGGTGCAGAA TGGTAATGAA CATCTGGTGC      50
    TGGAAGTTCA GCAGCAGCTC GGTGGCGGTA TCGTACGTAC CATCGCCATG      100
    GGTTCCTCCG ACGGCCTGCG TCGTGGTCTG GATGTGAAAG ACCTTGAGCA      150
    CCCGATCGAA GTCCCGGTAG GTAAAGCAAC GCTGGGTCGT ATCATGAACG      200
55  TACTGGGCGA ACCAGTAGAC ATGAAAGGCG AGATCGGTGA AGAAGAGCGT      250
    TGGGCTATCC ACCGTGCGGC ACCGTCCTAC GAAGAGTTGT CAAACTCTCA      300
    GGAAGTGCTG GAAACCGGTA TCAAAGTTAT CGACCTGATG TGCCCGTTCTG      350
    CGAAGGGCGG TAAAGTGGGT CTGTTCCGGT GTGCGGGTGT AGGTAAAACC      400
    GTAAACATGA TGGAGCTGAT CCGTAACATC GCGATCGAAC ACTCCGGTTA      450
50  CTCCGTGTTT GCGGGCGTAG GTGAACGTAC TCGTGAGGGT AACGACTTCT      500
  
```

	ACCACGAAAT	GACCGACTCC	AACGTTATCG	ACAAAGTATC	CCTGGTTTAC	550
	GGCCAGATGA	ACGAGCCGCC	GGGAAACCGT	CTGCGCGTTG	CGCTGACCGG	600
	CCTGACCATG	GCGGAGAAAT	TCCGTGACGA	AGGTCGTGAC	GTTCTGCTGT	650
	TCGTCGACAA	CATCTACCGT	TACACCCTGG	CCGGTACGGA	AGTATCCGCA	700
5	CTGCTGGGTC	GTATGCCTTC	AGCGGTAGGT	TACCAGCCGA	CCCTGGCGGA	750
	AGAGATGGGT	GTTTTGCAGG	AACGTATCAC	CTCCACCAAA	ACCGGTTCTA	800
	TCACCTCCGT	A				811

10

## 2) INFORMATION FOR SEQ ID NO: 263

## (i) SEQUENCE CHARACTERISTICS:

- 15 (A) LENGTH: 816 bases  
(B) TYPE: Nucleic acid  
(C) STRANDEDNESS: Double  
(D) TOPOLOGY: Linear

20

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Citrobacter farmeri*  
(B) STRAIN: ATCC 51112

25

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 263

	GATGCCGTAC	CGCGCGTGTA	CGATGCTCTT	GAGGTTATGA	ATGGTAAAGA	50
	GAGTCTGGTG	CTGGAAGTTC	AGCAGCAGCT	CGGCGGCGGT	ATCGTACGTA	100
	CCATCGCGAT	GGGTTCTTCC	GACGGTCTGC	GTCGTGGTCT	GGAAGTAAAA	150
30	GACCTCGAAC	ACCCGATCGA	AGTCCC GGTA	GGTAAAGCAA	CTCTGGGTCG	200
	TATCATGAAC	GTCCTGGGTC	ACCCGATCGA	CATGAAAGGC	GATATCGGTG	250
	AAGAAGAGCG	TTGGGCTATC	CACCGCGCAG	CGCCATCCTA	TGAAGAGCTG	300
	TCCAGCTCTC	AGGAACTGCT	GGAAACCGGT	ATCAAAGTTA	TCGACCTGAT	350
	GTGTCCGTTT	GCGAAGGGCG	GTAAAGTCGG	TCTGTTCGGT	GGTGCGGGTG	400
35	TAGGTAAAC	CGTAAACATG	ATGGAAGTCA	TCCGTAACAT	CGCGATCGAG	450
	CACTCCGGTT	ACTCCGTGTT	TGCGGGCGTA	GGTGAACGTA	CTCGTGAGGG	500
	TAACGACTTC	TACCACGAAA	TGACCGATTG	CAACGTTCTG	GATAAAGTAT	550
	CCCTGGTATA	TGGCCAGATG	AACGAGCCGC	CGGGAAACCG	TCTGCGCGTT	600
	GCGCTGACCG	GTCTGACCAT	GGCAGAGAAA	TTCCGTGACG	AAGGTCGTGA	650
40	CGTACTGCTG	TTCGTCGATA	ACATCTATCG	TTACACCCTG	GCCGGTACGG	700
	AAGTATCCGC	ACTGCTGGGC	CGTATGCCAT	CAGCGGTAGG	CTACCAGCCA	750
	ACCCTGGCGG	AAGAGATGGG	TGTTCTGCAG	GAACGTATCA	CTTCTACCAA	800
	AACCGGTTCT	ATTACC				816

45

## 2) INFORMATION FOR SEQ ID NO: 264

## (i) SEQUENCE CHARACTERISTICS:

- 50 (A) LENGTH: 819 bases  
(B) TYPE: Nucleic acid  
(C) STRANDEDNESS: Double  
(D) TOPOLOGY: Linear

55

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Citrobacter freundii*  
(B) STRAIN: ATCC 8090

60

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 264

	AGGATGCCGT	ACCGCGCGTG	TACGATGCTC	TTGAGGTTAT	GAATGGTAAA	50
	GAGAGCCTGG	TGCTGGAAGT	TCAGCAGCAG	CTCGGCGGCG	GTATCGTACG	100
5	TACCATCGCC	ATGGGTTCTT	CTGACGGTCT	GCGTCGTGGT	CTGGAAGTTA	150
	AAGACCTCGA	GCACCCGATC	GAAGTCCCGG	TAGGTAAAGC	AACGCTGGGT	200
	CGTATCATGA	ACGTTCTGGG	TCACCCGATC	GACATGAAAG	GCGATATCGG	250
	TGAAGAAGAG	CGTTGGGCTA	TCCACCGTGC	AGCACCTTCC	TACGAAGAGC	300
	TGTCAAGCTC	TCAGGAACTG	CTGGAAACCG	GTATCAAAGT	TATCGACCTG	350
10	ATGTGTCCGT	TCGCTAAGGG	CGGTAAAGTT	GGTCTGTTTC	GTGGTGCGGG	400
	TGTAGGTAAA	ACCGTAAACA	TGATGGAGCT	GATCCGTAAC	ATCGCGATCG	450
	AACACTCCGG	TTACTCCGTG	TTTGCGGGCG	TAGGTGAACG	TACTCGTGAG	500
	GGTAACGACT	TCTACCACGA	AATGACCGAC	TCCAACGTTC	TGGACAAAGT	550
	ATCCCTGGTA	TATGGCCAGA	TGAACGAGCC	GCCTGGAAAC	CGTCTGCGTG	600
15	TTGCGCTGAC	CGGTCTGACC	ATGGCTGAGA	AGTTCCGTGA	CGAAGGTCGT	650
	GACGTTCTGC	TGTTCTGTTA	TAACATCTAT	CGTTACACCC	TGGCCGGTAC	700
	AGAAGTATCT	GCACTGCTGG	GTCGTATGCC	ATCAGCGGTA	GGCTACCAGC	750
	CGACCCTGGC	GGAAGAGATG	GGTGTTCCTG	AGGAACGTAT	CACCTCCACC	800
20	AAAACCGGTT	CTATCACCT				819

## 2) INFORMATION FOR SEQ ID NO: 265

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 822 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Citrobacter koseri*
- (B) STRAIN: ATCC 27028

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 265

	GATGCCGTAC	CGCGCGTGTA	CGACGCCCTT	GAGGTGCAGA	ATGGTAATGA	50
40	ACATCTGGTG	CTGGAAGTTC	AGCAGCAGCT	CGGTGGCGGT	ATCGTACGTA	100
	CCATCGCCAT	GGGTTCTTCC	GACGGCCTGC	GTCGTGGTCT	GGATGTGAAA	150
	GACCTTGAGC	ACCCGATCGA	AGTCCCGGTA	GGTAAAGCAA	CGCTGGGTCG	200
	TATCATGAAC	GTA CTGGGCG	AACCAGTAGA	CATGAAAGGC	GAGATCGGTG	250
	AAGAAGAGCG	TTGGGCTATC	CACCGTGC GG	CACCGTCCTA	CGAAGAGTTG	300
45	TCAA ACTCTC	AGGAACTGTT	GGAAACCGGT	ATCAAAGTTA	TCGACCTGAT	350
	GTGTCCGTTT	GCGAAGGGCG	GTAAAGTGGG	TCTGTTCGGT	GGTGCGGGTG	400
	TAGGTAAAAC	CGTAAACATG	ATGGAGCTGA	TCCGTAACAT	CGCGATCGAA	450
	CACTCCGGTT	ACTCCGTGTT	TGCGGGCGTA	GGTGAACGTA	CTCGTGAGGG	500
	TAACGACTTC	TACCACGAAA	TGACCGACTC	CAACGTTATC	GACAAAGTAT	550
50	CCTTGGTTTA	CGGCCAGATG	AACGAGCCGC	CGGGAAACCG	TCTGCGCGTT	600
	GCGCTGACCG	GCCTGACCAT	GGCGGAGAAA	TTCCGTGACG	AAGGTCGTGA	650
	CGTTCTGCTG	TTCGTCGACA	ACATCTACCG	TTACACCCTG	GCCGGTACGG	700
	AAGTATCCGC	ACTGCTGGGT	CGTATGCCTT	CAGCGGTAGG	TTACCAGCCG	750
	ACCCTGGCGG	AAGAGATGGG	TGTTTTGCAG	GAACGTATCA	CCTCCACCAA	800
55	AACCGGTTCT	ATCACCTCCG	TA			822

## 2) INFORMATION FOR SEQ ID NO: 266

60



## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 820 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Citrobacter sedlakii*  
 (B) STRAIN: ATCC 51115

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 266

15	GATGCCGTAC	CGCGCGTGTA	CGACGCCCTT	GAGGTACAGA	ATGGTAATGA	50
	GCGTCTGGTG	CTGGAAGTTC	AGCAGCAGCT	CGGTGGCGGT	ATTGTACGTA	100
	CCATCGCCAT	GGGTTCTTCC	GACGGTCTGC	GTCGTGGTCT	GGAAGTAAAA	150
	GACCTTGAGC	ACCCGATCGA	AGTCCCGGTA	GGTAAAGCAA	CGCTGGGTCG	200
	TATCATGAAC	GTACTGGGCG	AACCAGTAGA	CATGAAAGGC	GACATCGGTG	250
20	AAGAAGAGCG	TTGGGCTATC	CACCGTGCCG	CGCCGTCCTA	TGAAGAGTTG	300
	TCTAACTCTC	AGGAACTGCT	GGAAACCGGC	ATCAAAGTTA	TCGACCTGAT	350
	GTGTCCGTTT	GCGAAGGGCG	GTAAAGTCGG	TCTGTTCCGT	GGTGCGGGCG	400
	TAGGTAAAC	CGTAAACATG	ATGGAGCTGA	TCCGTAACAT	CGCGATCGAG	450
	CACTCCGGTT	ACTCTGTGTT	TGCGGGCGTG	GGTGAACGTA	CTCGTGAGGG	500
25	TAACGACTTC	TACCACGAAA	TGACCGACTC	CAACGTTATC	GACAAAGTAT	550
	CCCTGGTGTA	CGGCCAGATG	AACGAGCCGC	CTGGAAACCG	TCTGCGCGTC	600
	GCACTGACCG	GTCTGACCAT	GGCTGAGAAG	TTCCGTGACG	AAGGTCGTGA	650
	CGTTCTGCTG	TTCGTGCGATA	ACATCTATCG	TTACACCCTG	GCCGGTACGG	700
	AAGTATCCGC	ACTGTGCGGT	CGTATGCCTT	CAGCGGTAGG	TTATCAGCCG	750
30	ACTCTGGCGG	AAGAGATGGG	TGTTCTGCAG	GAACGTATCA	CCTCAACCAA	800
	AACCGGTTCT	ATCACCTCCG				820

## 2) INFORMATION FOR SEQ ID NO: 267

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 806 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Citrobacter werkmanii*  
 (B) STRAIN: ATCC 51114

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 267

50	GCCGTACCGC	GCGTGTACGA	TGCTCTTGAG	GTTATGAATG	GTAAAGAGAG	50
	CCTGGTGCTG	GAAGTTCAGC	AGCAGCTCGG	CGGCGGTATC	GTACGTACCA	100
	TCGCCATGGG	TTCTTCCGAC	GGTCTGCGTC	GTGGTCTGGA	AGTTAAAGAC	150
	CTTGAGCACC	CGATCGAAGT	CCCGGTAGGT	AAAGCAACCC	TGGGTCGTAT	200
55	CATGAACGTC	CTGGGTCATC	CGATCGACAT	GAAAGGCGAT	ATCGGTGAAG	250
	AAGAGCGTTG	GGCTATCCAC	CGCGCAGCAC	CTACCTATGA	AGAACTGTCC	300
	AGTTCTCAGG	AACTGCTGGA	AACCGGCATC	AAAGTTATCG	ACCTGATGTG	350
	TCCGTTGCGG	AAGGGCGGTA	AAGTTGGTCT	GTTCGGTGGT	GCGGGTGTAG	400
	GTAAACCGT	AAACATGATG	GAGCTGATCC	GTAACATCGC	GATCGAACAC	450
50	TCCGGTTACT	CAGTGTTTGC	GGGCGTTGGT	GAACGTACTC	GTGAGGGTAA	500

	CGACTTCTAC	CACGAAATGA	CCGACTCCAA	CGTTCTGGAC	AAAGTATCCC	550
	TGGTATATGG	CCAGATGAAC	GAGCCGCCGG	GAAACCGTCT	GCGCGTTGCG	600
	CTGACCGGTC	TGACCATGGC	TGAGAAAGTT	CGTGACGAAG	GTCGTGACGT	650
	TCTGCTGTTT	GTTGATAACA	TCTATCGTTA	CACCCTGGCC	GGTACTGAAG	700
5	TATCTGCACT	GCTGGGTCGT	ATGCCATCAG	CGGTAGGCTA	CCAGCCAACC	750
	CTGGCGGAAG	AGATGGGTGT	TCTGCAGGAA	CGTATCACCT	CTACCAAAC	800
	CGGTTC					806

10

## 2) INFORMATION FOR SEQ ID NO: 268

## (i) SEQUENCE CHARACTERISTICS:

- 15 (A) LENGTH: 810 bases  
(B) TYPE: Nucleic acid  
(C) STRANDEDNESS: Double  
(D) TOPOLOGY: Linear

## 20 (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Citrobacter youngae*  
(B) STRAIN: ATCC 29935

## 25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 268

	GCCGTACCGC	GCGTGTACGA	TGCTCTTGAG	GTTATGAATG	GTAAAGAGAG	50
	CCTGGTGCTG	GAAGTTCAGC	AGCAGCTCGG	CGGCGGTATC	GTACGTACCA	100
	TCGCCATGGG	TTCTTCCGAC	GGTCTGCGTC	GTGGTCTGGA	AGTTAAAGAC	150
30	CTCGAGCACC	CGATCGAAGT	CCCGGTAGGT	AAAGCAACGC	TGGGTCGTAT	200
	CATGAACGTT	CTGGGTCACC	CGATCGACAT	GAAAGGCGAT	ATCGGAGAAG	250
	AAGAGCGTTG	GGCTATTAC	CGCGCAGCAC	CTTCCTATGA	AGAGCTGTCC	300
	AGCTCTCAGG	AACTGCTGGA	AACCGGCATC	AAAGTTATCG	ACCTGATGTG	350
	TCCGTTTCGCT	AAGGGCGGTA	AAGTTGGTCT	GTTCCGGTGGT	GCGGGTGTAG	400
35	GTAAAACCGT	AAACATGATG	GAGCTTATTC	GTAACATCGC	GATCGAGCAC	450
	TCCGGTTACT	CTGTGTTTGC	GGGTGTAGGT	GAACGTACTC	GTGAGGGTAA	500
	CGACTTCTAC	CACGAAATGA	CCGATTCCAA	CGTTCTGGAT	AAAGTATCCC	550
	TGGTTTATGG	CCAGATGAAC	GAGCCGCCGG	GAAACCGTCT	GCGCGTTGCG	600
	CTGACCGGTC	TGACCATGGC	TGAGAAATTC	CGTGACGAAG	GTCGTGACGT	650
40	ACTGCTGTTC	GTCGATAACA	TCTATCGTTA	TACCCTGGCC	GGTACGGAAG	700
	TATCCGCACT	GCTGGGTCGT	ATGCCATCAG	CGGTAGGTTA	CCAGCCGACC	750
	CTGGCGGAAG	AGATGGGTGT	TCTGCAGGAA	CGTATCACTT	CTACCAAAC	800
	CGGTTCTATC					810

15

## 2) INFORMATION FOR SEQ ID NO: 269

## (i) SEQUENCE CHARACTERISTICS:

- 50 (A) LENGTH: 827 bases  
(B) TYPE: Nucleic acid  
(C) STRANDEDNESS: Double  
(D) TOPOLOGY: Linear

## 55 (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Clostridium innocuum*  
(B) STRAIN: ATCC 14501

50

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 269

```

5   TTGAGAACGG AGATTTGCCG CAGCTATTGA CCGCTATTGA AATTCCTCTG      50
    AAAGACAGTG AATCTCTGAT TGTCGAAGTT GCTCAGCATA TCGGTGATGA      100
    ACGTGTCCGC TGTATCGCTA TGGGCGGTAC AGATGGTCTG GTTCGTGGAA      150
    TGGAAGCCAT TGATACAGGA TCCGCAATCC GTGTACCGGT GGGAAAAGAA      200
    ATTCTGGGAA GAATGTTCAA TGTCCTCGGA CGTGAAATTG ATGGTCTGGG      250
    ACCTGTAGGA ACGGATAACA CACTGCCGAT CCACAGACAG GCACCGGGCT      300
    TTGAGGAGCA GCAGACATCC GCAGAAATGC TGGAAACAGG AATTAAGGTC      350
10  ATTGACCTGT TATGTCCATA TTCGAAGGGT GGTAAAGATTG GTTTGTTTGG      400
    TGGTGCGGGA GTAGGTAAAA CCGTACTGAT TCAGGAGCTG ATTCATAATA      450
    TCGCCAAGGA ACATGGTGGA ATGTCCGTCG TTACCGGTGT AGGGGAGAGA      500
    ACCCGTGAAG GAAACGACAT GTATCATGAA ATGAAGGACA GCGGTGTCCT      550
    TGATAAGACC GTACTGGTTT ACGGACAGAT GAATGAATCA CCGGGTGCCA      600
15  GAATGCGTGT CGGTCTGACC GGGCTGACGA TGGCGGAATA TTTCCGTGAT      650
    CACGACCATC AGGATGTATT GCTGTTTATT GATAATATTT TCCGTTTTTAC      700
    CCAGGCGGGA AGTGAAGTAA GTGCCCTGCT GGGACGTATG CCAAGTGCAG      750
    TAGGCTATCA GCCGACACTT GCGACAGAAA TGGGACAGCT GCAGGAGCGC      800
    ATTACATCCA CGAAGGATGG TTCCATT                                827
20

```

## 2) INFORMATION FOR SEQ ID NO: 270

```

25  (i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 829 bases
    (B) TYPE: Nucleic acid
    (C) STRANDEDNESS: Double
    (D) TOPOLOGY: Linear
30
    (ii) MOLECULE TYPE: Genomic DNA

    (vi) ORIGINAL SOURCE:
    (A) ORGANISM: Clostridium perfringens
35  (B) STRAIN: ATCC 13124

```

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 270

```

40  GCAAATGATG AACTTCCTAA TATATTTAAT GCAATACACA TAAAAATGGA      50
    CGATGGAAAA ATCTTAGTTT GTGAGGTAGA GCAACACGTA GGAGACGATA      100
    TAGTTAGAAC TATAGCTATG GAAGCTACTG AAGGACTAAG AAGAGGTGTA      150
    GAAGCTGTTG ATACAGGAGC ACCTATATCA GTACCAGTTG GTGAATGCGT      200
    ATTAGGAAGA ATATTTAACG TATTAGGTAA ACCACTAGAT AGTGGAGCTG      250
    AAGTTAATAA CGAAGAAAAA TATCCAATTC ATAGACCAGC TCCATCATTT      300
45  GAAGAACAAT CAGTTGTTCC TCAAATGTTT GAGACAGGAA TAAAGGTTAT      350
    CGACCTTTTA GCACCTTACC AAAGAGGGGG AAAAATCGGT CTATTTGGAG      400
    GTGCAGGTGT TGGTAAAACA GTTCTTATCC AAGAGCTTAT AAACAACATA      450
    GCTAAAGAGC ACGGTGGACT TTCTGTATTC ACAGGAGTTG GAGAAAGATC      500
    AAGAGAAGGT AATGACCTTT ACTATGAAAT GATGGAATCA GGAGTTATAA      550
50  AAAATACAGC ATTAGTATTT GGACAAATGA ACGAACCACC TGGAGCAAGA      600
    ATGAGAGTTG CTTTAACAGG ACTTACTATG GCTGAGTACT TCAGAGACCA      650
    AGGTCAAGAC GTGTTATTAT TCATAGATAA CATATTCAGA TTCTCACAAG      700
    CTGGATCAGA GGTTCAGCT TTATTAGGAA GAATACCATC AGCTGTTGGT      750
    TACCAACCAA CTCTTGCTAC AGAGATGGGA GCTCTTCAAG AGAGAATCAC      800
55  ATCAACTACC CATGGATCAA TTACATCAG                                829

```

## 2) INFORMATION FOR SEQ ID NO: 271

50

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 bases  
(B) TYPE: Nucleic acid  
(C) STRANDEDNESS: Double  
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 271

TTGTCCACGT TGGATRTCTT CA

22

## 2) INFORMATION FOR SEQ ID NO: 272

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 818 bases  
(B) TYPE: Nucleic acid  
(C) STRANDEDNESS: Double  
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Corynebacterium diphtheriae*  
(B) STRAIN: ATCC 27010

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 272

30	CCCCGCGTGCG	GAGCTGCCGG	CACTGTACAA	CGCGTTGACT	GTCGAGGTCA	50
	CCCTCGAGGC	AGTCGCTAAG	ACCATTACCC	TTGAGGTTGC	CCAGCACTTG	100
	GGCGACAACC	TCGTTTCGCG	CGTGTCCATG	GCCCCTACCG	ACGGCCTCGT	150
	CCGTGGTGCT	GTTGTGACCG	ACTCGGGCAA	GCCAATCTCC	GTGCCAGTTG	200
35	GCGACGTTGT	TAAAGGCCAC	GTTTTCAACG	CACTGGGCGA	TTGCTTGGAT	250
	GAGCCAGGTC	TCGGCCGCGA	TGGTGAGCAG	TGGGGAATTC	ACCGCGATCC	300
	ACCACCATTC	GATCAGCTCG	AAGGTAAGAC	CGAAATCCTC	GAGACCGGTA	350
	TTAAGGTCAT	CGACTTGCTC	ACCCCTTACG	TTAAGGGCGG	CAAGATTGGT	400
	CTGTTCGGTG	GTGCAGGTGT	GGGTAAGACC	GTGCTCATCC	AGGAGATGAT	450
40	CACTCGTATT	GCTCGCGAGT	TCTCCGGTAC	CTCCGTCTTC	GCTGGCGTTG	500
	GTGAGCGTAC	CCGTGAGGGC	ACCGACCTCT	TCCTCGAAAT	GGAAGAAATG	550
	GGCGTTCTTC	AGGACACCGC	TCTCGTGTTT	GGCCAGATGG	ACGAGCCACC	600
	AGGAGTCCGT	ATGCGCGTTG	CTCTGTCCGG	TCTGACCATG	GCGGAGTACT	650
	TCCGCGATGT	TCAGCACCAG	GACGTGCTTC	TGTTTCATCGA	TAACATTTTC	700
45	CGTTTCACCC	AGGCCGGTTC	CGAGGTTTCG	ACCCTTCTTG	GTCGTATGCC	750
	TTCCGCCCGTG	GGTTACCAGC	CAACCTTGGC	TGACGAGATG	GGTGTTCTCC	800
	AGGAGCGTAT	TACCTCTA				818

## 2) INFORMATION FOR SEQ ID NO: 273

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 833 bases  
(B) TYPE: Nucleic acid  
(C) STRANDEDNESS: Double  
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Corynebacterium pseudodiphtheriticum*  
 (B) STRAIN: ATCC 10700

## 5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 273

	CGATGCCTGC	TCTGTACAAC	GCGCTGACTG	TCGAGGTCAC	CCTCGAGGCA	50
	GTCGCCAAGA	CCATCACGCT	TGAGGTTGCA	CAGCACCTCG	GCGATAACCT	100
	GATCCGGACC	ATTGCGTTGG	CACCTACGGA	CGGTCTCGTC	CGTGGCGCTG	150
10	AGGTTATCGA	CACCTGGTAAG	CCAATTACTG	TTCCCGTCGG	CGATGCCGTC	200
	AAAGGACACG	TCTTCAATGC	GCTCGGTGAG	TGTTTGGACG	AACCAGGATT	250
	GGGCCGCGAC	GGCGAACAGT	GGGGAATCCA	CCGCGATCCG	CCACCATTCTG	300
	ATGCGCTGGA	GGGCAAAACC	GAGATTCTGG	AGACTGGAAT	CAAGGTTATC	350
	GACCTCCTTA	CCCCTTACGT	TAAGGGTGCG	AAAATTGGTC	TGTTTCGGTGG	400
15	CGCCGGCGTC	GGCAAGACCG	TTCTTATCCA	GGAAATGATC	ACTCGTATCG	450
	CTCGTAACTT	CTCCGGTACT	TCCGTGTTTCG	CCGGCGTCGG	TGAGCGTACC	500
	CGTGAGGGTA	CTGACCTGTT	CCTGGAAATG	GAAGAGATGG	GCGTGTGCA	550
	AGACACCGCC	CTTGTCTTCG	GTCAAATGGA	CGAACCACCA	GGGGTTCGTA	600
	TGCGCGTGCG	CTTGTCTGGT	CTAACCATGG	CTGAATATTT	CCGCGACGTT	650
20	CAAACACCAGG	ACGTTTTGTT	GTTTCATTGAC	AACATCTTCC	GTTTTACTCA	700
	GGCAGGTTCC	GAGGTTTCCA	CGCTGTTGGG	CCGTATGCCT	TCCGCCGTGG	750
	GTTATCAGCC	AACATTGGCT	GATGAGATGG	GTGTTTTGCA	GGAACGGATT	800
	ACCTCTACAC	GTGGTAAGTC	AATTACTTCC	CTG		833

25

## 2) INFORMATION FOR SEQ ID NO: 274

## (i) SEQUENCE CHARACTERISTICS:

- 30 (A) LENGTH: 417 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

## 35 (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Corynebacterium ulcerans*  
 (B) STRAIN: NCTC 8665

40

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 274

	CCGTGCTCAT	CCAGGAGATG	ATCACCCGTG	TGGCCCGCAA	CTTCGGCGGC	50
	ACCTCTGTGT	TCGCCGGCGT	CGGCGAGCGC	ACCCGTGAGG	GCAACGACCT	100
15	CTGGGTCGAG	ATGGACGAGG	CCGACGTGCT	CAAGGACACC	GCCCTGGTGT	150
	TCGGCCAGAT	GGACGAGCCG	CCGGGAACCC	GTCTGCGCGT	GGCCCTGTCC	200
	GCGCTGACCA	TGGCGGAGTA	CTTCCGCGAT	GTGCAGAACC	AGGACGTGCT	250
	GCTGTTCATC	GACAACATCT	TCCGCTTCTC	CCAGGCCGGC	TCCGAGGTCT	300
	CCACCCTGCT	GGGCCGCATG	CCCTCCGCGG	TGGGCTACCA	GCCGAACCTG	350
50	GCGGACGAGA	TGGGTGTGCT	GCAGGAGCGC	ATCACCTCGA	CTCGCGGCCA	400
	CTCCATCACC	TCGATGC				417

## 55 2) INFORMATION FOR SEQ ID NO: 275

## (i) SEQUENCE CHARACTERISTICS:

- 50 (A) LENGTH: 835 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

5 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Corynebacterium urealyticum*

(B) STRAIN: ATCC 43042

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 275

10  
 GGGCAGCAGC CAGCACTATT CAACGCGCTG CACGTCGAGG TTGACCTCGA 50  
 GGCAGTTGCG AAGACCATTA CCCTGGAGGT CGCACAGCAC CTGGGTGACA 100  
 ACCTGGTGCG CACCGTCTCC ATGGCCCCGA CCGACGGCCT GGTCCGCGGT 150  
 GCAGAGGTCA AGGACACCGG TAAGCCGATC TCTGTGCCAG TCGGCGATGT 200  
 15 TGTCAAGGGG CACGTCTTCA ACGCCCTGGG CGACTGCCTG GATGAGCCAG 250  
 GTCTCGGCCG CGACGGCGAG CAGTGGGGCA TCCACCGCGA GCCACCGGCA 300  
 TTCGACGAGC TCGAGGGTAA GACCGAGATC CTGGAGACCG GCGTTAAGGT 350  
 CATCGACCTG CTGACCCCTT ACGTCAAGGG CGGCAAGATT GGCCTCTTCG 400  
 GTGGTGCAGG TGTGGGTAAG ACCGTCCTGA TTCAGGAGAT GATTACCCGT 450  
 20 ATCGCCCGCG AGTTCTCCGG TACCTCCGTG TTCGCCGGCG TCGGCGAGCG 500  
 TACCCGTGAG GGTACGGACC TCTTCCTCGA GATGGAGGAG ATGGGCGTGC 550  
 TCCAGGACAC CGCGCTGGTG TTCGGTCAGA TGGATGAGCC GCCGGGAGTC 600  
 CGTATGCGCG TGGCTCTGTC CGGTCTGACC ATGGCGGAGT ACTTCCGCGA 650  
 TGTTCAAGGC CAGGACGTGC TGCTGTTCAT CGACAACATC TTCCGTTTCA 700  
 25 CCCAGGCAGG TTCTGAGGTC TCCACGCTGC TCGGCCGCAT GCCGTCCGCA 750  
 GTGGGTTACC AGCCGACCCT GGCTGACGAG ATGGGTGTTC TGCAGGAGCG 800  
 CATTACCTCC ACGAAGGGTA AGTCCATTAC CTCCC 835

30  
 2) INFORMATION FOR SEQ ID NO: 276

(i) SEQUENCE CHARACTERISTICS:

35 (A) LENGTH: 818 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

40  
 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Coxiella burnetii*

(B) STRAIN: Nine Mile phase II

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 276

CCCGTCACGC TGTCCCGAAA GTGTACGATG CTTTGCAGGT GGATGAAAAT 50  
 AATTTAACGC TCGAAGTCCA ACAGCAACTC GGGGACGGTG TCGTGCGCAC 100  
 AATTGCCATG GGCAGCACTG AGGGCTTAAA ACGCGATATC GCCGTAAAAA 150  
 50 ATACGGAAAA ACCGATTGAA GTTCCCGTAG GAAAAGAAAC TTTAGGTCGT 200  
 ATCATGAACG TGCTGGGTGA GCCGATCGAT GAGTTAGGTC CCATTAATTC 250  
 AAAAGAAAAA CTCCCTATTC ATCGTCCTGC GCCGAGCTTT ATTGAGCAAT 300  
 CTGGCGCTAC CGAATTATTA GAAACCGGTA TTAAAGTGGT CGATTTGCTT 350  
 TGCCCCTTTG CTAAGGGAGG CAAAGTGGGT CTTTTTGGAG GCGCGGGCGT 400  
 55 TGGAAAAACG GTTAATATGA TGGAATTAAT CCGTAATATC GCCATTGAAC 450  
 ACAGCGGTTA TTCTGTTTTT GCGGGTGTGG GAGAAAGAAC GCGAGAAGGC 500  
 AATGATTTTT ATCATGAAAT GAAAGAATCC AATGTCTTGG ATAAAGTGGC 550  
 GTTGGTGTAC GGACAAATGA ACGAGCCGCC AGGGAACCGC TTGCGGGTGG 600  
 GTTTGACGGG GCTTACGCTG GCGGAAGCCT TCCGTGACGA AGGACGCGAC 650  
 50 GTTCTGTTAT TTATCGATAA TATCTTTCGT TACACTTTGG CAGGGGTGA 700

AGTCTCTGCC	CTCCTCGGTC	GGATGCCATC	GGCTGTGGGT	TATCAGCCGA	750
CGTTGGCCGA	AGAGATGGGG	GCCCTGCAAG	AACGCATTAC	TTCCACTAAA	800
AAAGGGTCCA	TTACGTCG				818

5

## 2) INFORMATION FOR SEQ ID NO: 277

## (i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 829 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

15 (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Edwardsiella hoshinae*  
 (B) STRAIN: ATCC 33379

20

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 277

TTCCCGCAGG	ACGCCGTGCC	GAAGGTGTAT	AACGCACTGG	AAGTAAAAGG	50
CGGTGCCACG	AAACTGGTAC	TGGAAGTGCA	GCAGCAGCTG	GGTGGCGGCG	100
25 TAGTTCGCTG	CATCGCGATG	GGCTCTTCCG	ACGGTCTGCG	CCGTGGGCTA	150
GAGGTTGAAG	ACCAAGACCA	TCCGATCGAG	GTTCTGTGTTG	GCAAGGCGAC	200
TCTGGGCCGT	ATCATGAACG	TACTGGGTGA	TCCGGTCGAC	ATGAAGGGCG	250
AGATCGGTGA	AGAAGAGCGT	TGGGCTATCC	ATCGTGCTGC	ACCGAGCTAT	300
GAAGATCTGT	CTAACTCTCA	GGAAGTCTG	GAGACCGGCA	TTAAGGTTAT	350
30 CGACCTGATT	TGCCCGTTTCG	CTAAAGGCGG	TAAAGTGGGC	CTGTTTCGGTG	400
GGGCCGGTGT	GGGTAAGACC	GTAAACATGA	TGGAGCTTAT	CCGTAACATC	450
GCTATCGAGC	ACTCCGGTTA	CTCAGTCTTC	GCCGGTGTGG	GTGAGCGTAC	500
CCGTGAGGGT	AACGACTTCT	ACCACGAGAT	GACCGATTCC	AACGTATTGG	550
ATAAAGTTTC	TCTGGTGTAT	GGTCAGATGA	ACGAGCCACC	GGGAAACCGT	600
35 CTGCGCGTGG	CGCTGACCGG	TCTGACCATG	GCGGAGAAAT	TCCGTGATGA	650
AGGTCGTGAT	GTAAGTGTGT	TCATCGATAA	CATCTACCGT	TATACCTTGG	700
CCGGTACTGA	AGTCTCCGCT	CTGCTGGGCC	GTATGCCGTC	GGCGGTAGGT	750
TATCAGCCGA	CTCTGGCGGA	GGAAATGGGG	GTGCTGCAAG	AGCGTATTAC	800
40 CTCCACTAAG	ACCGGGTCCA	TCACCTCTG			829

## 2) INFORMATION FOR SEQ ID NO: 278

## (i) SEQUENCE CHARACTERISTICS:

- 45 (A) LENGTH: 809 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

50

(ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Edwardsiella tarda*  
 (B) STRAIN: ATCC 15947

55

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 278

GCCGTGCCGA	AGGTGTATAA	CGCACTGGAA	GTAAAAGGCG	GTGCCACGAA	50
50 ACTGGTACTG	GAAGTGCAGC	AGCAGCTGGG	TGGCGGCGTC	GTTCGCTGCA	100

	TCGCGATGGG	CTCCTCCGAC	GGTCTGCGCC	GTGGGCTGGT	GGTTGAAGAC	150
	CAAGACCATC	CGATCGAGGT	TCCGGTCGGT	AAGGCGACCC	TGGGCCGTAT	200
	CATGAACGTA	CTGGGTGATC	CGGTCGACAT	GAAGGGCGAG	ATCGGCCGAAG	250
	AAGAGCGTTG	GGCTATCCAC	CGCGCGGCGC	CGAGCTATGA	AGATCTGTCC	300
5	AACTCTCAGG	AGCTGCTGGA	GACCGGCATC	AAGGTTATCG	ACCTGATTTG	350
	CCCGTTCGCC	AAAGGCGGTA	AAGTTGGCCT	GTTCCGGTGGT	GCCGGTGTGG	400
	GTAAGACCGT	TAACATGATG	GAGCTTATCC	GTAACATCGC	TATCGAGCAC	450
	TCCGGTTACT	CCGTATTTGC	CGGTGTAGGC	GAGCGTACCC	GTGAGGGTAA	500
	CGATTCTTAC	CACGAGATGA	CCGACTCCAA	CGTATTGGAT	AAAGTTTCTC	550
10	TGGTATACGG	CCAGATGAAT	GAGCCGCCGG	GAAACCGTCT	GCGTGTGGCG	600
	TTGACCGGTC	TGACCATGGC	GGAGAAATTC	CGTGATGAAG	GTCGCGATGT	650
	GTTGTTGTTT	ATCGATAACA	TTTATCGTTA	TACCTTGGCT	GGTACCGAAG	700
	TTTCTGCTCT	GCTGGGTCGT	ATGCCGTCGG	CGGTAGGTTA	TCAGCCGACC	750
	CTGGCGGAAG	AGATGGGTGT	GTTGCAAGAG	CGTATCACCT	CAACGAAGAC	800
15	GGGCTCTAT					809

## 2) INFORMATION FOR SEQ ID NO: 279

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 840 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Eikenella corrodens*
- (B) STRAIN: ATCC 23834

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 279

35	TTTCCGCGTA	CCGCCATTCC	GCGTGTTTAC	GATGCACTCA	AACTGGTTGA	50
	TACTGATTTG	ACGCTGGAAG	TACAGCAGCA	GCTTGGTGAC	GGCGTTGTCC	100
	GTACCATTGC	GATGGGTAAG	ACAGACGGTT	TGAAACGTGG	CTTGGCTGTG	150
	CAAAATACTG	GTGCACCGAT	TACTGTGCCG	GTGGGGAAAG	CCACCCTAGG	200
	CCGCATCATG	GACGTTCTGG	GCAACCCCGT	GGACGAACAA	GGTCCGATCG	250
40	GTTCTGACCA	AACCCGTGCT	ATTCATCAAT	TTGCACCTAA	GTTTCGACGAA	300
	CTCTCCAGCA	CTACCGAATT	GTTGGAAACA	GGCATTAAAG	TGATCGATTT	350
	GCTTTGTCCG	TTTGCTAAAG	GTGGTAAAGT	GGGTCTGTTT	GGCGGTGCCG	400
	GTGTGGGCAA	AACCGTGAAC	ATGATGGAGC	TGATTAAACA	CATTGCCAAA	450
	GCGCACAGTG	GTCTTTCCGT	ATTCGCCGGT	GTGGGTGAGC	GTACTCGTGA	500
45	AGGTAACGAC	TTCTACCACG	AAATGAAAGA	CTCCAACGTG	TTGGATAAAG	550
	TGGCAATGGT	GTATGGCCAG	ATGAACGAGC	CGCCTGGTAA	CCGCTTGCGT	600
	GTTGCTCTAA	CTGGTTTGTC	GATGGCTGAA	TACTTCCGTG	ACGAAAAAGA	650
	CGAAAACGGC	AAAGGCCGTG	ACGTATTATT	CTTTGTGGAT	AATATCTACC	700
	GCTATACTCT	GGCGGGTACC	GAAGTGTCGG	CTCTGCTTGG	CCGTATGCCT	750
50	TCTGCTGTGG	GTTATCAGCC	AACTTTGGCT	GAAGAAATGG	GTCGTTTGCA	800
	GGAGCGTATT	ACCTCCACCC	AACTGGTTC	CATTACCTCT		840

## 2) INFORMATION FOR SEQ ID NO: 280

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 803 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double



(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

5 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Enterobacter agglomerans*

(B) STRAIN: ATCC 27989

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 280

10  
 GCCGTACCAC GAGTGTACGA TGCAC TTGAG GTAAAGAATG GTGAAGAGCG 50  
 TCTGGTGCTG GAAGTTCAGC AACAGCTCGG CGGTGGCGTT GTACGTACCA 100  
 TCGCAATGGG TTCTTCTGAT GGTCTGCGTC GTGGTCTGGA AGTAACGGAC 150  
 CTGGCTCACC CGATCGAAGT CCCGGTAGGT AAAGCAACAC TGGGTCGTAT 200  
 15 CATGAACGTA CTGGGCGAAC CAGTAGACAT GAAAGGCGAC ATCGGTGAAG 250  
 AAGAGCGTTG GCGGATCCAC CGTGCAGCAC CGTCTTACGA AGAGTTGTCA 300  
 AACTCTCAGG AACTGCTGGA AACC GGATATC AAAGTTATCG ACCTGATGTG 350  
 TCCGTTTCGT AAGGGCGGTA AAGTGGGTCT GTTCGGTGGT GCGGGTGTAG 400  
 GTAAACCCTG AAACATGATG GAGCTTATTC GTAACATCGC GATCGAGCAC 450  
 20 TCCGGTTACT CTGTGTTTGC GGGCGTAGGT GAACGTACTC GTGAGGGTAA 500  
 CGACTTCTAC CACGAAATGA CCGACTCCAA CGTTATCGAC AAAGTATCCC 550  
 TGGTGTATGG TCAGATGAAC GAGCCGCCCG GAAACCGTCT GCGCGTTGCG 600  
 CTGACCGGTC TGACCATGGC TGAGAAGTTC CGTGACGAAG GTCGTGACGT 650  
 ACTGTTGTTT GTTGACAACA TCTACCGTTA CACCCTGGCC GGTACGGAAG 700  
 25 TATCCGCACT GCTGGGCCGT ATGCCTTCTG CGGTAGGTTA TCAGCCGACG 750  
 CTGGCGGAAG AGATGGGCGT TCTGCAGGAA CGTATCACCT CCACCAAAAC 800  
 CGG 803

30  
 2) INFORMATION FOR SEQ ID NO: 281

(i) SEQUENCE CHARACTERISTICS:

35 (A) LENGTH: 833 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

40  
 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Enterobacter amnigenus*

(B) STRAIN: ATCC 33072

45  
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 281

CGAATTCCCT CAGGATGCCG TACCGCGCGT GTACGATGCT CTTGAGGTAC 50  
 AGAATGGTAA CGAGAGTCTG GTGCTGGAAG TTCAGCAGCA GCTCGGTGGT 100  
 GGTATCGTAC GTACTATCGC CATGGGTTCT TCCGACGGTC TGCCTCGTGG 150  
 50 TCTGGCTGTT AAAGATCTCG AACACCCGAT CGAAGTCCCG GTAGGTAAAG 200  
 CAACACTGGG TCGTATCATG AACGTTTTGG GTCAACCAAT CGACATGAAA 250  
 GGCGACATCG GTGAAGAAGA CCGTTGGGCA ATCCACCGTG CAGCACCTTC 300  
 CTATGAAGAG CTGTCTAGCT CTCAGGAACT GCTGGAAACC GGCATCAAAG 350  
 TTATCGACCT GATGTGTCCG TTCGCTAAGG GCGGTAAAGT TGGTCTGTTC 400  
 55 GGCGGTGCGG GCGTGGGTAA AACTGTAAAC ATGATGGAGC TGATCCGTAA 450  
 CATCGCGATC GAGCACTCCG GTTACTCCGT GTTTGCAGGC GTGGGTGAGC 500  
 GTACTCGTGA GGGTAACGAC TTCTACCACG AAATGACCGA TTCCAACGTT 550  
 CTGGATAAAG TATCCCTGGT TTATGGCCAG ATGAACGAGC CACCAGGAAA 600  
 CCGTCTGCGC GTTGCGCTGA CCGGTCTGAC TATGGCTGAG AAGTTCCTGTG 650  
 50 ACGAAGGTCTG TGACGTACTG CTGTTCTGTAG ATAACATCTA CCGTTACACC 700

CTGGCCGGTA	CTGAAGTATC	TGCGCTGCTG	GGCCGTATGC	CTTCAGCGGT	750
AGGTTACCAG	CCGACCCTGG	CGGAAGAGAT	GGGCGTTCTG	CAGGAACGTA	800
TCACTTCTAC	CAAACCGGT	TCTATCACCT	CCG		833

5

## 2) INFORMATION FOR SEQ ID NO: 282

## (i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 810 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

15 (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterobacter asburiae*  
 (B) STRAIN: ATCC 35953

20

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 282

GCCGTACCAC	GCGTGTACGA	CGCGCTTGAG	GTACAGAATG	GTAACGAGAG	50
CCTGGTGCTG	GAAGTTCAGC	AGCAGCTCGG	CGGCGGTATC	GTGCGTACCA	100
25 TCGCGATGGG	TTCTTCCGAC	GGTCTGCGTC	GTGGTCTGGA	AGTCAAAGAC	150
CTTGAGCACC	CGATCGAAGT	CCCGTAGGT	AAAGCAACAC	TGGGTCGTAT	200
CATGAACGTA	TTGGGTCAAC	CAATCGACAT	GAAAGGCGAC	ATCGGTGAAG	250
AAGAGCGTTG	GGCTATCCAC	CGCGCGGCAC	CTTCCTACGA	AGAGCTGTCC	300
AGCTCTCAGG	AACTGCTGGA	AACCGGTATC	AAAGTTATCG	ACCTGATGTG	350
30 TCCGTTTCGG	AAGGGCGGTA	AAGTCGGTCT	GTTCGGTGGT	GCGGGTGTTG	400
GTAAAACCGT	AAACATGATG	GAGCTGATCC	GTAACATCGC	GATCGAGCAC	450
TCCGGTTACT	CCGTGTTTGC	GGGCGTAGGT	GAACGTACTC	GTGAGGGTAA	500
CGACTTCTAC	CACGAAATGA	CCGACTCCAA	CGTTCTGGAC	AAAGTATCCC	550
TGGTTTACGG	CCAGATGAAC	GAGCCACCAG	GAAACCGTCT	GCGCGTTGCG	600
35 CTGACCGGTC	TGACGATGGC	TGAGAAGTTC	CGTGATGAAG	GCCGTGACGT	650
TCTGCTGTTT	GTTGATAACA	TCTATCGTTA	CACCTGGCC	GGTACGGAAG	700
TATCTGCACT	GCTGGGTCGT	ATGCCTTCAG	CGGTAGGTTA	CCAGCCTACG	750
CTGGCGGAAG	AGATGGGTGT	TCTTCAGGAA	CGTATCACCT	CTACCAAAC	800
CGGTTCTATC					810

40

## 2) INFORMATION FOR SEQ ID NO: 283

## (i) SEQUENCE CHARACTERISTICS:

- 45 (A) LENGTH: 811 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

50

(ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterobacter cancerogenus*  
 (B) STRAIN: ATCC 35317

55

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 283

GCCGTACCGC	GCGTGTACGA	TGCTCTTGAG	GTACAGAATG	GTAACGAGAG	50
60 CCTGGTGCTG	GAAGTTCAGC	AGCAGCTCGG	CGGCGGTATC	GTACGTACTA	100

	TCGCCATGGG	TTCTTCCGAC	GGTCTGCGTC	GTGGTCTGGA	AGTAAAAGAC	150
	CTTGAGCACC	CGATCGAAGT	CCCGGTAGGT	AAAGCAACAC	TGGGTCGTAT	200
	CATGAACGTA	TTGGGTCAAC	CAATCGACAT	GAAAGGCGAC	ATCGGTGAAG	250
	AAGAGCGTTG	GGCTATCCAC	CGCGCAGCAC	CTTCTTACGA	AGAGCTGTCC	300
5	AGCTCTCAGG	AACTGCTGGA	AACCGGCATC	AAAGTTATCG	ACCTGATGTG	350
	TCCGTTTCGG	AAGGGCGGTA	AAGTCGGTCT	GTTCGGTGGT	GCGGGTGTAG	400
	GTAAAACCGT	AAACATGATG	GAGCTGATCC	GTAACATCGC	GATCGAGCAC	450
	TCCGGTTATT	CCGTGTTTGC	GGGCGTGGGT	GAACGTACTC	GTGAGGGTAA	500
	CGACTTCTAC	CACGAAATGA	CCGACTCCAA	CGTTCTGGAT	AAAGTATCCC	550
10	TGGTGTACGG	CCAGATGAAC	GAGCCACCAG	GAAACCGTCT	GCGCGTTGCG	600
	CTGACCGGCC	TGACCATGGC	TGAGAAGTTC	CGTGACGAAG	GTCGTGACGT	650
	ACTGCTGTTT	GTTGATAACA	TCTACCGTTA	CACCTTGGCC	GGTACCGAAG	700
	TATCTGCACT	GCTGGGTCGT	ATGCCTTCAG	CGGTAGGTTA	TCAGCCTACG	750
	CTGGCGGAAG	AGATGGGTGT	TCTTCAGGAA	CGTATCACCT	CAACCAAAC	800
15	CGGTTCTATC	A				811

## 2) INFORMATION FOR SEQ ID NO: 284

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 817 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterobacter cloacae*  
 (B) STRAIN: ATCC 13047

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 284

35	GCCGTACCAC	GCGTGTACGA	CGCGCTTGAG	GTACAGAATG	GTAACGAGAG	50
	CCTGGTGCTG	GAAGTTCAGC	AGCAGCTCGG	CGGCGGTATC	GTGCGTACCA	100
	TCGCGATGGG	GTCTTCCGAC	GGTCTGCGTC	GTGGTCTGGA	AGTTAAAGAC	150
	CTTGAGCACC	CGATCGAAGT	CCCGGTAGGT	AAAGCAACAC	TGGGTCGTAT	200
	CATGAACGTA	TTGGGTCAAC	CAATCGACAT	GAAAGGCGAC	ATCGGTGAAG	250
40	AAGAGCGTTG	GGCTATCCAC	CGCGCGGCAC	CTTCTTACGA	AGAGCTGTCC	300
	AGCTCTCAGG	AACTGCTGGA	AACCGGTATC	AAAGTTATCG	ACCTGATGTG	350
	TCCGTTTGGC	AAGGGCGGTA	AAGTTGGTCT	GTTCGGTGGT	GCGGGTGTAG	400
	GTAAAACCGT	AAACATGATG	GAGCTGATCC	GTAACATCGC	GATCGAGCAC	450
	TCCGGTTACT	CCGTATTTGC	GGGCGTAGGT	GAACGTACTC	GTGAGGGTAA	500
45	CGACTTCTAC	CACGAAATGA	CCGACTCCAA	CGTTCTGGAC	AAAGTATCCC	550
	TGGTTTACGG	CCAGATGAAC	GAGCCACCAG	GAAACCGTCT	GCGCGTTGCG	600
	CTGACTGGTC	TGACGATGGC	TGAGAAGTTC	CGTGACGAAG	GCCGTGACGT	650
	TCTGCTGTTT	GTTGATAACA	TCTACCGTTA	CACCTTGGCC	GGTACGGAAG	700
	TATCTGCACT	GCTGGGTCGT	ATGCCTTCAG	CGGTAGGTTA	TCAGCCTACG	750
50	CTGGCGGAAG	AGATGGGTGT	TCTTCAGGAA	CGTATCACCT	CTACCAAAC	800
	CGGTTCTATC	ACTTCCG				817

## 2) INFORMATION FOR SEQ ID NO: 285

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 766 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

5 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Enterobacter gergoviae*

(B) STRAIN: ATCC 33028

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 285

10  
 AATGAGAGCC TGGTGCTGGA AGTTCAGCAG CAGCTCGGCG GCGGTATCGT 50  
 GCGTACCATC GCAATGGGTT CTTCTGACGG TCTGCGTCGC GGTCTGGAAG 100  
 TTAAAGATCT CGAACATCCG ATCGAAGTCC CGGTAGGTAA AGCGACCCTC 150  
 GGCCGTATTA TGAACGTGCT GGGTCAGCCG GTTGATATGA AAGGCGATAT 200  
 15 CGGCGAAGAA GAGCGTTGGG CGATCCACCG CGCTGCGCCG TCCTATGAAG 250  
 AGCTCTCCAG CTCTCAGGAA CTGCTGGAAA CCGGTATCAA GGTAATGGAC 300  
 CTGATTGCGC CGTTCGCGAA GGGCGGTAAA GTCGGTCTGT TCGGCGGTGC 350  
 GGGCGTTGGT AAAACCGTAA ACATGATGGA GCTGATCCGT AACATCGCGA 400  
 TCGAGCACTC CGGCTACTCC GTGTTTGCGG GCGTGGGTGA ACGTACTCGT 450  
 20 GAGGGTAACG ACTTCTACCA CGAAATGACC GACTCCAACG TTATCGACAA 500  
 AGTATCCCTG GTGTACGGCC AGATGAACGA GCCGCCGGGA AACCGTCTGC 550  
 GCGTGGCGCT GACCGGTCTG ACCATGGCTG AGAAATTCCG TGACGAAGGT 600  
 CGTGACGTTT TGCTGTTCGT CGATAACATC TACCGCTATA CCCTCGCCGG 650  
 TACTGAAGTA TCCGCACTGC TGGGCCGTAT GCCTTCTGCA GTAGGTTACC 700  
 25 AGCCGACGCT GCGGAAGAG ATGGGTGTTC TGCAGGAACG TATCACCTCC 750  
 ACCAAAACCG GTTCTA 766

30 2) INFORMATION FOR SEQ ID NO: 286

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 805 bases

(B) TYPE: Nucleic acid

35 (C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

40 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Enterobacter hormaechei*

(B) STRAIN: ATCC 49162

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 286

45  
 GCCGTACCAC GCGTGTACGA CGCGCTTGAG GTACAGAATG GTAACGAGAG 50  
 CCTGGTGCTG GAAGTTCAGC AGCAGCTCGG CGGCGGTATC GTGCGTACCA 100  
 TCGCCATGGG TTCTTCCGAC GGTCTGCGTC GTGGTCTGGA AGTGAAAGAC 150  
 CTTGAGCACC CGATCGAAGT CCCGGTAGGT AAAGCAACGC TGGGTCGTAT 200  
 50 CATGAACGTA TTGGGTCAGC CAATCGACAT GAAAGGCGAC ATCGGTGAAG 250  
 AAGAGCGTTG GGCTATCCAC CGCGCGGCAC CTTCTACGA AGAGCTGTCC 300  
 AGCTCTCAGG AACTGCTGGA AACCGGCATC AAAGTTATCG ACCTGATGTG 350  
 TCCGTTTGCG AAGGGCGGTA AAGTTGGTCT GTTCGGTGGT GCGGGTGTAG 400  
 GTAAAACCGT AAACATGATG GAGCTGATCC GTAACATCGC GATCGAGCAC 450  
 55 TCCGGTTACT CCGTGTTCGC GGGCGTGGGT GAACGTACTC GTGAGGGTAA 500  
 CCACTTCTAC CACGAAATGA CCGACTCCAA CGTTCTGGAC AAAGTATCCC 550  
 TGGTTTACGG CCAGATGAAC GAGCCACCAG GAAACCGTCT GCGCGTTGCG 600  
 CTGACTGGCC TGACGATGGC TGAGAAGTTC CGTGACGAAG GCCGTGACGT 650  
 TCTGCTGTTT GTCGATAACA TCTACCGTTA CACCTGGCC GGTACGGAAG 700  
 50 TATCTGCACT GCTGGGTTCG ATGCCTTCAG CGGTAGGTTA TCAGCCAACG 750

CTTGCGGAAG AGATGGGTGT TCTTCAGGAA CGTATCACCT CGACCAAAAC 800  
CGGTT 805

5

## 2) INFORMATION FOR SEQ ID NO: 287

## (i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 791 bases  
(B) TYPE: Nucleic acid  
(C) STRANDEDNESS: Double  
(D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

15

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterobacter sakasaki*  
(B) STRAIN: ATCC 29544

20

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 287

25 TACGACGCCC TTGAGGTAAC GAATGGTAAT GAGCGTCTGG TGCTGGAAGT 50  
CCAGCAGCAG CTCGGCGGCG GTATCGTACG TACCATCGCG ATGGGCTCTT 100  
CCGACGGTCT GCGTCGCGGT CTGCCTGTTG CAGACCTTGA GCACCCGATC 150  
GAAGTGCCGG TAGGTAAAGC GACGCTGGGT CGTATCATGA ACGTCCTGGG 200  
TCAGCCTATC GACATGAAAG GCGACATCGG CGAAGAAGAG CGTTGGGCGA 250  
TTCATCGCGC GCGCGCGTCC TATGAAGAGC TGTCCAGCTC TCAGGAACTG 300  
CTGGAAACCG GCATCAAAGT TATCGACCTG ATGTGTCCGT TCGCGAAGGG 350  
CGGTAAAGTC GGTCTGTTTC GTGGTGCAGG TGTAGGTAAA ACCGTAAACA 400  
30 TGATGGAGCT TATTCGTAAC ATCGCGATTG AGCACTCCGG TTA CTCCGTG 450  
TTTGCGGGCG TGGGCGAACG TACCCGTGAA GGTAACGACT TCTACCACGA 500  
AATGACCGAC TCCAACGTAC TGGATAAAGT ATCCCTGGTG TACGGCCAGA 550  
TGAACGAGCC GCCGGGAAAC CGTCTGCGCG TTGCGCTGAC CGGCCTGACC 600  
ATGGCTGAGA AATTCCGTGA CGAAGGTCGT GACGTTCTGC TGTTCTGTCGA 650  
35 CAACATCTAC CGTTACACCC TGGCCGGTAC TGAAGTATCC GCACTGCTGG 700  
GCCGTATGCC TTCAGCGGTA GGTTATCAGC CGACCCTGGC GGAAGAGATG 750  
GGTGTCTG C AGGAGCGTAT CACCTCCACC AAAACCGGTT C 791

40

## 2) INFORMATION FOR SEQ ID NO: 288

## (i) SEQUENCE CHARACTERISTICS:

- 45 (A) LENGTH: 839 bases  
(B) TYPE: Nucleic acid  
(C) STRANDEDNESS: Double  
(D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

50

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus avium*  
(B) STRAIN: ATCC 14025

55

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 288

50 TTTCTTTAGA TCAATCCTTA CCAGACATCA ACAATGCGTT GATTGTTTAC 50  
AAAAAAGATA AAACAAAAGT TGTTCTTGAA GTTGCTTTGG AACTTGGTGA 100  
TGGTGTTATC CGCACAAATCG CTATGGAGGC TACTGATGGA TTGCAACGTG 150  
GAATGGAAGT TGTCGATACT GGCAAATCAA TCTCCGTTCC TGTAGGTAAA 200

	GATACTCTAG	GTCGTGTGTT	TAACGTATTA	GGTGAAACGA	TTGATAAAGA	250
	AGCACCTTTT	CCAGAAGATG	CAGAAAGAAG	CGGCATTTCAT	AAAAAGGCGC	300
	CTGCTTTTGA	AGACCTTAGT	ACAAGTAACG	AGATTTTGGG	AACAGGGATC	350
	AAGGTTATCG	ACTTATTAGC	CCCTTATTTA	AAAGGTGGGA	AAGTCGGACT	400
5	ATTCGGTGGT	GCCGGTGTG	GTAAAACCGT	TTTGATCCAA	GAATTAATTC	450
	ATAATATCGC	CCAAGAACAC	GGTGGTATTT	CAGTGTTTAC	CGGTGTTGGG	500
	GAACGTACTC	GTGAAGGGAA	CGACCTTTAT	TATGAAATGA	AAGACTCTGG	550
	CGTTATTGAG	AAAACAGCCA	TGGTGTTCGG	ACAAATGAAC	GAGCCGCCTG	600
	GTGCACGTAT	GCGTGTGTC	TTGACTGGTT	TGACATTAGC	TGAATATTTT	650
10	CGTGATGAAG	AAGGACAAGA	TGTGTTGCTA	TTTATTGACA	ACATCTTCCG	700
	CTTTACTCAA	GCCGGATCAG	AAGTTTCTGC	CTTATTAGGA	CGTATGCCAT	750
	CAGCCGTTGG	GTATCAACCA	ACTTTGGCAA	CTGAAATGGG	GCAATTACAA	800
	GAACGAATCA	CTTCAACCAA	AAAAGGTTTC	ATCACTTCA		839

15

## 2) INFORMATION FOR SEQ ID NO: 289

## (i) SEQUENCE CHARACTERISTICS:

- 20 (A) LENGTH: 847 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

## 25 (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus casseliflavus*  
 (B) STRAIN: ATCC 25788

30

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 289

	TTCTCTCTAG	ACCAATCATT	ACCAGATATC	AACAATGCGT	TGATTGTTTA	50
	CAAAAAAGAT	GAGCAGAAAA	CAAAAGTTGT	GTTAGAAGCT	GCCTTAGAAC	100
35	TTGGCGACGG	CGTTATCCGT	ACGATTGCCA	TGGAATCAAC	AGATGGCTTA	150
	CAACGAGGAA	TGGAAGTAAT	CGATACAGGC	GCCTCCATTT	CTGTTCCAGT	200
	TGGGACAGAA	ACCTTAGGAC	GGGTGTTTAA	TGTCTTAGGG	GACACCATCG	250
	ATTTAGAAGC	GCCGTTCCCT	GAAGAAGCAC	CCCGCAGTGG	GATTCACAAA	300
	AAAGCACCTG	ACTTTGATGA	ATTGTCAACA	AGTACGGAGA	TCCTTGAAAC	350
40	TGGGATCAAA	GTTATCGATT	TGTTAGCCCC	TTATTTAAAA	GGGGGGAAAG	400
	TTGGACTTTT	CGGTGGTGCC	GGTGTGTTGA	AAACCGTCTT	GATCCAAGAA	450
	TTGATCCACA	ACATCGCCCA	AGAGCATGGT	GGGATCTCTG	TCTTCACAGG	500
	TGTTGGTGAA	CGGACACGTG	AAGGAAATGA	CCTTTATAAT	GAAATGAAAG	550
	AATCTGGCGT	TATCGAAAAA	ACAGCCATGG	TGTTTGGACA	AATGAACGAA	600
45	CCACCAGGTG	CTCGGATGCG	GGTAGCCTTG	ACTGGTTTGA	CATTAGCCGA	650
	GTAATTCCGT	GATGTGGAAG	GACAAGACGT	GCTCTTGTTT	ATCGATAATA	700
	TCTTCCGCTT	CACTCAAGCA	GGTTCTGAAG	TATCTGCCTT	ACTAGGTCGG	750
	ATGCCGTCTG	CCGTTGGGTA	TCAGCCAACA	TTAGCAACTG	AGATGGGGCA	800
50	ATTACAAGAA	CGGATCACAT	CGACGAAGAA	AGGTTCCGTT	ACGTCTA	847

## 2) INFORMATION FOR SEQ ID NO: 290

## (i) SEQUENCE CHARACTERISTICS:

- 55 (A) LENGTH: 845 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

50

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Enterococcus durans*

(B) STRAIN: ATCC 19432

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 290

```

10  TTTCTTTAGA CCAATCCTTA CCAGATATCA ACAACGCTTT AGTTGTTTAT      50
    AAAAATGATG AGAAGAAATC GAAAGTTGTT CTTGAAACAG CGCTAGAATT      100
    AGGTGACGGT GTCATCCGTA CAATCGCGAT GGAATCAACA GATGGTTTAC      150
    AACGCGGAAT GGAAGTCATT GATACAGAAA AAGCAATTTC TGTACCAAGT      200
    GGTAAAGAAA CGTTAGGTCG TGTATTCAAT GTATTAGGAG ATACGATCGA      250
    TTTATCTGCA CCTTTCCTCAG AAGATGCAAA ACGTAGCGAA ATCCATAAAA      300
15  AAGCACCAAA CTTTGATGAG TTAAGTACAA GTACTGAGAT CCTTGAAACT      350
    GGGATCAAAG TTATTGACTT GCTTGCTCCT TACTTAAAAG GTGGGAAAGT      400
    TGGATTATTC GGTGGTGCCG GTGTAGGTAA AACTGTATTG ATCCAAGAAT      450
    TGATCCATAA TATCGCTCAA GAACACGGTG GTATTTCTGT ATTTACTGGT      500
    GTTGGTGAAC GTACACGTGA AGGTAATGAC CTTTATTATG AAATGAAAGA      550
20  TTCAGGAGTT ATTGAAAAAA CAGCCATGGT GTTTGGTCAA ATGAACGAAC      600
    CACCAGGTGC ACGTATGCGT GTTGCCCTGA CTGGTTTGAC GATTGCTGAA      650
    TACTTCCGTG ATGTTGAAGG GCAAGACGTG CTATTGTTTA TTGATAATAT      700
    TTTCCGTTTC ACTCAAGCCG GTTCAGAAGT TTCTGCCCTA TTAGGTCGTA      750
    TGCCTTCTGC CGTTGGGTAC CAACCAACGC TAGCAACAGA AATGGGTCAA      800
25  TTACAAGAAC GGATCACTTC AACGAAAAAA GGTTCATCA CTTCA          845

```

2) INFORMATION FOR SEQ ID NO: 291

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 840 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Enterococcus faecalis*

(B) STRAIN: ATCC 29212

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 291

```

15  TTAGATCAAT CCTTACCCGA TATTAACAAC GCTTTAGTCG TTTATAAAAA      50
    TGGCGAAGCA AAACAAAAAG TAGTACTTGA AGTCGCTTTA GAAC TAGGTG      100
    ATGGAGTGAT TCGTTCTATC GCCATGGAAT CGACAGATGG TTTACAACGT      150
    GGAATGGAAG TTATCGATAC AGGAAAATCA ATTTCA GTTC CTGTTGGTAA      200
    AGATACATTA GGTTCGTGTGT TTAACGTTTT AGGAGACACA ATTGACTTAG      250
50  AAGCGCCATT CCCTGCAGAT GCTGAACGTA GTGGGATTCA TAAAAAAGCG      300
    CCAGCATTTG ATGAATTAAG TACCAGTAAT GAAATTTTAG AAACAGGGAT      350
    TAAAGTTATT GACTTATTAG CACCTTATCT AAAAGGTGGT AAAGTCGGAC      400
    TTTTCGGTGG TGCCGGTGTG GGTAAAACCG TCTTAATTCA AGAATTAATT      450
    CATAATATTG CCCAAGAACA TGGAGGGATT TCCGTCTTTA CTGGTGTGTTGG      500
55  TGAACGGACA CGTGAAGGGA ACGATCTGTA CTATGAAATG AAAGATTTCAG      550
    GCGTTATTGA AAAACAGGCC ATGGTTTTTG GTCAAATGAA CGAACCGCCA      600
    GGTGCACGGA TGCGTGTGGC CTTAACTGGG TTAACGATTG CTGAATATTT      650
    CCGTGATGTG GAAGGACAAG ACGTGCTATT ATTTATTGAT AACATTTTCC      700
    GTTTCACCCA AGCCGGTTCA AGAGTTTCTG CCCTTTTAGG TCGGATGCCG      750
50  TCAGCCGTTG GTTACCAACC AACCTTAGCG ACTGAAATGG GACAATTACA      800

```

AGAACGGATT ACTTCAACGA AAAAAGGATC AATTACCTCT

840

## 5 2) INFORMATION FOR SEQ ID NO: 292

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 831 bases  
 (B) TYPE: Nucleic acid  
 10 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

## 15 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus faecium*  
 (B) STRAIN: ATCC 19434

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 292

20 TTTCTTTAGA CCAATCCTTA CCAGATATCA ACAACGCATT AGTTGTTTAT 50  
 AAAAATGACG AAAATAAATC AAAAGTTGTT CTTGAAGCAG CGTTAGAATT 100  
 AGGGGACGGA GTGATCCGGA CCATTGCGAT GGAATCAACA GATGGTTTAC 150  
 AAAGAGGAAT GGAAGTCATT GATACAGGCA AAGCAATCTC TGTTCCCTGTA 200  
 25 GGTAAAGAAA CATTAGGTCG CGTATTCAAC GTACTAGGAG ATACGATCGA 250  
 TTTAGAAACA CCTTTCCAG AAGATGCGGA AAGAAGCGAA ATTCATAAAA 300  
 AAGCACCAGC CTTTGACGAA TTAAGTACAA GTACAGAAAT TTTGGAAACA 350  
 GGGATCAAAG TTATCGATTT GCTTGCCCCA TATTTAAAAG GTGGGAAAGT 400  
 CGGACTATTC GGTGGTGCCG GTGTTGGTAA AACCGTACTG ATCCAAGAAC 450  
 30 TGATCCATAA TATCGCCCAA GAACATGGTG GTATTTCTGT ATTTACCGGT 500  
 GTAGGTGAAC GTACTCGTGA AGGTAATGAC TTGTATTATG AAATGAAAGA 550  
 TTCAGGAGTT ATCGAAAAAA CAGCCATGGT GTTCGGACAA ATGAACGAAC 600  
 CACCAGGTGC ACGTATGCGT GTTGCTTTGA CTGGTTTGAC GATTGCGGAA 650  
 TATTTCCGTG ATGTAGAAGG TCAAGATGTA CTGTTGTTTA TCGACAACAT 700  
 35 TTTCCGTTTC ACTCAAGCTG GATCTGAAGT ATCAGCCTTG TTAGGACGGA 750  
 TGCCTTCTGC GGTGTTTAT CAACCAACAT TGGCAACAGA AATGGGTCAA 800  
 TTGCAAGAAC GTATCACATC TACGAAAAA G 831

## 40 2) INFORMATION FOR SEQ ID NO: 293

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 826 bases  
 45 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

## 50 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus gallinarum*  
 (B) STRAIN: ATCC 49573

## 55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 293

CCTTACCAGA TATCAACAAT GCGTTGATCG TTTACAAAAA AGACGAGAAA 50  
 AAAACAAAAG TAGTATTGGA AGCCGCTTTA GAACTAGGGG ATGGTGTGAT 100  
 CCGCACCATC GCAATGGAAT CTACAGACGG TTTGCAACGA GGAATGGAAG 150  
 60 TCATCGATAC CGGTGCCTCA ATCTCTGTCC CTGTAGGAAC AGATACTCTA 200

175



	GGCCGAGTAT	TTAATGTACT	AGGCGATACT	ATCGACTTGG	AAGCACCATT	250
	CCCAGAAGAT	GCCAAACGTA	GTGGCATCCA	CAAAAAAGCC	CCAGATTTTCG	300
	ATGAATTGTC	AACAAGTACA	GAAATCCTTG	AAACTGGGAT	CAAAGTTATC	350
	GATTTATTAG	CTCCTTACTT	AAAAGGTGGT	AAAGTCGGCT	TGTTCCGGTGG	400
5	TGCCGGTGTT	GGTAAAACCG	TATTGATTCA	AGAATTGATT	CACAATATCG	450
	CTCAAGAGCA	TGGGGGAATT	TCAGTATTTA	CCGGTGTGTT	CGAACGGACG	500
	CGTGAAGGTA	ATGACTTGTA	TTATGAAATG	AAAGAATCAG	GCGTTATCGA	550
	AAAGACAGCC	ATGGTTTTTCG	GTCAAATGAA	TGAACCACCA	GGTGCCCGGA	600
	TGCGGGTTGC	TTTGACTGGT	TTGACCATTG	CTGAGTATTT	CCGTGACGTT	650
10	GAAGGACAAG	ATGTGCTCTT	GTTTATCGAT	AATATTTTCC	GTTTCACACA	700
	AGCGGGTTCT	GAAGTATCTG	CCTTGTTAGG	CCGGATGCCA	TCAGCCGTTG	750
	GTTATCAACC	AACTCTAGCA	ACTGAAATGG	GTCAATTACA	AGAACGAATC	800
	ACTTCTACGA	AAAAAGGATC	TGTAAC			826

15

## 2) INFORMATION FOR SEQ ID NO: 294

## (i) SEQUENCE CHARACTERISTICS:

- 20 (A) LENGTH: 846 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

## 25 (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus saccharolyticus*  
 (B) STRAIN: ATCC 43076

30

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 294

	TTTCTTTGGA	CCAATCCTTA	CCAGACATCA	ACAATGCGTT	GGTGGTCTAT	50
	AAAAAGAATG	ATGAAAAAAC	AAAAGTG GTA	CTTGAAACAG	CTTTAGAACT	100
35	TGGTGATGGT	GTCGTACGTA	CGATTGCTAT	GTCGTCAACA	GACGGTTTGC	150
	AACGTGGGAT	GGAAGTCATC	GATACAGGAG	CATCAATTTC	TGTTCCCTGTT	200
	GGGAAAGAGA	CATTAGGACG	TGTATTTAAC	GTTTTAGGGG	AGACTATCGA	250
	CTTAGATGGT	CCATTCCCAG	AAGAAGTAGC	ACGAGATGGT	ATTCATAAAA	300
	AGGCACCTGA	TTTTGATGAA	TTAAGTACAA	GTACGGAGAT	TCTTGAAACA	350
40	GGATTAAAG	TAATCGATTT	ATTAGCGCCT	TACTTAAAAG	GTGGGAAAGT	400
	TGGTTTATTC	GGTGGTGCCG	GTGTAGGTAA	AACGGTATTA	ATTCAAGAAT	450
	TGATTAACAA	TATTGCGCAA	GAACATGGTG	GTATTTTCAGT	ATTTGCGGGT	500
	GTTGGTGAGC	GTA CT CGTGA	AGGAAATGAC	CTTTATTATG	AAATGAAAGA	550
	GTCGGGCGTT	ATTGAGAAAA	CAGCGATGGT	TTTTGGACAA	ATGAACGAAC	600
15	CACCAGGTGC	ACGTATGCGA	GTTGCTTTAA	CTGGTTTAAAC	CATTGCAGAA	650
	TACTTCCGTG	ATGTTGAAGG	ACAAGATGTA	TTACTATTTA	TTGATAACAT	700
	TTTCCGTTTT	ACTCAAGCTG	GTT CAGAAGT	TTCAGCTTTA	TTAGGACGTA	750
	TGCCTTCAGC	GGTAGGGTAT	CAACCGACAT	TAGCAACAGA	AATGGGACAA	800
50	TTACAAGAAC	GTATTACGTC	AACGAAAAAA	GGCTCAATTA	CATCAA	846

## 2) INFORMATION FOR SEQ ID NO: 295

## (i) SEQUENCE CHARACTERISTICS:

- 55 (A) LENGTH: 803 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

50

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Escherichia fergusonii*  
 5 (B) STRAIN: ATCC 35469

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 295

	GCCGTACCGC	GCGTGTACGA	TGCTCTTGAG	GTGCAAAATG	GTAATGAGCG	50
10	TCTGGTGCTG	GAAGTTCAGC	AGCAGCTCGG	CGGTGGTATC	GTGCGTACCA	100
	TCGCAATGGG	GTCCTCCGAC	GGTCTGCGTC	GCGGTCTGGA	TGTAAAAGAC	150
	CTCGAACACC	CGATCGAAGT	CCCGGTAGGT	AAAGCGACTC	TGGGCCGTAT	200
	CATGAACGTA	CTGGGTGAAC	CGGTCGACAT	GAAAGGCGAG	ATCGGTGAAG	250
	AAGAGCGTTG	GGCGATTAC	CGCGCAGCAC	CTTCCTACGA	AGAGCTGTCA	300
15	AACTCTCAGG	AACTGCTGGA	AACCGGTATC	AAAGTTATCG	ACCTGATGTG	350
	TCCGTTTCGCT	AAGGGCGGTA	AAGTCGGTCT	GTTCCGGTGGT	GCGGGTGTAG	400
	GTAACACTGT	AAACATGATG	GAGCTTATTC	GTAACATCGC	GATCGAGCAC	450
	TCCGGTTACT	CTGTGTTTGC	GGGCGTAGGT	GAACGTACTC	GTGAGGGTAA	500
	CGACTTCTAC	CACGAAATGA	CTGACTCCAA	CGTTATCGAC	AAAGTATCCC	550
20	TGGTATATGG	CCAGATGAAC	GAGCCGCCCG	GAAACCGTCT	GCGCGTTGCA	600
	CTGACCGGCC	TGACCATGGC	TGAGAAATTC	CGTGACGAAG	GTCGTGACGT	650
	TCTGCTGTTT	GTTGACAACA	TCTATCGTTA	CACCCTGGCC	GGTACGGAAG	700
	TATCCGCACT	GCTGGGCCGT	ATGCCTTCAG	CGGTAGGTTA	TCAGCCGACT	750
	CTGGCGGAAG	AGATGGGCGT	TCTTCAGGAA	CGTATCACCT	CCACCAAAC	800
25	TGG					803

2) INFORMATION FOR SEQ ID NO: 296

30

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 822 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 35 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 40 (A) ORGANISM: *Escherichia hermannii*  
 (B) STRAIN: ATCC 33650

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 296

45	GATGCCGTAC	CGCGCGTGTA	CGATGCTCTT	GAGGTGCAAA	ATGGTGATGA	50
	GCGTCTGGTG	CTGGAAGTGC	AGCAGCAGCT	CGGCGGCGGT	ATCGTGCGTA	100
	CCATCGCAAT	GGGTTCTTCC	GACGGTCTGC	GTCGTGGTCT	GACTGTCGTC	150
	GACCTCGAGC	ACCCGATCGA	AGTCCCGGTA	GGTAAAGCGA	CCCTGGGCCG	200
	TATCATGAAC	GTGCTGGGTC	AGCCGATCGA	CATGAAAGGC	GATATCGGTG	250
50	AAGAAGAGCG	TTGGGCGATT	CACCGCGCGG	CGCCGTCCTA	TGAAGAGCTG	300
	TCCAGCTCTC	AGGAACTGCT	GGAAACCGGC	ATCAAAGTTA	TCGACCTGAT	350
	GTGTCCGTTT	GCGAAGGGCG	GTAAAGTCGG	TCTGTTCCGGT	GGTGCGGGCG	400
	TAGGTAAAAC	CGTAAACATG	ATGGAGCTGA	TCCGTAACAT	CGCGATCGAG	450
	CACTCCGGTT	ACTCTGTGTT	TGCGGGCGTG	GGTGAACGTA	CTCGTGAGGG	500
55	TAACGACTTC	TACCATGAAA	TGACCGACTC	CAACGTTCTG	GACAAAGTAT	550
	CCCTGGTTTA	CGGCCAGATG	AACGAACCGC	CGGGAAACCG	TCTGCGCGTT	600
	GCACTGACCG	GCCTGACCAT	GGCTGAGAAA	TTCCGTGACG	AAGGTCGTGA	650
	CGTTCTGTTG	TTCGTCGACA	ACATCTACCG	TTACACCCTG	GCCGGTACTG	700
	AAGTATCCCG	ACTGCTGGGC	CGTATGCCTT	CTGCGGTAGG	TTACCAGCCG	750
50	ACCCTGGCGG	AAGAGATGGG	CGTTCTGCAG	GAGCGTATCA	CCTCCACCAA	800

AACCGGTTCT ATCACCTCCG TA

## 5 2) INFORMATION FOR SEQ ID NO: 297

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 808 bases  
 (B) TYPE: Nucleic acid  
 10 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

## 15 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Escherichia vulneris*  
 (B) STRAIN: ATCC 33821

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 297

20 CCGAACGTGT ACGACGCCCT CGAAGTGACA AATGGTAATG AGCGTCTGGT 50  
 GCTGGAAGTT CAGCAGCAGC TCGGCGGCGG TATCGTACGT ACCATCGCTA 100  
 TGGGTCTTTC CGACGGTCTG CGTCGTGGTC TGGAAGTTCA GGACCTCGAG 150  
 CACCCGATCG AAGTGCCGGT AGGTAAAGCG ACCCTGGGTC GTATCATGAA 200  
 25 CGTACTGGGT CAGCCGATCG ATATGAAAGG CGACATCGGT GAAGAAGAGC 250  
 GTTGGGCTAT TCACCGTGCA GCACCGTCCT ATGAAGAGCT CTCCAGCTCT 300  
 CAGGAAGTGC TGGAAACCGG CATCAAGGTT ATCGACCTGA TGTGTCCGTT 350  
 CGCCAAGGGC GGTAAAGTCG GCCTGTTTCGG CGGCGCGGGC GTGGGTAAAA 400  
 CCGTAAACAT GATGGAGCTG ATCCGTAACA TCGCGATCGA GCACTCCGGT 450  
 30 TACTCCGTGT TTGCAGGCGT GGGTGAGCGT ACTCGTGAGG GTAACGACTT 500  
 CTACCACGAG ATGACCGACT CCAACGTTCT GGACAAAGTA TCCCTGGTGT 550  
 ACGGCCAGAT GAACGAGCCG CCGGGAAACC GTCTGCGCGT GGCCTGACC 600  
 GGCCTGACCA TGGCTGAGAA GTTCCGTGAC GAAGGTCGTG ACGTTCTGCT 650  
 GTTCGTTGAC AACATCTATC GTTACACCCT GGCCGGTACG GAAGTATCTG 700  
 35 CACTGCTGGG CCGTATGCCT TCAGCGGTAG GTTACCAGCC GACGCTGGCG 750  
 GAAGAGATGG GCGTTCTGCA GGAGCGTATC ACCTCCACCA AAACCGGTTT 800  
 TATCACCT 808

## 40 2) INFORMATION FOR SEQ ID NO: 298

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 843 bases  
 45 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

## 50 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Eubacterium lentum*  
 (B) STRAIN: ATCC 43055

## 55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 298

TTTCCCCCTG ATCAGCTGCC GCGGATTAC AACGCGCTGA CGGTTGATGC 50  
 CAAGACCCTG GCGGGCGACT TGCACCTCGT GCTCGAGGTC GAGACGCACC 100  
 TGCCGGGCAA CCTTGTCCGC TCGGTGGCCA TGAGCTCGAC GGACGGTCTC 150  
 50 GTCCGCGGCC TCGAGGTCGT CGACACGGC AACCCGATCA TGATGCCCGT 200

	GGGTCCCGAG	ACCCTGGGTC	GCATCTGGAA	CGTCATGGGC	GAGCCCGT <sup>~</sup> CG	250
	ACGAGAAGCC	GATGCCCCGAG	GTGAAGGGCT	ACATGCCCCAT	CCACCGTCCG	300
	GCTCCGGACT	ACGACGAGCT	GTCCACCACC	ACCGAGATCT	TCGAGACCGG	350
	CATCAAGGCC	ATCGACCTCG	TCGAGCCCTT	CGTCAAGGGC	GGCAAGACGG	400
5	GTCTGTTCGG	CGGCGCCGGC	GTGGGCAAGA	CGGTTATCAT	CCAGGAGCTC	450
	ATCAACAACC	TGGCCCAGGA	GCACGGCGGC	ACGTCGGTGT	TCACGGGCGT	500
	GGGCGAGCGT	ACCCGCGAGG	GTACCGACCT	CTACCTGGAG	ATGAGCGACT	550
	CGGGCGTCAT	CAACAAGACC	TGCCTCGTGT	ACGGTCAGAT	GAACGAGCCT	600
	CCGGGAGCGC	GTCTGCGCGT	GGGTCTCGCG	GGCCTCACCG	AGGCGGAGTA	650
10	CTTCCGCGAT	CAGGGCCAGG	ACGTGCTTCT	GTTCGTGGAC	AACATCTTCC	700
	GCTTCACGCA	GGCCGGCTCC	GAGGTGTCCG	CTCTGCTGGG	CCGCATGCCC	750
	TCTGCCGTGG	GTTACCAGCC	GACGCTGGCA	ACCGAGATGG	GCGACCTGCA	800
	GGAGCGCATC	ACGTCGACGT	CCACCGGCTC	CATCACGTCC	GTG	843

15

## 2) INFORMATION FOR SEQ ID NO: 299

## (i) SEQUENCE CHARACTERISTICS:

- 20 (A) LENGTH: 829 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

## 25 (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Ewingella americana*  
 (B) STRAIN: ATCC 33852

30

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 299

	TCCCTCAGGA	TGCAGTACCG	AACGTGTACA	ATGCTCTTGA	GGTAGAAAAC	50
	GGTGCCTCCA	AACTGGTTCT	GGAAGTTCAG	CAACAGTTAG	GCGGCGGCGT	100
35	TGTTTCGTTGT	ATCGCAATGG	GTACCTCAGA	CGGCCTTCGT	CGCGGTCTGA	150
	AAGTGAACAA	CCTGGAACAC	CCAATTGAAG	TTCCGGTTGG	TAAAGCGACT	200
	CTGGGTCGTA	TCATGAACGT	ATTGGGTGAA	CCAATCGACA	TGAAAGGTGA	250
	AATCGGCGAA	GAAGAACGTC	GTGCAATTCA	CCGTCCAGCG	CCTTCTTATG	300
	AAGAGCTGGC	TAACTCCCAA	GAATTGCTGG	AAACCGGTAT	CAAAGTTATG	350
40	GACCTGATGT	GTCCGTTTCG	TAAGGGCGGT	AAAGTCGGTC	TGTTTCGGTGG	400
	TGCGGGTGTT	GGTAAAACTG	TAAACATGAT	GGAGCTGATC	CGTAACATCG	450
	CGATCGAGCA	CTCCGGTTAC	TCAGTGTTTG	CAGGCGTGGG	TGAGCGTACT	500
	CGTGAGGGTA	ACGACTTCTA	CCACGAAATG	ACTGACTCCA	ACGTTATCGA	550
	CAAAGTTTCC	CTGGTCTATG	GTCAGATGAA	TGAGCCACCA	GGTAACCGTC	600
45	TGCGCGTTGC	ACTGACCGGC	CTGACCATGG	CGGAGAAATT	CCGTGATGAA	650
	GGTCGTGACG	TACTGCTGTT	CGTTGACAAC	ATTTACCGTT	ACACCCTGGC	700
	AGGTACCGAA	GTGTCCGCAC	TTCTGGGCCG	TATGCCATCG	GCGGTAGGTT	750
	ATCAGCCAAC	GCTGGCGGAA	GAGATGGGTG	CTCTGCAAGA	GCGTATCACC	800
50	TCTACCAAAA	GTGGTTCTAT	CACCTCCGT			829

## 2) INFORMATION FOR SEQ ID NO: 300

## (i) SEQUENCE CHARACTERISTICS:

- 55 (A) LENGTH: 805 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 60 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 5 (A) ORGANISM: *Francisella tularensis*  
 (B) STRAIN: LVS

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 300

```

10 AACACGCCTA AAGTATATGA TGCTTTAAAT GTAGTAGAAG CTGGTTTAGT      50
ATTAGAAGTT CAGCAACAAA TTGGTGATGG CGTAGTTCGT ACAATTGCTA      100
TGGGATCTAG TGATGGTCTT AGACGTGGTA TGGAAAGTTAA GAACACAAAT      150
GCGCCTATTT CTGTTCCAGT TGGACATGGC ACACTTGGAC GTATCATGAA      200
TGTTTTAGGT GAACCAATTG ATGAAGCTGG TCCAATTGAA TATACTGAGA      250
AAAGATCTAT CCATCAAGCT CCTCCTGCAT ATGATGAGTT AGCATTAAGT      300
15 ACAGAAATAT TAGAAACAGG TATCAAAGTA GTTGACCTTA TTTGTCCATT      350
TGCTAAGGGC GGTAAAGTTG GTTTATTTGG CGGTGCAGGT GTTGGTAAAA      400
CTGTAACGAT GATGGAACCTT ATCAACAATA TTGCAAAAGA ACATAGTGGC      450
TACTCTGTAT TTTCCGGTGT TGGTGAAAGA ACTCGTGAAG GTAATGACTT      500
CTACTATGAG ATGAAATATT CTAATGTATT GGATAAAGTA TCATTAGTAT      550
20 ATGGTCAGAT GAATGAGCCG CCTGGAAACA GATTAAGAGT AGCTCTTAGT      600
GGCTTAACAA TAGCAGAAGG ATTCCGTGAT GAAAAGCGTG ATGTTTTGAT      650
GTTTATCGAT AACATCTATC GTTATACATT AGCAGGTACA GAGGTATCGG      700
CGCTACTTGG TCGTATGCCA TCTGCTGTGG GTTATCAGCC AACGCTTGCA      750
GCTGAGATGG GTGCTTTACA GGAGCGTATT ACATCTACTA AGACAGGATC      800
25 TATTA
TATTA
805

```

2) INFORMATION FOR SEQ ID NO: 301

- 30 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 825 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 35 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 40 (A) ORGANISM: *Fusobacterium gonidiaformans*  
 (B) STRAIN: ATCC 25563

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 301

```

45 GACGAATTGC CAAAAATATA CAATGCATTA AAGGTGCAAG TTGGAGAAAA      50
AGAACTTGTA TTGGAAGTGC AACAAACATTT GGGAAATAAT GTTGTGAGAA      100
CAGTAGCGAT GGA CTCAACA GATGGATTGC TTCGAGGAAT GGAAGTAATG      150
GATACCGGAG CACCGATTAC TGTTCCAGTA GGGAAAGGCGG TTTTAGGAAG      200
AATATTGAAT GTTTTGGGAG AGCCTGTGGA TCAAAAAGGG CCTGTGGAAA      250
50 CAGAAGAATA TTTACCTATC CATAGAGAAG CACCAAAATT TGAAGAACAA      300
GAAACAGTAA CAGAAATTTT TGAAACAGGA ATTAAAGTCA TAGATTTGTT      350
AGCCCCTTAT ATCAAAGGAG GAAAGACAGG TCTATTCCGT GGAGCCGGAG      400
TAGGGAAAAC AGTTTTTAATT ATGGAATTAA TTAATAACAT TGCAAAGGGC      450
CACGGAGGAA TTTCTGTGTT TGCAGGAGTT GGAGAAAGAA CAAGAGAAGG      500
55 AAGAGATTTA TACAACGAAA TGACAGAGTC CGGAGTTTGT AATAAGACCT      550
CGTTGGTGTA TGGTCAAATG AATGAGCCGC CCGGAGCAAG ACTTCGTGTG      600
GCGTTGACAG GATTACGGT TGCTGAAAAC TTTAGAGATA AAGAAGGGCA      650
AGATGTATTG TTGTTTATCG ACAATATCTT CCGTTTCACA CAAGCAGGAT      700
CAGAAGTATC GGCTCTATTG GGAAGAATTC CATCGGCAGT AGGATATCAA      750
50 CCGAAGTTAG CGACAGAAAT GGGAACTTTA CAAGAAAGAA TTACTTCTAC      800

```

AAAATCAGGA TCTATCACTT CGGTA

## 5 2) INFORMATION FOR SEQ ID NO: 302

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 806 bases  
 (B) TYPE: Nucleic acid  
 10 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

## 15 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Fusobacterium necrophorum* subsp. *necrophorum*  
 (B) STRAIN: ATCC 25286

## 20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 302

ACAATGCATT	AAAGGTACAG	GTGGGAGAAA	GGGAACTTGT	GTTGGAAGTG	50
CAGCAACATT	TAGGAAATAA	TGTTGTCAGA	ACAGTAGCAA	TGGATTCAAC	100
AGACGGATTA	CTTCGGGGAA	TGGAAGTGAG	AGATACAGGA	GTTCCCATTA	150
25 CTGTTCCGGT	AGGAAAGGCG	GTTTTGGGAA	GAATATTAAA	TGTCTTAGGG	200
GAGCCTGTGG	ACGAAAAAGG	TCCGATAGAG	ACAGAAGAAT	ATTTACCAAT	250
ACATAGAGAA	GCACCGAAAT	TGAAGAACA	GGAAACGGTG	ACAGAAATTT	300
TTGAAACAGG	AATTAAAGTC	ATTGATTTGT	TAGCTCCTTA	TATTAAAGGA	350
GGAAAAACAG	GCCTATTCGG	AGGAGCCGGA	GTAGGAAAAA	CCGTTTTGAT	400
30 TATGGAAGTG	ATCAATAATA	TTGCAAAAGG	TCATGGAGGA	ATTTCTGTTT	450
TTGCAGGAGT	TGGAGAAAGA	ACGAGAGAGG	GAAGAGATCT	ATACAACGAA	500
ATGACAGAGT	CCGGAGTTTT	GAATAAAACT	TCTTTGGTAT	ATGGGCAAAT	550
GAATGAGCCG	CCCGGAGCAA	GACTTCGAGT	GGCTTTAACC	GGACTTACTG	600
TTGCCGAAAA	TTTCAGAGAT	AAAGAGGGAC	AGGATGTCTT	ATTGTTTATT	650
35 GACAATATTT	TCCGTTTCAC	ACAAGCAGGT	TCGGAAGTAT	CGGCACTTTT	700
GGGGAGAATT	CCTTCTGCAG	TGGGATATCA	ACCGAACTTG	GCGACAGAAA	750
TGGGAAGCTT	ACAAGAAAGA	ATTACTTCTA	CAAAATCCGG	TTCTATCACT	800
TCCGTG					806

40

## 2) INFORMATION FOR SEQ ID NO: 303

## (i) SEQUENCE CHARACTERISTICS:

- 45 (A) LENGTH: 821 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

## 50 (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Fusobacterium nucleatum* subsp. *polymorphum*  
 (B) STRAIN: ATCC 10953

55

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 303

GATGAATTGC	CTGCAATATA	TAATGCTTTA	AAAGTAAAAT	TAGAAGATAA	50
GGAACCTTGT	CTAGAAGTTG	AACAACATCT	TGGTAACAAT	GTTGTAAGAA	100
50 CTGTTGCTAT	GGATTCAACT	GATGGATTAA	AAAGAGGAAT	GGAAGTTATA	150

	GATACAGGTA	AACCAATTAC	AGTACCAGTT	GGTAAAGCTG	TTCTTGGTAG	200
	AATATTAAAT	GTTTTAGGAG	AACCTGTTGA	TAATCAAGGT	CCTATAAATG	250
	CTGAAACATT	TTTACCTATT	CATAGAGAAG	CACCAGAATT	TGATGACTTA	300
	GAAACTGAAA	CTGAAATATT	TGAAACAGGA	ATAAAAGTTA	TAGACTTATT	350
5	AGCACCATAT	ATTAAAGGTG	GAAAAATAGG	ATTATTTGGT	GGAGCTGGAG	400
	TAGGAAAAAC	AGTTTTAATA	ATGGAACTTA	TCAACAACAT	TGCAAAAAGGA	450
	CATGGAGGAA	TTTCAGTTTT	TGCAGGAGTT	GGAGAAAGAA	CAAGAGAAGG	500
	TAGAGACTTA	TATGGTGAAA	TGACTGAATC	AGGAGTTATC	ACAAAAACAG	550
	CTCTTGTTTA	TGGACAAATG	AATGAGCCAC	CTGGAGCAAG	ACTTAGAGTT	600
10	GCATTAAACAG	GGCTTACTGT	TGCAGAAAAC	TTTAGAGATA	AAGATGGGCA	650
	AGATGTTCTT	CTATTTATAG	ATAATATATT	TAGATTTACA	CAAGCAGGTT	700
	CAGAAGTTTC	AGCTTTACTT	GGAAGAATAC	CATCAGCTGT	TGGATATCAA	750
	CCAAACCTAG	CAACTGAAAT	GGGTGCTTTA	CAAGAAAGAA	TAACATCTAC	800
	AAAATCTGGT	TCAATTACAT	C			821

## 2) INFORMATION FOR SEQ ID NO: 304

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 864 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Gardnerella vaginalis*  
 (B) STRAIN: ATCC 49145

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 304

	TTCCCAGTTG	GCTATCTTCC	AGATATTTAT	AATGCTCTCA	AGGTTGATAT	50
35	CAACACCGTT	GGAAACACGG	AGGGAGATAC	CGTCCACGAG	ATTACATTGG	100
	AAGTTGAGCA	GCACCTTGGT	GATTCAACTG	TGCGAGCAGT	GGCACTTAAG	150
	CCTACGGACG	GCTTGGTCCG	TGGTGCTTTA	GTGCGAGATA	CTGGTGGCCC	200
	AATTTCTGTG	CCTGTTGGAG	ATGTTACAAA	AGGTCACGTT	TTTGACGTAA	250
	CTGGTAACAT	TTTAAACGCT	AAACCAGGCG	AAAACATTGA	GGTGACCGAG	300
40	CGCTGGCCAA	TCCACGCAA	CCCACCTGCT	TTCGATCAGC	TTGAGTCTAA	350
	GACTCAAATG	TTTGAAACAG	GCATTAAGGT	TATCGATTG	CTTACGCCTT	400
	ACGTTACAGG	CGGAAAGATT	GGTCTGTTTC	GTGGTGCAGG	CGTTGGTAAA	450
	ACTGTGTTGA	TTCAGGAGAT	GATTACGCGC	GTTGCACAGA	ACCACGGCGG	500
	TGTGTCTGTG	TTTGCTGGCG	TTGGCGAACC	TACTCGTGAG	GGTAACGATT	550
45	TGATTGGCGA	AATGGCTGAG	GCTGGCGTTT	TGGAGAAAAC	AGCGCTTGTC	600
	TTTGGTCAGA	TGGATGAGCC	TCCTGGGACT	CGTCTTCGTG	TGCCCTTTAC	650
	TGCTTTGACT	ATGGCTGAGT	ATTTCCGTGA	TGTTCAGAAT	CAGGATGTGT	700
	TGCTGTTTAT	CGACAACATC	TTCCGCTTTA	CTCAGGCAGG	TTCTGAGGTT	750
	TCCACGTTGC	TTGGTCGTAT	GCCTTCTGCA	GTTGGTTATC	AGCCAAACTT	800
50	GGCGGATGAA	ATGGGTGCGT	TGCAGGAGCG	CATTACTTCT	ACGCGCGGTC	850
	ATTCTATTAC	GTCG				864

## 2) INFORMATION FOR SEQ ID NO: 305

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 848 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

5 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Gemella haemolysans*

(B) STRAIN: ATCC 10379

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 305

10 TCGAATCAGG GCATATGCCA AATCTATTAA ACGCTTTAGA AGTTTACATA 50  
 GAAAAAGGCG ATGGGAAAAA AGAAAAATTA GTTCTTGAAG TTTCTCTTGA 100  
 AATTGGTGAT AACGTAAGTAA GAACAATCGC TATGTCATCT ACTGATGGAT 150  
 TAAATAGGGG AGCAGAAGTA GTAGATACAG GAGCACCAAT TACAGTTCCT 200  
 15 GTAGGTAAGT ACACATTAGG TCGTGTGTTT AACGTATTAG GTGAAGCAGT 250  
 TGACCACGGT GAAGAAGCAG GAGCAGAAGT TCGTAAAGAT TCAATTCACA 300  
 AAGAAGCTCC AACATTTCGAT GAATTATCAA CTCACGTTGA GGTTCCTGAA 350  
 ACAGGTATTA AAGTTATCGA CTTACTTGCA CCATATATTA AAGGTGGTAA 400  
 AATCGGTCTT TTCGGTGGTG CGGGAGTTGG TAAACGGTT CTTATCCAAG 450  
 20 AACTTATCAA CAACGTTGCG CAACAACACG GTGGATTATC AGTATTCACA 500  
 GGTGTAGGTG AGCGTACTCG TGAAGGAAAT GACTTATACT ATGAAATGAA 550  
 AGATTCTGGT GTTATTAACA AAACAGCCAT GGTATTCGGA CAAATGAACG 600  
 AACCACCAGG TGCTCGTATG CGTGTAGCAT TAACAGGATT AACAATGGCG 650  
 GAATACTTCC GTGATGAAGA AGGACAAGAC GTGCTTCTAT TCATCGATAA 700  
 25 CATTTTCCGT TTCACACAAG CAGGTTCTGA GGTTTCTGCG TTATTAGGAC 750  
 GTATGCCATC AGCCGTTGGT TACCAACCAA CACTTGCTAC AGAGATGGGA 800  
 CGTTTACAAG AACGTATAAC ATCAACTAAA AAAGGTTCTG TTACATCT 848

30 2) INFORMATION FOR SEQ ID NO: 306

(i) SEQUENCE CHARACTERISTICS:

35 (A) LENGTH: 848 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

40 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Gemella morbillorum*

(B) STRAIN: ATCC 27824

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 306

TCGAATCAGG GCATATGCCT AATCTACTAA ACGCTTTAGA AGTTTATATA 50  
 GAAAAAGGCG ATGGAAAAAA AGAAAAATTA GTTCTTGAAG TTTCTCTTGA 100  
 AATCGGGGAT AATGTCGTAA GAACTATTGC GATGTCATCT ACTGATGGAT 150  
 50 TAAACAGAGG GGCAGAAGTA GTTGATACTG GAGCGCCAAT TACAGTGCCA 200  
 GTAGGTAAGT ATACATTAGG ACGTGTGTTT AACGTATTAG GTGAAGCAGT 250  
 TGACCACGGA GAAGAAGCTG GAGCAGAAGT TCAAAAAGAA TCTATTACATA 300  
 AAGAAGCTCC AACTTTCGAA GAATTATCAA CACATGTTGA GGTATTAGAA 350  
 ACAGGTATTA AAGTTATCGA CCTTCTTGCA CCATATATTA AAGGTGGTAA 400  
 55 GATTGGACTA TTCGGTGGTG CTGGAGTTGG GAAAACAGTT CTTATCCAAG 450  
 AACTTATTAA CAACGTAGCA CAACAACACG GAGGACTTTC AGTATTTACT 500  
 GGGGTAGGTG AACGTAAGT TGAAGGTAAC GACTTGTAAT ATGAAATGAA 550  
 AGACTCTGGA GTTATTAATA AAAGTGGCAT GGTATTTGGT CAAATGAATG 600  
 AGCCACCAGG TGCACGTATG CGTGTGTCCT TAACAGGATT AACAATGGCA 650  
 50 GAGTACTTCC GTGATGAAGA AGGACAAGAC GTACTATTAT TTATCGATAA 700



TATCTTCCGT	TTCACACAAG	CAGGGTCTGA	GGTATCTGCA	TTATTAGGGC	750
GTATGCCTTC	AGCCGTTGGA	TATCAACCAA	CTCTTGCAAC	AGAAATGGGA	800
CGTCTTCAAG	AACGTATTAC	ATCAACTAAA	AAAGGATCTG	TTACATCT	848

5

## 2) INFORMATION FOR SEQ ID NO: 307

## (i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 813 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

15 (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Haemophilus ducreyi*  
 (B) STRAIN: DSM 8925

20

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 307

GATGCAGTAC	CAAAAGTATA	TGATGCTTTA	AAAGTTGAAT	CAGGTTTAAC	50
CTTAGAAGTT	CAACAACAAT	TAGGTGGTGG	TTTAGTACGT	TGTATCGCAT	100
25 TAGGTACCTC	AGATGGTTTA	AAGCGTAGCT	TAAAGGTTGT	AAATACAGGT	150
AACCTTATTC	AAGTTCCTGT	AGGCACTAAA	ACATTAGGCC	GTATTATGAA	200
TGTATTAGGC	GAACCAATTG	ATGAAAAAGG	ACCTATTAGC	GAAGAAGCTC	250
GTTGGGATAT	TCATCGTGCG	GCTCCAAATT	ATGAAGAACA	GTCAAATAGT	300
ACTGAATTAC	TTGAAACCGG	TATCAAAGTT	ATTGACTTAA	TTTGTCCATT	350
30 TGCAAAAGGT	GGTAAAGTCG	GCTTATTTGG	TGGAGCTGGT	GTAGGTAAAA	400
CCGTTAATAT	GATGGAATTG	ATCCGTAATA	TTGCTATTGA	GCACTCAGGT	450
TATTCGGTTT	TTGCTGGTGT	AGGTGAGCGT	ACTCGTGAAG	GTAATGATTT	500
TTATCATGAA	ATGACGGATT	CTAATGTATT	AGATAAAGTA	TCACTAGTAT	550
ATGGTCAAAT	GAATGAACCA	CCAGGTAACC	GCCTACGTGT	TGCGTTAACA	600
35 GGTTTAACTA	TGGCTGAAAA	ATTCCGTGAT	GAAGGTCGTG	ATGTATTATT	650
TTTCGTAGAT	AATATTTATC	GTTATACTTT	AGCCGGTACA	GAAGTTTCTG	700
CTTTATTAGG	CCGTATGCCA	TCAGCGGTAG	GTTATCAACC	AACCCTTGCA	750
GAAGAAATGG	GTGTATTACA	AGAACGTATT	ACCTCAACTA	AAACTGGTTC	800
10 AATCACGGCA	GTA				813

## 2) INFORMATION FOR SEQ ID NO: 308

## (i) SEQUENCE CHARACTERISTICS:

- 15 (A) LENGTH: 826 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

50

(ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Haemophilus haemolyticus*  
 55 (B) STRAIN: ATCC 33390

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 308

TGAATTTCCA	CAAGATGCAG	TGCCAAAAGT	TTACGATGCA	TTAAAAGTTG	50
50 AATCAGGTTT	AACACTTGAG	GTGCAACAAC	AATTAGGTGG	CGGTGTGGTA	100

	CGTTGTATCG	CATTAGGTGC	TTCTGACGGT	TTAAAACGTG	GTTTAAAAGT	150
	AGAAAACACG	AATGATCCGA	TTCAAGTACC	GGTAGGCACA	AAAACCCTTG	200
	GTCGTATCAT	GAATGTATTG	GGTGAACCAA	TTGACGAACA	AGGTCCAATC	250
	GGTGAAGAAG	AGCGTTGGGC	TATCCATCGT	TCTGCACCAA	GCTATGAAGA	300
5	ACAATCAAAC	AGTACGGAAT	TATTAGAGAC	TGGTATCAAA	GTTATCGACT	350
	TAATTTGTCC	ATTTCGAAAA	GGTGGTAAAG	TTGGTCTATT	CGGTGGTGC	400
	GGTGTAGGTA	AAACCGTTAA	CATGATGGAA	TTAATCCGTA	ACATCGCGAT	450
	CGAGCACTCA	GGTACTCCG	TATTTGCGGG	TGTAGGTGAA	CGTACTCGTG	500
	AAGGTAACGA	CTTCTATCAT	GAAATGAAAG	ATTCTAACGT	ATTAGATAAA	550
10	GTATCTTTGG	TTTATGGTCA	GATGAATGAG	CCACCAGGTA	ACCGTTTACG	600
	TGTTGCGTTA	ACTGGTTTAA	CCATGGCAGA	AAAATTCCGC	GATGAAGGTC	650
	GTGATGTATT	ATTCTTCGTG	GATAATATCT	ATCGTTATAC	CCTTGCTGGT	700
	ACGGAAGTAT	CTGCGTTATT	AGGTCGTATG	CCATCTGCGG	TAGGTTACCA	750
	ACCAACTCTT	GCTGAAGAAA	TGGGTGTGTT	ACAAGAACGT	ATCACTTCAA	800
15	CCAAAACAGG	TTCTATTACA	TCTGTA			826

## 2) INFORMATION FOR SEQ ID NO: 309

20

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 809 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

25

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Haemophilus parahaemolyticus*  
 (B) STRAIN: ATCC 10014

30

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 309

35	GATGCAGTAC	CAAAAGTATA	TGATGCGTTA	AAAGTTGAAT	CAGGTTTAAAC	50
	GCTTGAAGTT	CAACAACAAT	TAGGCGGTGG	CTTAGTGCGC	TGTATCGCAT	100
	TAGGTACGTC	TGATGGTTTA	AAACGTGGCT	TAAAAGTAGA	AAATACAGGC	150
	AACCCAATTG	AAGTGCCAGT	GGGCACTAAA	ACCCTTGGTC	GTATTATGAA	200
	CGTATTGGGT	GAGCCGATTG	ACGAAAAAGG	TCCTATCGGT	GAAGAAGCAC	250
40	GCTGGGCAAT	CCACCGTGCA	GCACCAAGCT	ACGAAGAGCA	ATCAAATAGC	300
	ACGGAATTAC	TCGAAACAGG	TATCAAAGTT	ATCGACTTAA	TCTGCCCCATT	350
	CGCAAAAGGG	GGTAAAGTTG	GTTTATTTGG	TGGTGCAGGT	GTAGGTAAAA	400
	CCGTAAATAT	GATGGAGTTA	ATCCGTAACA	TCGCGATCGA	ACACTCTGGT	450
	TACTCTGTAT	TTGCAGGGGT	AGGTGAGCGT	ACTCGTGAAG	GTAATGACTT	500
45	CTACCACGAA	ATGACAGACT	CTAACGTATT	AGATAAAGTA	TCGTTAGTGT	550
	ATGGTCAAAT	GAACGAACCA	CCAGGTAACC	GTTTACGCGT	AGCTTTAACA	600
	GGCTTAACCA	TGGCGGAAAA	ATTCCGCGAT	GAAGGTCGTG	ACGTATTATT	650
	CTTCGTCGAT	AACATCTACC	GTTATACCCT	AGCAGGTACG	GAAGTGTCAG	700
	CACCTTCTCGG	TCGTATGCCA	TCTGCGGTAG	GTTATCAGCC	AACCTTAGCA	750
50	GAAGAAATGG	GTGTATTACA	AGAGCGTATC	ACTTCAACCA	AAACTGGTTC	800
	TATCACCTC					809

## 55 2) INFORMATION FOR SEQ ID NO: 310

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 824 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double

60

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

5 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Haemophilus parainfluenzae*

(B) STRAIN: ATCC 7901

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 310

10  
 CGAATTTCCA CAAGATGCAG TACCAAAAGT TTATGATGCA TTAAAAGTTG 50  
 AATCGGGTTT AACCTTGAA GTTCAACAAC AATTAGGTGG TGGTGTGGTA 100  
 CGTTGTATCG CACTGGGAGC TTCTGACGGT TTAAAACGCA GTTTAAGCGT 150  
 TGAAAATACC AATAAACCAA TTTCAGTACC GGTGTTGGTGA AAAACTCTCG 200  
 15 GTCGTATTAT GAACGTATTG GCGAACC GAATTCACCGT TCTACTCCAA GTTATGAAGA 250  
 GGTGCGGAAG AAGAATGGGC AATTCACCGT TCTACTCCAA GTTATGAAGA 300  
 ACAGTCCAAC AGTACCGAAT TATTAGAAAC CGGTATCAAA GTTATCGACT 350  
 TAATTTGTCC ATTCGCGAAG GGTGGTAAAG TTGGTTTATT CGGTGGTGGC 400  
 GGTGTAGGTA AGACCGTAAA TATGATGGAA TTAATCCGTA ATATTGCGAT 450  
 20 TGAGCACTCA GGTACTCCG TATTTGCCGG TGTAGGTGAG CGTACCCGTG 500  
 AAGGTAACGA CTTCTACCAT GAAATGACAG AATCTAACGT ATTAGACAAA 550  
 GTATCCCTAG TTTACGGACA AATGAATGAG CCGCCGGGTA ACCGTTTACG 600  
 TGTGCTTTA ACCGGTTTAA CCATGGCAGA AAAATTCCGT GACGAAGGTC 650  
 GTGATGTATT ATTCTTCGTG GATAACATCT ATCGTTATAC CCTTGCAGGG 700  
 25 ACTGAAGTAT CGGCACTTT AGGCCGTATG CCATCAGCGG TAGGTTATCA 750  
 GCCGACACTT GCAGAAGAAA TGGGTGTGTT ACAAGAACGT ATTACATCAA 800  
 CCAAACAGG TTCTATTACT TCTG 824

30

2) INFORMATION FOR SEQ ID NO: 311

(i) SEQUENCE CHARACTERISTICS:

35 (A) LENGTH: 811 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

40

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Hafnia alvei*

(B) STRAIN: ATCC 13337

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 311

GCCGTGCCTA AAGTGTATAA CGCACTTGAG GTGAAAGGCG GTGCCACTAA 50  
 ACTGGTACTG GAAGTTCAGC AGCAGCTAGG CGGCGGCGTT GTACGCTGTA 100  
 TCGCTATGGG TACTTCTGAC GGTCTGCGTC GCGGACTGGA CGTTGTTGAC 150  
 50 CTGGAGCACC CGATTGAAGT CCCAGTAGGT AAAGCGACCT TAGGCCGCAT 200  
 TATGAACGTA CTGGGTGAGC CAATTGATAT GAAGGGTGAT ATCGGCGAAG 250  
 AAGATCGCTG GGCTATTAC CGTGAAGCTC CAAGCTACGA AGAACTGTCT 300  
 AACTCGCAAG AACTGCTGGA AACTGGTATC AAGGTAATGG ACCTGATTTG 350  
 TCCGTTTCGCT AAGGGCGGTA AAGTTGGTCT GTTCGGTGGT GCGGGTGTG 400  
 55 GTAAAACAGT AAACATGATG GAGCTGATCC GTAACATCGC GATCGAGCAC 450  
 TCAGGTTACT CTGTATTTGC CGGCGTGGGT GAACGTACTC GTGAGGGTAA 500  
 CGACTTCTAC CACGAAATGA CCGACTCCAA CGTATTGGAC AAAGTATCAC 550  
 TGGTTTATGG CCAGATGAAC GAGCCACCAG GAAACCGTCT GCGCGTTGCG 600  
 CTGACCGGTC TGAATATGGC TGAGAAGTTC CGTGACGAAG GTCGTGACGT 650  
 60 ACTGCTGTTC ATCGATAACA TCTACCGTTA TACCTTGCC GGTACCGAAG 700

TATCTGCACT	GTTGGGTCGT	ATGCCTTCTG	CGGTAGGTTA	TCAGCCAACG	750
CTGGCGGAAG	AGATGGGTGT	TCTGCAAGAA	CGTATCACCT	CGACCAAAAC	800
GGGTTCAATC	A				811

5

## 2) INFORMATION FOR SEQ ID NO: 312

## (i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 831 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

## 15 (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Kingella kingae*  
 (B) STRAIN: ATCC 23330

20

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 312

GCGATGCTAT	TCCACGCGTT	TACGATGCGT	TGAAACTGGT	TGATGTGGAC	50
TTGACATTAG	AAGTGCAACA	ACAACTGGGC	GATGGCGTAG	TGCGTACCAT	100
25 TGCGATGGGT	AGTACCGATG	GTTTGAAACG	CGGCTTAGCC	GTGAACAACA	150
CAGGCGCACC	TATTACAGTG	CCTGTTGGTA	AAGCAACATT	GGGTCGTATT	200
ATGGACGTAT	TGGGTAATCC	TGTTGATGAA	GCAGGTCCAA	TTGGTTCTGA	250
CCAAACGCGT	GCTATTCACC	AACCAGCTCC	TAAATTTGAT	GAAGTGTCTA	300
GCGCAACCGA	ATTGCTGGAA	ACAGGCATCA	AAGTGATTGA	CTTGCTTTGC	350
30 CCATTTGCAA	AAGGTGGTAA	AGTAGGTTTG	TTTGGTGGTG	CAGGTGTGGG	400
CAAAACTGTG	AACATGATGG	AGTTGATTAA	CAACATTGCC	AAAGCGCACA	450
GTGGTTTGTC	TGTATTTGCA	GGCGTGGGTG	AACGTACTCG	CGAAGGTAAT	500
GACTTCTATC	ACGAGATGAA	AGATTCTAAC	GTGTTGGATA	AAGTTGCCAT	550
GGTGTATGGT	CAAATGAATG	AACCTCCTGG	CAACCGTTTG	CGCGTTGCAT	600
35 TGA CTGGTTT	GTCTATGGCA	GAACACTTCC	GTGATGAAAA	AGACGAAAAT	650
GGCAAAGGTC	GCGATGTATT	GTTCTTTGTG	GACAACATCT	ATCGCTACAC	700
ATTGGCAGGT	ACAGAAGTAT	CGGCATTGCT	GGGTCGTATG	CCCTCTGCGG	750
TAGGTTATCA	ACCAACATTG	GCAGAAGAAA	TGGGTCGTTT	GCAAGAGCGT	800
ATTACTTCAA	CGCAAACAGG	TTCGATTACT	T		831

40

## 2) INFORMATION FOR SEQ ID NO: 313

## (i) SEQUENCE CHARACTERISTICS:

- 15 (A) LENGTH: 812 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

50

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Klebsiella pneumoniae* subsp. *ozaenae*  
 55 (B) STRAIN: ATCC 11296

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 313

ATGCCGTACC	ACGCGTGTAC	GAAGCCCTTG	AGGTACAGAA	TGGTAATGAA	50
50 GTTCTGGTGC	TGGAAGTTCA	GCAGCAGCTG	GGCGGCGGTA	TCGTACGTAC	100

	CATCGCCATG	GGTTCTTCTG	ATGGTCTGCG	CCGCGGTCTG	GATGTAAAG	150
	ACCTCGAGCA	CCCGATCGAA	GTCCCGGTAG	GTAAAGCAAC	GCTGGGTCGT	200
	ATCATGAACG	TACTGGGTCA	ACCGGTTGAC	ATGAAAGGCG	ACATCGGCGA	250
	AGAAGAGCGT	TGGGCTATCC	ACCGCGCGGC	ACCGTCCTAT	GAAGAGCTGT	300
5	CCAGCTCTCA	GGAAGTCTG	GAAACCGGCA	TCAAAGTTAT	CGACCTGATG	350
	TGTCCGTTTC	CCAAGGGCGG	TAAAGTTGGT	CTGTTCGGCG	GTGCGGGTGT	400
	AGGTAAAACT	GTAAACATGA	TGGAGCTGAT	CCGTAACATC	GCGATCGAGC	450
	ACTCCGGTTA	CTCTGTGTTT	GCGGGCGTAG	GTGAGCGTAC	TCGTGAGGGT	500
	AACGACTTCT	ACCACGAAAT	GACCGACTCC	AACGTTATCG	ATAAAGTATC	550
10	CCTGGTGTAC	GGCCAGATGA	ACGAGCCGCC	GGGAAACCGT	CTGCGCGTTG	600
	CGCTGACCGG	CCTGACCATG	GCTGAGAAAT	TCCGTGACGA	AGGTCGTGAC	650
	GTAAGTCTGT	TCGTGATAAA	CATCTATCGT	TACACCCTGG	CCGGTACTGA	700
	AGTATCCGCG	CTGCTGGGTC	GTATGCCTTC	AGCGGTAGGT	TATCAGCCGA	750
	CCCTGGCGGA	AGAGATGGGC	GTTCTGCAGG	AACGTATCAC	CTCCACCAAA	800
15	ACCGGTTCTA	TC				812

## 2) INFORMATION FOR SEQ ID NO: 314

20

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 812 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

25

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Klebsiella ornithinolytica*  
 (B) STRAIN: ATCC 31898

30

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 314

35	ATGCCGTACC	GCGCGTGTAC	GATGCTCTTG	AGGTACAGAA	TGGTAATGAG	50
	AGCCTGGTGC	TGGAAGTTCA	GCAGCAGCTC	GGCGGTGGTA	TCGTACGTGC	100
	TATCGCCATG	GGTTCTTCCG	ACGGTCTGCG	TCGTGGTCTG	GAAGTTAAAG	150
	ACCTTGAGCA	CCCGATCGAA	GTCCCGGTTG	GTAAAGCAAC	GCTGGGTCGT	200
	ATCATGAACG	TGCTGGGTCA	GCCAATCGAT	ATGAAAGGCG	ACATCGGCGA	250
40	AGAAGAGCGT	TGGGCTATTC	ACCGTGCAGC	TCCGTCCTAT	GAAGAGCTGT	300
	CCAGCTCTCA	GGAAGTCTG	GAAACCGGCA	TCAAAGTTAT	CGACCTGATG	350
	TGTCCGTTTC	CTAAGGGCGG	TAAAGTTGGT	CTGTTCGGTG	GTGCGGGTGT	400
	AGGTAAAAAC	GTAAACATGA	TGGAGCTGAT	CCGTAACATC	GCGATCGAGC	450
	ACTCCGGTTA	CTCCGTGTTT	GCGGGCGTAG	GTGAACGTAC	TCGTGAGGGT	500
45	AACGACTTCT	ACCACGAAAT	GACCGACTCC	AACGTTCTGG	ATAAAGTATC	550
	CCTGGTTTAT	GGCCAGATGA	ACGAGCCGCC	GGGAAACCGT	CTGCGCGTTG	600
	CTCTGACCGG	CCTGACCATG	GCTGAGAAAT	TCCGTGACGA	AGGTCGTGAC	650
	GTTCTGCTGT	TCGTGATAAA	CATCTATCGT	TATACCCTGG	CCGGTACTGA	700
	AGTATCCGCA	CTGCTGGGTC	GTATGCCTTC	AGCGGTAGGT	TATCAGCCGA	750
50	CCCTGGCGGA	AGAGATGGGT	GTTCTGCAGG	AACGTATCAC	CTCCACCAAA	800
	ACCGGTTCTA	TC				812

## 55 2) INFORMATION FOR SEQ ID NO: 315

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 813 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double

50

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

5 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Klebsiella oxytoca*

(B) STRAIN: ATCC 33496

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 315

10  
 GTACCGCGCG TGTACGAGGC TCTTGAGGTA CAAAATGGTA GTGAGAATCT 50  
 GGTGCTGGAA GTTCAGCAGC AGCTCGGCGG CGGTATTGTT CGTACCATCG 100  
 CCATGGGTTC TTCCGACGGT CTGCGTCGCG GTCTGGAAGT CAAAGACCTC 150  
 GAGCATCCGA TCGAAGTCCC GGTAGGTAAA GCAACGCTGG GTCGTATCAT 200  
 15 GAACGTACTG GGCCAACCGG TAGACATGAA AGGCGACATC GGCGAAGAAG 250  
 AGCGTTGGGC GATTCAACGC GCAGCGCCTT CCTACGAAGA GTTGTCAAAC 300  
 TCTCAGGAAC TGCTGGAAAC CGGCATCAAA GTTATCGACC TGATGTGTCC 350  
 GTTTGC GAAG GCGGTAAAG TTGGTCTGTT CCGTGGTGCG GGTGTAGGTA 400  
 AAACCGTAAA CATGATGGAG CTGATCCGTA ACATCGCGAT CGAGCACTCC 450  
 20 GGT TACTCCG TGTTTGCGGG CGTAGGTGAA CGTACTCGTG AGGGTAACGA 500  
 CTTCTACCAC GAAATGACCG ACTCCAACGT TATCGATAAA GTATCCCTGG 550  
 TGTATGGCCA GATGAACGAG CCGCCGGGAA ACCGTCTGCG CGTTGCGCTG 600  
 ACCGGCCTGA CCATGGCTGA GAAGTTCCGT GACGAAGGTC GTGACGTTCT 650  
 GCTGTTTCGTC GATAACATCT ATCGTTACAC CCTGGCCGGT ACTGAAGTAT 700  
 25 CCGCACTGCT GGGTCGTATG CCTTCAGCGG TAGGTTACCA GCCGACTCTG 750  
 GCGGAAGAGA TGGCGTTCT GCAGGAACGT ATCACCTCCA CAAAACGGG 800  
 TTCTATCACT TCC 813

30

2) INFORMATION FOR SEQ ID NO: 316

(i) SEQUENCE CHARACTERISTICS:

35 (A) LENGTH: 822 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

40

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Klebsiella planticola*

(B) STRAIN: ATCC 33531

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 316

GATGCCGTAC CGCGCGTGTA CGATGCTCTT GAGGTACAGA ATGGTAATGA 50  
 GAGCCTGGTG CTGGAAGTTC AGCAGCAGCT CGGCGGTGGT ATCGTACGTG 100  
 CTATCGCCAT GGGTTCTTCT GACGGTCTGC GTCGTGGTCT GGAAGTTAAA 150  
 50 GACCTTGAGC ACCCGATCGA AGTCCCGGTT GGTAAAGCAA CGCTGGGTCG 200  
 TATCATGAAC GTGCTGGGTC AGCCGATCGA TATGAAAGGC GACATCGGCG 250  
 AAGAAGAGCG TTGGGCTATT CACCGCGCAG CTCCGTCTTA TGAAGAGCTG 300  
 TCCAGTTCTC AGGAACTGCT GGAAACCGGC ATCAAAGTTA TCGACCTGAT 350  
 GTGTCCGTTT GCTAAGGGCG GTAAAGTAGG TCTGTTCCGT GGTGCGGGCG 400  
 55 TAGGTAAAC CGTAAACATG ATGGAGCTGA TCCGTAACAT CGCGATCGAG 450  
 CACTCCGGTT ACTCCGTGTT TGCGGGCGTC GGTGAACGTA CTCGTGAGGG 500  
 TAACGACTTC TACCACGAAA TGACCGACTC CAACGTTCTG GATAAAGTAT 550  
 CCCTGGTTTA TGGCCAGATG AACGAGCCGC CGGGAAACCG TCTGCGCGTT 600  
 GCTCTGACCG GCCTGACCAT GGCTGAGAAA TTCCGTGACG AAGGTCGTGA 650  
 50 CGTTCTGCTG TTCGTGATA ACATCTATCG TTATACCCTG GCCGCTACTG 700

AAGTATCCGC	ACTGCTGGGT	CGTATGCCTT	CAGCGGTAGG	TTATCAGCCG	750
ACCCTGGCGG	AAGAGATGGG	TGTTCTGCAG	GAACGTATCA	CCTCCACCAA	800
AACCGTTTCT	ATCACTTCCG	TA			822

5

## 2) INFORMATION FOR SEQ ID NO: 317

## (i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 785 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

15 (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Klebsiella pneumoniae* subsp. *pneumoniae*  
 (B) STRAIN: ATCC 13883

20

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 317

AGAATGGTAA	TGAAGTTCTG	GTGCTGGAAG	TTCAGCAGCA	GCTGGGCGGC	50
GGTATCGTAC	GTACCATCGC	CATGGGTTCT	TCTGATGGTC	TGCGCCGCGG	100
25 TCTGGATGTA	AAAGACCTCG	AGCACCCGAT	CGAAGTCCCG	GTAGGTAAAG	150
CAACGCTGGG	TCGTATCATG	AACGTACTGG	GTCAACCGGT	TGACATGAAA	200
GGCGACATCG	GCGAAGAAGA	GCGTTGGGCT	ATCCACCGCG	CGGCACCGTC	250
CTATGAAGAG	CTGTCCAGCT	CTCAGGAACT	GCTGGAAACC	GGCATCAAAG	300
TTATCGACCT	GATGTGTCCG	TTCGCCAAGG	GCGGTAAAGT	TGGTCTGTTC	350
30 GGCGGTGCGG	GTGTAGGTAA	AACTGTAAAC	ATGATGGAGC	TGATCCGTAA	400
CATCGCGATC	GAGCACTCCG	GTTACTCTGT	GTTTGCGGGC	GTAGGTGAGC	450
GTA CTCTGTA	GGGTAATGAC	TTCTACCACG	AAATGACCGA	CTCCAACGTT	500
ATCGATAAAG	TATCCCTGGT	GTACGGCCAG	ATGAACGAGC	CGCCGGGAAA	550
CCGTCTGCGC	GTTGCGCTGA	CCGGCCTGAC	CATGGCTGAG	AAATTCCGTG	600
35 ACGAAGGTCG	TGACGTACTG	CTGTTTCGTCG	ATAACATCTA	TCGTTACACC	650
CTGGCCGGTA	CTGAAGTATC	CGCACTGCTG	GGTCGTATGC	CTTCAGCGGT	700
AGGTTATCAG	CCGACCCTGG	CGGAAGAGAT	GGGCGTTCTG	CAGGAACGTA	750
TCACCTCCAC	CAAACCGGT	TCTATCACCT	CCGTA		785

10

## 2) INFORMATION FOR SEQ ID NO: 318

## (i) SEQUENCE CHARACTERISTICS:

- 15 (A) LENGTH: 759 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

50 (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Kluyvera ascorbata*  
 (B) STRAIN: ATCC 33433

55

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 318

CTGGTGCTGG	AAGTTCAGCA	GCAGCTCGGC	GGCGGTATCG	TACGTWCCAT	50
CGCTATGGGT	TCTTCCGACG	GTCTGCGTCG	CGGTCTGGAT	GTAAAGATC	100
50 TCGAGCACCC	AATCGAAGTT	CCGGTMGGTA	AAGCAACMCT	GGGTCGTATC	150

	ATGAACGTAC	TGGGTCACCC	AGTMGACATG	AAAGGCGACA	TCGGTGAAGA	200
	AGAGCGTTGG	GCTATCCACC	GCGCTGCACC	TTCCTACGAA	GAGCTGTCTA	250
	GCTCTCAGGA	ATTGCTGGAA	ACCGGTATCA	AAGTTATCGA	CCTGATGTGT	300
	CCGTTGCTA	AGGGCGGTAA	AGTCGGTCTG	TTCGGTGGTG	CSGGTGTGG	350
5	TAAAACCGTA	AACATGATGG	AGCTGATCCG	TAACATCGCG	ATCGAGCACT	400
	CCGGTTACTC	CGTGTTCGCG	GGCGTAGGTG	AACGTACTCG	TGAGGGTAAC	450
	GACTTCTACC	ACGAAATGAC	CGACTCCAAC	GTTATCGATA	AAGTATCCCT	500
	GGTATATGGC	CAGATGAACG	AGCCACCGGG	AAACCGTCTG	CGCGTTGCTC	550
	TGACCGGTCT	GACCATGGCT	GAGAAATTCC	GTGACGAAGG	TCGTGACGTA	600
10	CTGCTGTTTCG	TCGATAACAT	CTATCGTTAC	ACCCTGGCCG	GTACTGAAGT	650
	ATCTGCWCTG	CTGGGTCGTA	TGCCTTCAGC	GGTAGGTTAC	CAGCCGACCC	700
	TGGCGGAAGA	GATGGGCGTT	CTGCAGGAAC	GTATCACCTC	CACCAAGACC	750
	GGTTCTATC					759

15

## 2) INFORMATION FOR SEQ ID NO: 319

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 831 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Kluyvera cryocrescens*

(B) STRAIN: ATCC 33435

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 319

	TTCCCTCAGG	ATGCCGTACC	GCGTGTGTAC	GAAGCCCTTG	AGGTTTCAGAA	50
	TGGTAATGAA	GTGCTGGTGC	TGGAAGTTCA	GCAGCAGCTC	GGCGGCGGTA	100
35	TCGTACGTAC	CATCGCTATG	GGTTCTTCCG	ACGGTCTGCG	TCGTGGTCTG	150
	GATGTAAAAG	ACCTCGAGCA	CCCGATCGAA	GTCCCGGTAG	GTAAAGCAAC	200
	ACTGGGTCGT	ATCATGAACG	TACTGGGCCA	ACCGGTAGAC	ATGAAAGGCG	250
	ACATCGGTGA	AGAAGAACGT	TGGGCTATCC	ACCGTGCAGC	ACCTTCCTAC	300
	GAAGAGCTGT	CAAGCTCTCA	GGAAGTGTCTG	GAAACCGGCA	TCAAAGTTAT	350
10	CGACCTGATG	TGTCCGTTTG	CGAAGGGCGG	TAAAGTTGGT	CTGTTCCGGTG	400
	GTGCGGGTGT	AGGTAAAACC	GTAAACATGA	TGGAGCTTAT	TCGTAACATC	450
	GCGATTGAGC	ACTCCGGTTA	TTCTGTGTTT	GCGGGCGTAG	GTGAACGTAC	500
	TCGTGAGGGT	AACGACTTCT	ACCACGAAAT	GACCGACTCC	AACGTTATCG	550
	ATAAAGTTTC	CCTGGTTTAC	GGCCAGATGA	ACGAGCCACC	AGGAAACCGT	600
15	CTGCGCGTTG	CGCTGACTGG	TCTGACTATG	GCTGAGAAGT	TCCGTGACGA	650
	AGGTCGCGAC	GTAAGTGTGT	TCGTGATAAA	CATCTATCGT	TACACCCTGG	700
	CCGGTACAGA	AGTATCTGCA	CTGCTGGGTC	GTATGCCTTC	AGCGGTAGGT	750
	TACCAGCCGA	CTCTGGCGGA	AGAGATGGGC	GTTCTGCAGG	AACGTATCAC	800
50	CTCCACCAAA	ACCGTTCTA	TCACCTCCGT	A		831

50

## 2) INFORMATION FOR SEQ ID NO: 320

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 810 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

50



(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 5 (A) ORGANISM: *Kluyvera georgiana*  
 (B) STRAIN: ATCC 51603

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 320

```

10 GCCGTACCGC GCGTGTACGA AGCCCTTGAG GTACAGAATG GTAATGAAGT      50
   GCTGGTGTCTG GAAGTTCAGC AGCAGCTCGG TGGCGGTATC GTGCGTACCA      100
   TCGCCATGGG TTCCTCCGAC GGTCTGCGTC GCGGTCTGGA AGTTAAAGAT      150
   CTCGAGCACC CGATCGAAGT TCCGGTAGGT AAAGCAACAC TGGGTCGTAT      200
   CATGAACGTA CTGGGTACAC CCGTAGACAT GAAAGGCGAC ATCGGTGAAG      250
   AAGAGCGTTG GGCTATCCAC CGCGCTGCGC CTTCCTACGA AGAGCTGTCC      300
15 AGCTCTCAGG AACTGCTGGA AACC GGATATC AAAGTTATCG ACCTGATGTG      350
   TCCGTTTCGCG AAGGGCGGTA AAGTCGGTCT GTTCGGCGGT GCGGGTGTG      400
   GTAAAACCGT AAACATGATG GAGCTGATCC GTAACATCGC GATCGAGCAC      450
   TCCGGTTACT CTGTGTTTGC GGGCGTAGGT GAACGTACTC GTGAGGGTAA      500
   CGACTTCTAC CACGAAATGA CCGACTCCAA CGTTATCGAT AAAGTATCCC      550
20 TGGTGTATGG CCAGATGAAC GAGCCGCCGG GAAACCGTCT GCGCGTTGCG      600
   CTGACCGGCC TGACCATGGC TGAGAAATTC CGTGACGAAG GTCGTGACGT      650
   ACTGCTGTTT GTCGATAACA TCTATCGTTA CACCCTGGCC GGTACTGAAG      700
   TATCTGCACT GCTGGGTCGT ATGCCTTCAG CGGTAGGTTA CCAGCCGACT      750
   CTGGCGGAAG AGATGGGCGT TCTGCAGGAA CGTATCACCT CCACCAAGAC      800
25 CGGTTCTATC                                         810

```

2) INFORMATION FOR SEQ ID NO: 321

(i) SEQUENCE CHARACTERISTICS:

- 30 (A) LENGTH: 834 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 35 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 40 (A) ORGANISM: *Lactobacillus acidophilus*  
 (B) STRAIN: ATCC 4356

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 321

```

45 TCGATAAGAA TTTACCTGAT ATTAACAACG CCTTACGTGT AATCAAGTCC      50
   GAAGATGAAA GCATCGTTCT TGAAGTTACA CTTGAACTCG GTGATGGTGT      100
   TTAAAGAACA ATCGCCATGG AATCTACCGA TGGTCTTCGT CGTGGTATGA      150
   AAGTCGAAGA TACTGGCGCT CCAATTTTCTG TTCCAGTTGG AGAAGACACT      200
   TTAGGTCGTG TGTTTAAACGT TTTAGGACAG CCTATTGATG GTGGTCCAGC      250
50 CTTTCCAAAG GATCACCCAC GTGAGGGTAT CCACAAGGAA GCACCTAAAT      300
   ATGAAGATTT AACTACTAGT CGTGAAATTC TTGAAACTGG TATCAAGGTT      350
   ATCGACCTTC TTGAACCATA TGTTCTGGT GGTAAAGTTG GTTTGTTTGG      400
   TGGTGCCGGT GTTGGTAAAA CTACTATTAT TCAAGAATTA ATTCACAACA      450
   TCGCTCAAGA ACACGGTGGT ATTTCCGTAT TTAAGTGGT TGGTGAAAGA      500
55 ACTCGTGAAG GTAATGACCT TTACTTTGAA ATGAAAGCTT CAGGCGTTTT      550
   AAGTAAGACT GCCATGGTAT TTGGTCAGAT GAACGAGCCG CCTGGTGCCA      600
   GAATGCGTGT TGCATTAACC GGTGTTGACAC TTGCTGAATA CTTTAGAGAT      650
   GTTGAAGGTC AAGACGTATT GCTCTTTATT GACAATATCT TTAGATTTAC      700
   TCAGGCTGGT TCAGAGGTAT CTGCTTTGCT TGGTCGTATG CCAAGTGCCG      750
50 TAGGTTATCA GCCAACTTTG GCAACAGAAA TGGGTCAATT GCAGGAAAGA      800

```

ATTACTTCTA CTAAGAAGGG TTCAATTACT TCAA

## 5 2) INFORMATION FOR SEQ ID NO: 322

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 824 bases  
 (B) TYPE: Nucleic acid  
 10 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

## 15 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Legionella pneumophila* subsp. *pneumophila*  
 (B) STRAIN: ATCC 33152

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 322

20 TTCCTCGTGA TAGCGTGCCT AAAGTCAATG ATGCGTTAAA GCTTGTTGAT 50  
 AGTGATCTGG TTTTGAAGT GCAGCAGCAA CTTGGAGACG GAGTTGTGCG 100  
 TACTATTGCC ATGGGAACAA CCGATGGTTT AAAGCGAGGA TTAAAAGCAG 150  
 AAAATACAGG CCATCCTATT CAAGTGCCAG TAGGTAAGAA AACTTTGGGA 200  
 25 CGCATTATGG ATGTTCTTGG GCGTCCTGTA GATGATGCTG GGCCTATCGA 250  
 TGCTGAAGAG ACTTGGGCTA TTCATCGTAA AGCACCAAGT TATGAAGAGC 300  
 AAGCTGGCAG CCAGGAATTA TTGGAAACTG GTATTAAAGT AATTGATTG 350  
 CTTTGCCCTT TTGCCAAGGG AGGTAAAGTT GGTCTATTCG GTGGTGCCGG 400  
 TGTAGGCAAA ACCGTTAACA TGATGGAATT AATACGAAAC ATTGCAATTG 450  
 30 AGCATAGCGG TTATTCAGTG TTTGCAGGGG TTGGTGAACG TACCCGTGAA 500  
 GGAAACGACT TCTATCATGA GATGAAAGAC TCTAATGTAT TGGATAAAGT 550  
 ATCGCTTGTT TATGGTCAGA TGAATGAGCC GCCAGGAAAC CGTTTGCGTG 600  
 TTGCTCTAAC CGGTTTGACT ATGGCTGAAA AATTCCGGGA TGAAGGGCGA 650  
 GACGTTCTTT TGTTTATCGA TAATATTTAT CGTTATACCT TGGCTGGGGT 700  
 35 TGAAGTATCT GCGCTGTTAG GCCGTATGCC TTCTGCAGTA GGATATCAGC 750  
 CGACATTAGC AGAGGAAATG GGTATGCTGC AAGAGCGCAT TACCTCCACA 800  
 AAAACAGGTT CTATTACTTC CATA 824

40

## 2) INFORMATION FOR SEQ ID NO: 323

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 818 bases  
 45 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

50

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Legionella grimontii*  
 (B) STRAIN: ATCC 33999

## 55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 323

GACGCCGTAC CGAAAGTGTA CGATGCGCTT GAAGTTCAAA TTGATGCCAA 50  
 GCTGGTTCTG GAAGTTCAAC AGCAGCTCGG CGGCGGCGTT GTTCGCTGCA 100  
 TCGCGATGGG TACTTCAGAC GGCTTAAGCC GCGGTCTGGA CGTGCTCGAT 150  
 60 CTGGAACACC CGATTGAAGT ACCGGTGGGC AAAGCGACGC TGGGCCGCAT 200

	CATGAACGTG	CTTGGTCACC	CTATCGACAT	GAAGGGCGAC	ATCGGCGAAG	250
	AAGAGCGTTG	GGCTATTAC	CGCGCAGCGC	CGAGCTACGA	AGACCTGTCTG	300
	GGCGCAACCG	AGCTGCTGGA	GACCGGCATC	AAGGTTATCG	ACCTGATTTG	350
	TCCGTTTCGCC	AAAGGGCGGTA	AAGTCGGCCT	GTTTCGGCGGC	GCCGGCGTAG	400
5	GTAAAACCGT	AAACATGATG	GAGCTCATTC	GCAACATTGC	GACCGAGCAC	450
	TCCGGTTACT	CCGTGTTTGC	AGGCGTAGGT	GAACGTACCC	GTGAGGGTAA	500
	CGACTTCTAC	CACGAAATGA	CTGAATCCAA	CGTATTGGAC	AAGGTGTCTGC	550
	TGGTATACGG	TCAGATGAAC	GAGCCGCCTG	GAAACCGTCT	GCGCGTAGCG	600
	TTAACGGGCT	TGACCATGGC	GGAGAAGTTC	CGTGATGAAG	GCCGTGACGT	650
10	TCTGCTGTTT	ATCGACAACA	TTTACCGCTA	TACCCTGGCC	GGTACGGAAG	700
	TATCCGCACT	GCTGGGCCGT	ATGCCTTCAG	CCGTAGGCTA	CCAGCCGACT	750
	CTGGCTGAGG	AAATGGGCGT	GCTTCAAGAG	CGTATTACCT	CTACCAAGAC	800
	GGGGTCTATC	ACCTCCGT				818

15

## 2) INFORMATION FOR SEQ ID NO: 324

## (i) SEQUENCE CHARACTERISTICS:

- 20 (A) LENGTH: 835 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

## 25 (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Listeria monocytogenes*

## 30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 324

	GTGGAAACTT	ACCTGAAATC	TACAATGCCC	TAGTTATTGA	ATATAAATCT	50
	GATGCAGAAG	AAGCACCAAC	TAGCCAACCT	ACTTTAGAAG	TAGCCATCCA	100
	ATTAGGTGAT	GATGTTGTAC	GTACAATCGC	AATGGCATCA	ACAGATGGTG	150
35	TTCAAAGAGG	TATGGAAGTT	ATTGATACTG	GGAGCCCAAT	TACAGTTCCT	200
	GTAGGTACAG	TAACTCTTGG	TCGTGTATTT	AATGTATTAG	GAAACACCAT	250
	CGATTTGGAC	GAACCACTTC	CAAGCGATAT	TAAACGTAAT	AAAATTCCACC	300
	GCGAAGCTCC	AACTTTTCGAT	CAATTAGCAA	CGACAACAGA	AATTCTTGAA	350
	ACAGGAATTA	AAGTAGTTGA	CTTGCTAGCT	CCTTACTTAA	AAGGTGGTAA	400
40	AATCGGATTG	TTCGGTGGTG	CCGGTGTGG	TAAACCGTT	CTAATTC AAG	450
	AGCTTATCCA	TAATATCGCA	CAAGAACATG	GTGGTATTTC	TGTGTTTCGCT	500
	GGCGTTGGAG	AACGTACTCG	TGAAGGTAAC	GACCTTTACT	TCGAAATGAA	550
	AGATTCAGGC	GTTATTGAAA	AAACAGCGAT	GGTATTCGGT	CAAATGAACG	600
	AGCCACCAGG	TGCGCGTATG	CGTGTTGCCT	TAACTGGTCT	AACAATTGCT	650
45	GAATATTTCC	GTGATGAAGA	ACATCAAGAT	GTACTTTTAT	TCATTGATAA	700
	CATTTTCCGT	TTACACACAAG	CTGGTTCAGA	GGTTTCGGCT	TTACTAGGTC	750
	GTATGCCATC	TGCGGTAGGT	TACCAACCAA	CCCTAGCTAC	TGAAATGGGT	800
	CAACTACAAG	AACGTATTAC	ATCTACTAAC	GTTGG		835

50

## 2) INFORMATION FOR SEQ ID NO: 325

## (i) SEQUENCE CHARACTERISTICS:

- 55 (A) LENGTH: 828 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

## 60 (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Micrococcus lylae*

(B) STRAIN: ATCC 27566

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 325

5  
 10  
 15  
 20  
 25

CCCCGCGTGGC	GAGTTGCCCGG	CACTGTTCAA	CGCGCTGACT	GTCGAGGTCA	50
CCCTCGAAGC	AGTCGCTAAA	ACCATTACCC	TTGAGGTTGC	TCAGCACCTC	100
GGCGACAAC	TGGTTCGTGC	CGTGTCATG	GCACCGACCG	ACGGTCTCGT	150
CCGTGGCGCT	GCTGTGATCG	ACAGCGGTAA	GCCGATCTCA	GTTCCCCTTG	200
GTGACGTAGT	CAAGGGACAC	GTCTTCAACG	CTCTGGGTGA	TTGCCTCGAT	250
GAGCCAGGTC	TTGGCCGTGA	CGGTGAGCAG	TGGGGCATCC	ACCGCGATCC	300
GCCACCTTTT	GACCAGCTTG	AGGGTAAGAC	CGAGATTCTG	GAAACCGGTA	350
TTAAGGTCAT	CGACCTGCTG	ACCCCGTATG	TTAAGGGCGG	CAAGATCGGC	400
CTGTTCCGGT	GTGCTGGTGT	GGGTAAGACC	GTTCTTATCC	AGGAAATGAT	450
CACCCGTATC	GCTCGCGAGT	TCTCCGGTAC	CTCGGTGTTC	GCAGGCGTGG	500
GTGAGCGTAC	CCGTGAGGGC	ACCGACCTCT	TCCTGGAAAT	GGAAGAGATG	550
GGCGTTCTCC	AGGACACCGC	TCTTGTGTTC	GGCCAGATGG	ACGAGCCTCC	600
AGGAGTTCGT	ATGCGCGTGG	CGCTGTCCGG	CCTGACCATG	GCGGAGTACT	650
TCCGCGATGT	GCAGCACCAG	GACGTGCTTC	TGTTTCATCGA	CAACATCTTC	700
CGTTTCACCC	AGGCAGGTTT	CGAGGTTTCC	ACCCTCCTAG	GCCGCATGCC	750
TTCTGCCGTG	GGTTACCAGC	CAACGCTGGC	AGACGAGATG	GGTGTTCTGC	800
AGGAGCGTAT	TACCTCCACA	AAGGGTAA			828

## 2) INFORMATION FOR SEQ ID NO: 326

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 822 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Moellerella wisconsensis*

(B) STRAIN: ATCC 35017

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 326

45  
 50  
 55  
 60

GATGCCGTAC	CAAAAGTGTA	CGATGCTCTT	GAGGTTCTTA	ACGGTAAAGA	50
AAAATTGGTG	CTGGAAGTTC	AGCAACAATT	AGGCGGTGGT	GTTGTTTCGTT	100
GTATCGCAAT	GGGTACATCA	GATGGTTTAA	GCCGCGGTTT	AGAAGTTAAA	150
AATACAGATC	ATCCGATCGA	AGTTCCTGTC	GGTGTTAAAA	CGCTTGGCCG	200
TATCATGAAC	GTGCTGGGTG	ACCCAATCGA	CATGAAAGGT	GATATCGGCG	250
AAGAAGAACG	CTGGTCAATT	CACCGCGCAG	CACCAAGCTA	TGAAGATCTG	300
GCTAACTCAA	CAGAACTTCT	AGAAACAGGT	ATCAAAGTTA	TGGACCTGAT	350
TTGCCCATTC	GCTAAAGGGG	GTAAAGTGGG	TCTGTTCGGT	GGTGCGGGTG	400
TCGGTAAAC	AGTTAACATG	ATGGAGCTTA	TTCGTAATAT	CGCGATTGAG	450
CACTCAGGTT	ATTCTGTATT	CGCGGGTGTT	GGTGAACGTA	CTCGTGAAGG	500
TAACGATTTT	TACCATGAAA	TGACAGACTC	AAACGTTCTG	GATAAAGTTT	550
CATTGGTTTA	TGGCCAGATG	AATGAGCCAC	CAGGAAACCG	TCTGCGTGTT	600
GCTCTGACTG	GTCTGACTAT	GGCAGAGAAA	TTCCGTGACG	AAGGTCGTGA	650
CGTACTGTTA	TTCGTAGATA	ATATTTATCG	TTATACCTTA	GCAGGGACAG	700
AAGTATCTGC	ACTGCTGGGT	CGTATGCCTT	CAGCGGTGGG	TTATCAGCCA	750
ACGCTGGCGG	AAGAGATGGG	TGTTCTGCAA	GAACGTATCA	CCTCGACTAA	800
GACCGGCTCT	ATCACTTCCG	TA			822

## 2) INFORMATION FOR SEQ ID NO: 327

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 854 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Branhamella catarrhalis*  
 (B) STRAIN: ATCC 43628

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 327

```

20  CCGTGGCGAT  GTCCCCCAA  TCTTTGATGC  ACTTCATGTT  GATGGTACTG      50
    AAACCACCCT  TGAAGTCCAA  CAACAGTTAG  GTGATGGTGT  GGTGCGTACC      100
    ATTGCCATGG  GTTCTACCGA  AGGCTTAAAG  CGTGGCTTGC  CTGTCTCTAA      150
    TTCAGGTGCA  CCCATTTCGG  TACCAGTCGG  TCAAGCAACA  CTGGGTCGCA      200
    TTATGGATGT  CCTAGGTCGC  CCAATCGATG  AAGCAGGTCC  GGTAATGCT       250
25  GAACAAAAAT  GGTCCATTCA  TCGTGAAGCA  CCAAGTTATG  ATGAACAGTC      300
    AAATAGTACA  GAACTTTTAG  AAACAGGCAT  CAAAGTGATT  GATTTGCTTT      350
    GTCCATTTGC  CAAAGGTGGT  AAAGTCGGTC  TGTTCCGGTG  TGCTGGTGTT      400
    GGTAAGACCG  TTAACATGAT  GGAGCTTATC  AATAATATCG  CCCTAAAACA      450
    CTCAGGTCTG  TCGGTTTTTG  CTGGTGTGGG  TGAGCGTACT  CGTGAGGGTA      500
30  ATGACTTCTA  CCATGAAATG  CAAGAAGCAG  GCGTTGTTAA  TACCGAAGAT      550
    TTTACTCAGT  CAAAAGTTGC  CATGGTTTAT  GGTCAGATGA  ATGAGCCACC      600
    AGGAAACCGT  CTGCGTGTTG  CCTTAACTGG  TTTGACCATG  GCAGAGTATT      650
    TCCGTGATGA  AAAAGACGAA  GCAACGGGCA  AAGGCCGTGA  TGTTCTGCTG      700
    TTCGTTGATA  ATATTTATCG  TTACACATTG  GCAGGTACTG  AGGTATCAGC      750
35  ACTTTTAGGT  CGTATGCCAT  CTGCGGTAGG  TTATCAGCCG  ACTTTGGCCG      800
    AAGAGATGGG  CTTGCTACAA  GAGCGTATCA  CCTCCACCCA  ATCAGGCTCA      850
    ATTA

```

## 2) INFORMATION FOR SEQ ID NO: 328

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 831 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Moraxella osloensis*  
 (B) STRAIN: ATCC 19976

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 328

```

    CCGTCAAAGC  GTACCAAGAA  TTTATGATGC  CTTAAAAGTT  GAAGGCACAG      50
    AAACACTATT  AGAAGTACAA  CAACAATTGG  GTGATGGTAT  CGTACGTACT      100
    ATTGCCATGG  GTTCTACTGA  AGGTCTAAAA  CGTGGTCTAC  CAGTTAGCAA      150
50  CACTGGCGCA  CCAATCTCTG  TACCTGTGGG  TAAAGGTACA  CTAGGTCGTA      200

```

	TCATGGACGT	TTTAGGACAC	CCAATCGATG	AGGCAGGTCC	GGTAGAGCAT	250
	AGTAACACTT	GGGCGATTCA	CCGTGAAGCG	CCAAGCTATG	ATGAACAATC	300
	AAACTCTACT	GAACCTTTAG	AAACCGGTAT	TAAAGTAATT	GACTTACTAT	350
	GCCCATTTGC	TAAAGGTGGT	AAAGTCGGTC	TGTTCCGGTGG	CGCGGGTGTT	400
5	GGTAAACCG	TTAACATGAT	GGAACCTATC	AATAACATCG	CAAAAGCACA	450
	CTCAGGTTTA	TCGGTATTTG	CTGGTGTAGG	TGAGCGTACT	CGTGAAGGTA	500
	ATGACTTCTA	CCACGAGATG	AAAGACTCAA	ACGTACTTGA	TAAAGTTGCG	550
	ATGGTGTATG	GTCAGATGAA	TGAGCCACCA	GGAAACCGTT	TACGTGTTGC	600
	CCTGACAGGT	TTAACCATGG	CAGAATACTT	CCGTGACGAA	AAAGATGAAA	650
10	ACGGTAAAGG	TCGTGACGTA	TTATTGTTTCG	TTGACAATAT	TTATCGTTAC	700
	ACGCTAGCGG	GTACCGAAGT	ATCAGCATTG	TTAGGTCGTA	TGCCATCTGC	750
	AGTAGGGTAT	CAGCCAACGC	TTGCAGAAGA	GATGGGTGTA	CTACAAGAAC	800
	GTATTACTTC	AACCCAATCA	GGCTCTATTA	C		831

15

## 2) INFORMATION FOR SEQ ID NO: 329

## (i) SEQUENCE CHARACTERISTICS:

- 20 (A) LENGTH: 835 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

## 25 (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Morganella morganii* subsp. *morganii*  
 (B) STRAIN: ATCC 25830

30

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 329

	CGAATTTTCT	CAGGATGCAG	TACCGAAAGT	GTACGATGCG	CTTGAGGTAA	50
	CAAATGGTAA	AGAAAACTG	GTGCTGGAAG	TTCAGCAGCA	GTTAGGCGGC	100
35	GGGGTTGTCC	GTTGTATCGC	TATGGGTACA	TCTGATGGTC	TGAGCCGTAA	150
	TCTGGAAGTA	ACCGATTTAG	GCCACCCGAT	CGAAGTCCCT	GTCGGCGTGA	200
	AAACCTTAGG	ACGTATCATG	AACGTTCTGG	GTGATCCGAT	CGATATGAAA	250
	GGTGACATCG	GCGCAGAAGA	AAAATGGTCT	ATTCACCGTG	CTGCACCAAC	300
	ATACGAAGAA	CTGTCTAACT	CCCAGGAACT	GCTGGAAACA	GGTATCAAAG	350
40	TAATGGACCT	GATCTGCCCC	TTGCGGAAGG	GTGGTAAAGT	CGGTCTGTTC	400
	GGTGGTGCGG	GTGTGGGTAA	AACCGTAAAC	ATGATGGAAC	TGATCCGTAA	450
	CATCGCGATC	GAGCACTCCG	GTTACTCTGT	ATTCGCAGGG	GTCGGTGAGC	500
	GTACCCGTGA	AGGTAACGAC	TTCTATCATG	AAATGACAGA	CTCCAACGTT	550
	CTGGACAAAG	TATCACTCGT	GTACGGCCAG	ATGAACGAGC	CACCGGGAAA	600
45	CCGTCTGCGC	GTTGCTCTGA	CCGGTCTGAC	CATGGCGGAA	AAATTCCGTG	650
	ATGAAGGCCG	CGATGTACTG	CTGTTCTGTT	ATAACATCTA	CCGTTATACC	700
	CTGGCCGGTA	CTGAAGTATC	CGCGTGTGTA	GGCCGTATGC	CTTCAGCGGT	750
	AGGTTACCAG	CCGACACTGG	CGGAAGAAAT	GGGTGTGCTT	CAGGAACGTA	800
50	TCACATCGAC	CAAAACAGGC	TCTATCACGT	CTGTA		835

## 2) INFORMATION FOR SEQ ID NO: 330

## 55 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 824 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

50

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Pantoea agglomerans*  
 5 (B) STRAIN: ATCC 27155

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 330

	GACGCGGTAC	CGCAAGTGTA	CAGCGCCCTC	GAGGTTATGA	ATGGTGATGC	50
10	GCGTCTGGTG	CTGGAAGTTC	AGCAGCAGCT	CGGCGGCGGC	GTA GTACGTA	100
	CCATCGCAAT	GGGTACGTCT	GACGGCCTGA	AGCGTGGTCT	GAGCGTCAAC	150
	GACCTGCAGA	AACCGATTCA	GGTACCCGTC	GGTAAAGCGA	CCCTGGGCCG	200
	TATCATGAAC	GTTCTCGGCG	AGCCAATCGA	TATGAAAGGC	GAGCTGAAAG	250
	AAGAAGATGG	CAGCGCAGTA	GAGATCGCCT	CTATTCACCG	CGCAGCCCCT	300
15	TCTTATGAAG	ATCAGTCTAA	CTCGCAGGAA	CTGCTGGAAA	CCGGCATCAA	350
	GGTTATCGAC	CTGATGTGTC	CGTTTGCTAA	AGGCGGTAAA	GTCGGTCTGT	400
	TCGGTGGTGC	GGGTGTAGGT	AAAACCGTCA	ACATGATGGA	ACTGATCCGT	450
	AACATCGCGG	CTGAACACTC	AGGTACTCA	GTGTTTGCCG	GTGTGGGTGA	500
	GCGTACTCGT	GAGGGTAACG	ACTTCTACCA	CGAAATGACT	GACTCTAACG	550
20	TTATCGATAA	AGTTGCACTG	GTCTATGGCC	AGATGAACGA	GCCGCCGGGT	600
	AACCGTCTGC	GCGTAGCACT	GACCGGTCTG	ACCATGGCGG	AAAAATTCCG	650
	TGATGAAGGT	CGCGACGTTT	TGCTGTTTAT	CGATAACATC	TACCGTTATA	700
	CCCTGGCCGG	TACAGAAGTT	TCTGCACTGC	TGGGTCGTAT	GCCATCTGCG	750
	GTAGGTTACC	AGCCAACGCT	GGCAGAAGAG	ATGGGTGTGT	TGCAGGAGCG	800
25	TATTACCTCC	ACCAAGACCG	GTTC			824

2) INFORMATION FOR SEQ ID NO: 331

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 808 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 35 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Pantoea dispersa*  
 40 (B) STRAIN: ATCC 14589

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 331

45	TATACAGCGC	TCTCGAGGTA	AAAAATGGTG	ATGCTCGTCT	GGTGCTGGAA	50
	GTACAGCAGC	AGCTGGGCGG	TGGCGTGGTG	CGTACCATCG	CCATGGGTTC	100
	TTCTGACGGC	CTGAAGCGCG	GTCTGGAAGT	CACCGACCTG	AAAAAACCTA	150
	TCCAGGTTCC	GGTTGGTAAA	GCAACACTCG	GCCGTATCAT	GAACGTGCTG	200
	GGTGAGCCAA	TCGACATGAA	AGGCGACCTG	AAAGAAGAAG	ACGGCAGCGC	250
50	TGTAGAGGTT	TCCTCTATTC	ATCGCGCAGC	GCCTTCTTAT	GAAGATCAGT	300
	CAAACCTCGA	GGAAC TGCTG	GAAACCGGCA	TCAAGGTTAT	CGACCTGATG	350
	TGTCCGTTTC	CGAAGGGCGG	TAAAGTCGGT	CTGTTCCGGT	GTGCGGGTGT	400
	AGGTAAAACC	GTAAACATGA	TGGAGCTGAT	CCGTAACATC	GCGGCTGAGC	450
	ACTCAGGTTA	TTCGGTCTTT	GCCGGCGTGG	GTGAGCGTAC	TCGTGAGGGT	500
55	AACGACTTCT	ACCACGAAAT	GACGGACTCC	AACGTTATCG	ATAAAGTAGC	550
	GCTGGTGTAT	GGCCAGATGA	ACGAGCCGCC	GGGTAAACCGT	CTGCGCGTAG	600
	CACTGACCGG	TCTGACCATG	GCGGAAAAAT	TCCGTGATGA	AGGCCGTGAC	650
	GTTCTGCTGT	TCATCGACAA	CATCTACCGT	TACACCCTGG	CCGGTACAGA	700
	GGTTTCTGCA	CTGCTGGGTC	GTATGCCATC	GGCGGTAGGT	TATCAGCCAA	750
50	CGCTGGCTGA	AGAGATGGGT	GTGCTGCAGG	AGCGTATTAC	CTCCACCAAG	800

ACCGGTTC

## 5 2) INFORMATION FOR SEQ ID NO: 332

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 805 bases  
 (B) TYPE: Nucleic acid  
 10 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

## 15 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Pasteurella multocida*  
 (B) STRAIN: NCTC 10322

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 332

20 GATGCAGTAC CAAAAGTATA TGATGCCTTA AATGTTGAAA CAGGTTTAGT 50  
 ACTTGAAGTT CAACAACAAT TAGGTGGTGG TGTAGTTCGC TGTATCGCAA 100  
 TGGGATCATC TGATGGATTA AAACGCGGTT TAAGCGTAAC AAATACGAAT 150  
 AACCCAATTT CTGTTCCAGT GGAACGAAA ACATTGGGTC GTATCATGAA 200  
 25 CGTATTGGGT GAACCAATCG ATGAGCAAGG TGAAATCGGT GCAGAAGAGA 250  
 ATTGGTCTAT TCACCGTGCG CCACCAAGTT ATGAAGAACA ATCTAACAGT 300  
 ACTGAACTTT TAGAAACGGG AATTAAAGTT ATCGACTTAG TTTGTCCGTT 350  
 TCGGAAAGGG GGTAAAGTAG GTTTATTTCGG TGGTGCGGGT GTCGGTAAAA 400  
 CCGTCAATAT GATGGAATTA ATCCGTAACA TCGCAATTGA GCACTCAGGT 450  
 30 TACTCTGTCT TTGCGGGGGT AGGTGAGCGT ACGCGTGAAG GTAACGACTT 500  
 CTATCATGAG ATGAAAGACT CTAACGTATT AGATAAAGTG TCTCTTGTTT 550  
 ATGGTCAAAT GAACGAGCCA CCAGGTAACC GTTTACGTGT GGCATTAACA 600  
 GGCTTAACTA TGGCGGAAAA ATTCCGTGAT GAAGGTCGTG ATGTCTTATT 650  
 CTTTCGTTGAT AATATTTATC GTTATACTCT TGCTGGTACA GAAGTTTCTG 700  
 35 CATTATTAGG TCGTATGCCA TCTGCGGTAG GTTATCAACC AACCTTGCA 750  
 GAAGAAATGG GTGTTCTGCA AGAGCGTATT ACCTCAACCA AAACAGGTTC 800  
 TATTA 805

## 10 2) INFORMATION FOR SEQ ID NO: 333

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 828 bases  
 15 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

## 50 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Pragia fontium*  
 (B) STRAIN: ATCC 49100

## 55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 333

TTTCCTCAAG ACGCCGTACC AAAAGTGTAC GACGCGCTTG AAGTTCAGAA 50  
 CGATGCCAAG CTGGTGCTGG AAGTTCAACA ACAGCTCGGT GGTGGTGTCG 100  
 TTCGTTGTAT CGCAATGGGT ACTTCCGATG GCTTAAGCCG CGGTTTAAAA 150  
 50 GTGCTTGATT TAGAACATCC TATCGAAGTA CCGGTTGGTA CTGCGACGCT 200



	GGGCCGTATT	ATGAACGTGC	TCGGTCAGCC	AATCGATATG	AAAGGCGATA	250
	TTGGTGAAGA	AGAGCGTTGG	GCTATTCACC	GTGAAGCACC	AAGTTATGAA	300
	GATTTATCTG	GCGCCAATGA	ACTGCTGGAA	ACGGGTATCA	AGGTTATCGA	350
	CCTGATTTGT	CCGTTTGCTA	AAGGTGGTAA	AGTTGGTCTG	TTTGGTGGTG	400
5	CGGGTGTAGG	TAAAACCGTA	AACATGATGG	AGCTGATTCG	TAACATTGCG	450
	ACTGAGCACT	CAGGTTACTC	CGTATTCGCC	GGTGTAGGGG	AACGTACCCG	500
	TGAAGGTAAT	GACTTCTACC	ACGAAATGAC	CGAATCAAAC	GTACTGGATA	550
	AAGTATCTCT	GGTTTATGGC	CAGATGAACG	AGCCACCAGG	AAACCGTCTG	600
	CGCGTGGCGT	TAACGGGTTT	GACCATGGCT	GAAAAATTCC	GTGATGAAGG	650
10	TCGTGACGTT	CTGTTATTTA	TCGATAACAT	TTATCGCTAT	ACCTTAGCCG	700
	GTACCGAAGT	ATCAGCACTG	TTGGGGCGTA	TGCCATCAGC	GGTAGGTTAT	750
	CAGCCAACGT	TAGCAGAAGA	GATGGGTGTG	TTGCAGGAAC	GTATTACTTC	800
	AACCAAACCC	GGTTCAATCA	CTTCTGTA			828

15

## 2) INFORMATION FOR SEQ ID NO: 334

## (i) SEQUENCE CHARACTERISTICS:

- 20 (A) LENGTH: 807 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

## 25 (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Proteus mirabilis*  
 (B) STRAIN: ATCC 25933

30

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 334

	GTCCCTAAAG	TATACGACGC	TCTTGAGGTT	ATGAATGGTA	AAGAAAAACT	50
	GGTGCTGGAA	GTTTCAGCAAC	AGTTAGGCGG	TGGTATCGTT	CGTTGTATCG	100
35	CAATGGGTAC	ATCAGACGGT	TTAAGCCGTG	GCTTAAAGGT	TGAAGATTTA	150
	GGCCACCCAA	TTGAAGTACC	AGTAGGTAAA	GCGACTTTAG	GACGTATCAT	200
	GAACGTTCTG	GGTACACCTA	TTGATATGAA	AGGTGAGATT	GAAACCGAAG	250
	AGCGTTGGTC	AATCCACCGT	GAAGCACCAA	CTTACGAAGA	GTTATCAAAC	300
	TCTCAAGAAC	TGCTTGAAAC	CGGTATCAAA	GTTATGGACT	TAATCTGTCC	350
40	ATTTGCTAAA	GGTGGTAAAG	TCGGTCTGTT	CGGTGGTGCG	GGTGTGGGTA	400
	AAACAGTTAA	CATGATGGAA	TTGATCCGTA	ATATCGCGAT	CGAGCACTCA	450
	GGTTACTCTG	TATTTGCTGG	TGTTGGTGAG	CGTACTCGTG	AGGGTAACGA	500
	CTTCTATCAT	GAAATGACAG	ATTCTAACGT	TCTTGACAAA	GTATCGTTAG	550
	TTTACGGTCA	GATGAATGAG	CCACCAGGAA	ACCGTCTGCG	TGTTGCACTG	600
15	ACTGGTCTGA	CTATGGCTGA	GAAATTCCGT	GATGAAGGCC	GTGACGTACT	650
	GTTATTTCGT	GATAACATCT	ATCGTTACAC	CTTAGCCGGT	ACAGAAGTAT	700
	CAGCACTGTT	AGGTCGTATG	CCATCAGCGG	TAGGTTACCA	ACCAACATTG	750
	GCTGAAGAGA	TGGGTGTTCT	GCAAGAGCGT	ATCACTTCAA	CCAAAACAGG	800
	TTCTATC					807

50

## 2) INFORMATION FOR SEQ ID NO: 335

## (i) SEQUENCE CHARACTERISTICS:

- 55 (A) LENGTH: 811 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

50

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Proteus vulgaris*  
 5 (B) STRAIN: ATCC 13315

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 335

```

10 CCCTAAAGTA TACGACGCTC TTGAGGTTAT GAATGGTAAA GAGAAACTGG      50
   TGCTAGAAGT TCAGCAACAG TTAGGCGGTG GTATCGTTCG TTGTATCGCA      100
   ATGGGTACAT CAGACGGTTT AAGCCGTGGC TTAAAAGTTG AAAACTTAGG      150
   CCACCCAATT GAAGTACCAG TAGGTAAAGC AACACTGGGA CGTATCATGA      200
   ACGTTCTGGG TACACCTATC GATATGAAAG GTGATATTGC AACTGAAGAA      250
   CGTTGGTCTA TTCACGCGCA AGCGCCAACC TATGAAGAGT TATCAAGCTC      300
15 TCAAGAACTA CTAGAAACCG GTATCAAAGT AATGGACTTA ATCTGTCCGT      350
   TTGCTAAAGG TGGTAAAGTA GGTCTCTTCG GTGGTGCGGG TGTTGGTAAA      400
   ACAGTTAACA TGATGGAATT GATCCGTAAC ATCGCGATTG AGCACTCAGG      450
   TTATTCTGTA TTTGCAGGTG TTGGTGAGCG TACTCGTGAG GGTAACGACT      500
   TCTATCATGA AATGACAGAT TCTAACGTTT TTGACAAAGT ATCGTTAGTT      550
20 TATGGTCAGA TGAATGAGCC ACCAGGAAAC CGTCTACGTG TAGCACTGAC      600
   GGGTTTAACC ATGGCGGAAA AATTCCGTGA TGAAGGCCGT GACGTACTGT      650
   TATTCGTCGA TAACATCTAT CGTTACACCT TAGCCGGTAC CGAAGTATCA      700
   GCACTGTTAG GCCGTATGCC ATCAGCAGTA GGTTACCAAC CAACATTGGC      750
   TGAAGAGATG GGTGTTCTGC AAGAACGTAT CACTTCAACC AAAACAGGTT      800
25 CAATCACCTC T                                     811

```

2) INFORMATION FOR SEQ ID NO: 336

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 806 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 35 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 40 (A) ORGANISM: *Providencia alcalifaciens*  
 (B) STRAIN: ATCC 9886

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 336

```

45 TCAAGATAAC GTACCAAAAG TGTACGATGC TCTTGAGGTT ATTAACGGTA      50
   AAGAAAAACT GGTGTTGGAA GTTCAACAAC AGTTAGGTGG TGGTGTGTC      100
   CGTTGTATCG CAATGGGTAC ATCAGATGGT CTGAGCCGTG GTTTAGAAGT      150
   TGTAAACTTA GAGCACCCAA TCGAAGTACC AGTCGGTAAA GCAACTCTGG      200
   GACGTATCAT GAACGTTCTG GGTGAACCAA TCGACATGAA AGGTGATATC      250
50 GCGGAAGAAG AGCGCTGGTC TATTCACCGT GCTGCACCAA GCTACGAAGA      300
   ATTAGCTAAC TCAACTGAAC TGCTGGAAAC CGGTATCAAA GTAATGGACT      350
   TAATCTGTCC ATTGCGGAAA GGTGGTAAAG TAGGTCTGTT CGGTGGTGCG      400
   GGTGTTGGTA AAACCGTAAA CATGATGGAA CTGATCCGTA ACATCGCGAT      450
   TGAGCACTCA GGTTACTCAG TGTTGCTGGT TGTTGGTGAG CGTACCCGTG      500
55 AAGGTAACGA CTTCTATCAT GAAATGACAG ACTCAAACGT TCTGGATAAA      550
   GTATCACTGG TTTATGGCCA GATGAACGAG CCACCAGGAA ACCGTCTGCG      600
   TGTTGCGCTG ACTGGTCTGA CTATGGCTGA AAAATTCCGT GACGAAGGTC      650
   GTGACGTACT GCTGTTCTGT GACAACATTT ATCGTTATAC ACTGGCAGGT      700
   ACTGAAGTAT CAGCACTGTT AGGTCGTATG CCATCAGCGG TAGGTTACCA      750
50 ACCAACGCTG GCGGAAGAGA TGGGTGTTCT TCAAGAACGT ATTACCTCAA      800

```

CTCAAA

## 5 2) INFORMATION FOR SEQ ID NO: 337

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 830 bases  
 (B) TYPE: Nucleic acid  
 10 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

## 15 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Providencia rettgeri*  
 (B) STRAIN: ATCC 9250

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 337

20 TTCCCTCAAG ATGACGTACC AAAAGTGTAC GACGCTCTTG AGGTTGTTAA 50  
 CGGTAAAGAA ACACCTGGTGC TGGAAAGTTCA GCAACAGTTA GCGGGTGGTG 100  
 TTGTCCGTTG TATCGCAATG GGTACATCAG ATGGCCTGAG CCGTGGTTTA 150  
 GAAGTTGTAA ACTTAGAGCA CCCAATTGAA GTACCAGTAG GTAAAGCAAC 200  
 25 TTTAGGACGT ATCATGAACG TTCTGGGTCA GCCTATTGAT ATGAAAGGTG 250  
 ATATCGGCGA AGAAGAGCGC TGGTCAATTC ACCGTGCTGC ACCTAGCTAC 300  
 GAAGAGTTAG CTAACCTAAC AGAGCTGCTG GAAACCGGTA TCAAAGTAAT 350  
 GGACTTAATC TGTCCATTTC CGAAAGGTGG TAAAGTTGGT CTGTTCCGTG 400  
 GTGCGGGTGT TGGTAAAACA GTAAACATGA TGGAACTGAT CCGTAACATC 450  
 30 GCGATTGAGC ACTCAGGTTA CTCAGTATTC GCTGGTGTG GTGAGCGTAC 500  
 TCGTGAAGGG AACGACTTCT ATCATGAAAT GACTGACTCA AACGTTCTGG 550  
 ATAAAGTATC ACTGGTTTAT GGCCAGATGA ATGAGCCACC AGGAAACCGT 600  
 CTGCGCGTTG CGTTGACTGG TCTGACTATG GCTGAAAAAT TCCGTGACGA 650  
 AGGTCGTGAC GTACTACTGT TCGTTGACAA CATCTATCGT TATACTACTG 700  
 35 CAGGTACTGA AGTATCAGCA CTGTTAGGTC GTATGCCTTC AGCGGTAGGT 750  
 TATCAGCCAA CGCTGGCGGA AGAGATGGGT GTTCTGCAAG AACGTATTAC 800  
 CTCAACTCAA ACGGGTTCTA TCACTTCCGT 830

## 10 2) INFORMATION FOR SEQ ID NO: 338

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 812 bases  
 15 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

## 50 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Providencia rustigianii*  
 (B) STRAIN: ATCC 33673

## 55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 338

AGCGTACCAA AAGTGTACGA TGCTCTTGAG GTTATTAACG GTAAAGAAAA 50  
 ACTGGTGTG GAAGTTCAGC AGCAGTTAGG CGGTGGTGTG GTCCGTTGTA 100  
 TCGCAATGGG TACATCAGAT GGTCTGAGCC GTGGTTTAGA AGTTGTAAAC 150  
 50 TTAGAACACC CAATTGAAGT ACCAGTAGGT AAAGCAACTC TGGGACGTAT 200

	CATGAACGTT	CTGGGTGACC	CTATTGATAT	GAAAGGTGAT	ATCGGCGAAG	250
	AAGAGCGCTG	GTCTATTCAC	CGTTCAGCGC	CAAGCTATGA	AGAATTAGCT	300
	AACTCAACAG	AACTGCTAGA	AACCGGTATC	AAAGTAATGG	ACTTAATCTG	350
	TCCATTTCGCG	AAAGGTGGTA	AAGTTGGTCT	GTTTCGGTGGT	GCGGGTGTTG	400
5	GTAACACAGT	AAACATGATG	GAAGTATGAT	GTAACATCGC	GATTGAGCAC	450
	TCAGGTTACT	CAGTATTCGC	TGGTGTGGT	GAGCGTACCC	GTGAAGGTAA	500
	CGACTTCTAT	CATGAAATGA	CTGATTCTAA	CGTTCTGGAT	AAAGTATCAC	550
	TGGTTTATGG	CCAGATGAAC	GAGCCACCAG	GAAACCGTCT	GCGTGTGCG	600
	CTGACTGGTC	TGACTATGGC	TGAAAAATTC	CGTGACGAAG	GTCGTGACGT	650
10	ACTGCTGTTT	GTTGACAACA	TTTATCGTTA	TACACTGGCA	GGTACTGAAG	700
	TATCAGCACT	GTTAGGTCGT	ATGCCCTCAG	CGGTAGGTTA	TCAGCCAACA	750
	TTGGCAGAAG	AGATGGGTGT	TCTACAAGAA	CGTATCACTT	CTACCAAAC	800
	CGTTTCTATC	AC				812

15

## 2) INFORMATION FOR SEQ ID NO: 339

## (i) SEQUENCE CHARACTERISTICS:

- 20 (A) LENGTH: 819 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

25 (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Providencia stuartii*  
 (B) STRAIN: ATCC 33672

30

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 339

	TCAAGATGCA	GTACCAAAAG	TGTACGATGC	GCTTGAGGTT	GTTAACGGTA	50
	AAGAAAAACT	GGTGCTGGAA	GTTTACGCAAC	AGTTAGGCGG	TGGTGTGTC	100
35	CGTTGTATCG	CAATGGGTAC	ATCAGATGGC	CTAAGCCGTG	GTTTAGAAGT	150
	TAAAAATTTA	GAACACCCAA	TTGAAGTACC	AGTAGGTAAA	GCAACACTCG	200
	GACGTATCAT	GAACGTTCTG	GGTGACCTTA	TTGATATGAA	AGGTGATATC	250
	GGCGAAGAAG	AGCGTTGGTC	TATTCACCGC	GCTGCACCAA	GCTACGAAGA	300
	GCTATCGAGC	TCAACTGAAC	TGCTAGAGAC	AGGTATCAAA	GTCATGGACT	350
10	TGATCTGTCC	ATTCGCGAAA	GGTGGTAAAG	TTGGTCTGTT	CGGTGGTGCG	400
	GGTGTGTTGTA	AAACGGTAAA	CATGATGGAA	CTTATCCGTA	ACATCGCGAT	450
	TGAGCACTCA	GGTTACTCAG	TATTCGCAGG	TGTTGGTGAG	CGTACCCGTG	500
	AAGGTAACGA	CTTCTATCAT	GAAATGACAG	ATTCAAACGT	TCTTGACAAA	550
	GTATCACTGG	TTTATGGTCA	GATGAATGAG	CCACCAGGAA	ACCGTCTACG	600
15	CGTAGCATTG	ACTGGTTTGA	CTATGGCTGA	GAAATTCCGT	GACGAAGGCC	650
	GTGATGTTCT	GTTGTTTCGTG	GATAACATCT	ATCGTTATAC	ACTGGCAGGT	700
	ACAGAAGTAT	CGGCTCTGTT	AGGTCGTATG	CCATCAGCAG	TAGGTTATCA	750
	GCCAACATTG	GCAGAAGAGA	TGGGTGTTCT	TCAAGAACGT	ATCACTTCTA	800
50	CTAAGACAGG	TTCTATCAC				819

## 2) INFORMATION FOR SEQ ID NO: 340

## (i) SEQUENCE CHARACTERISTICS:

- 55 (A) LENGTH: 907 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

50

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Psychrobacter phenylpyruvicus*  
 5 (B) STRAIN: ATCC 23333.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 340

```

10 AACCGCACTG ACGTGCCTCA AATTTATGAC GCGTTAGTTG TAGATGGTAC      50
   CGAAACCACC CTAGAAGTTC AGCAGCAGCT GGGCGATGGT GTGGTACGTA      100
   CTATTGCAAT GGGATCTACT GAAGGTCTTA AGCGTGGTTT ACCAGTAACA      150
   AACACTGGTG CCCCAATTAC AGTTCCAGTA GGTGATGCGA CTTTAGGTCTG      200
   TATTATGGAC GTTTTAGGTC GTCCAATTGA CGAACAAGGT CCAGTTAATT      250
   CTGAAGACCA TTGGTCAATC CACCGTCAAG CGCCATCATA TGATGAGCAA      300
15  GCTAACAGTA CTGACCTATT AGAGACAGGT ATTAAAGTAA TTGACTTACT      350
   TTGTCCGTTT GCTAAAGGGG GTAAAGTTGG TCTGTTCGGT GGTGCCGGTG      400
   TTGGTAAAC  CGTAAACATG ATGGAATTGA TTAATAACAT CGCTCTTAAG      450
   CACTCAGGTT TATCAGTATT CGCTGGTGTG GGTGAGCGTA CTCGTGAAGG      500
   TAACGACTTC TACCACGAGA TGCAAGAAGC GGGTGTGTGT GACGTTGAAA      550
20  ACTTCACCAA CTCAAAGTT GCGATGGTTT ATGGTCAGAT GAATGAGCCA      600
   CCAGGTAACC GTTTACGTGT TGCGTTAACC GGTCTGACTA TGGCTGAGTA      650
   CTTCCGTGAT CAAAAAGATG AAAACGGTAA AGGTAAAGAC GTTCTATTAT      700
   TCGTTGATAA CATCTACCGC TACACGCTAG CCGGTACTGA AGTATCAGCA      750
   CTTCTAGGTC GTATGCCATC AGCAGTAGGT TATCAGCCAA CACTAGCGGA      800
25  AGAGATGGGT GTACTACAAG AGCGTATTAC TTCAACTCAG ACTGGTTCTA      850
   TTACTTC                                     907

```

30 2) INFORMATION FOR SEQ ID NO: 341

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 832 bases  
 (B) TYPE: Nucleic acid  
 35 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

40 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Rahnella aquatilis*  
 (B) STRAIN: DSM 4594

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 341

```

45 GTTCCCTCAG GATGCAGTAC CGAACGTGTA CAATGCTCTT GAGGTAGAAA      50
   ACGGTACCTC CAAACTGGTG CTGGAAGTTC AGCAACAGTT AGGCGGCGGC      100
   GTTGTTTCGTT GTATCGCAAT GGGTACCTCA GACGGCCTGC GTCGCGGTCT      150
   GAAAGTGAAC AACCTGGAAC ACCCAATTGA AGTACCGGTA GGTAAGCGA      200
50  CTCTGGGTCG TATCATGAAC GTATTGGGTG AACCAATCGA CATGAAAGGT      250
   GAAATCGGCG AAGAAGAACG TCGTGCTATT CACCGTGCTG CGCCTTCTTA      300
   TGAAGAGCTG GCAAACCTCC AGGAATTGCT GGAAACCGGT ATCAAAGTTA      350
   TGGACCTGAT GTGTCCGTTT GCTAAGGGCG GTAAAGTTGG TCTGTTCGGT      400
   GGTGCGGGTG TAGGTAAAC  TGTGAACATG ATGGAGCTGA TCCGTAACAT      450
55  TGCATCGAG  CACTCCGTTT ATTCTGTGTT TGCAGGCGTG GGTGAACGTA      500
   CTCGTGAGGG TAACGACTTC TACCACGAAA TGACTGATTC CAACGTTATC      550
   GACAAAGTTT CCCTGGTGTA TGGCCAGATG AATGAGCCAC CAGGTAACCG      600
   TCTGCGCGTT GCACTGACCG GCCTGACCAT GGCGGAAAAA TTCCGTGATG      650
   AAGGTCGTGA CGTACTGCTG TTCGTTGACA ACATTTACCG TTACACCCTG      700
60  GCCGGTACCG AAGTGTCCGC ACTTCTGGGC CGTATGCCAT CGGCGGTAGG      750

```

TTATCAGCCA ACGCTGGCGG AAGAGATGGG CGCTCTGCAA GAACGTATCA' 800  
 CCTCGACCAA AAGTGGTTCT ATCACCTCCG TA 832

5

## 2) INFORMATION FOR SEQ ID NO: 342

## (i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 824 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

15

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Salmonella choleraesuis* subsp. *arizonae*  
 (B) STRAIN: ATCC 13314

20

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 342

TTCCCTCAGG ATGCCGTACC ACGCGTGTAC GATGCTCTTG AGGTGCAGAA 50  
 TGGTAATGAG AAGCTGGTGC TGGAAGTTCA GCAGCAGCTT GCGGCGGTA 100  
 TCGTGCGTAC CATCGCGATG GGGTCTTCTG ACGGTCTGCG TCGCGGTCTT 150  
 25 GATGTAAAG ATCTCGAACA CCCGATCGAA GTCCCGGTAG GTAAAGCCAC 200  
 GCTGGGTCGT ATCATGAACG TCCTGGGCGA ACCGGTCGAT ATGAAAGGCG 250  
 AGATCGGCGA AGAAGAGCGT TGGGCTATTC ACCGCGCGGC GCCGTCCTAC 300  
 GAAGAGTTGT CAAACTCTCA GGAAGTGTG GAAACCGGTA TAAAGTTAT 350  
 CGACCTGATG TGTCCGTTTC CGAAGGGCGG TAAAGTCGGT CTGTTTCGGT 400  
 30 GCGCGGGTGT AGGTAAAACC GTAAACATGA TGGAGCTTAT CCGTAACATC 450  
 GCGATCGAGC ACTCCGGTTA CTCTGTGTTT GCGGGCGTAG GTGAACGTAC 500  
 TCGTGAGGGT AACGACTTCT ACCACGAAAT GACCGACTCT AACGTTATCG 550  
 ATAAAGTATC CCTGGTGTAT GGCCAGATGA ACGAGCCACC GGGAAACCGT 600  
 CTGCGCGTTG CATTGACCGG CCTGACCATG GCGGAAAAAT TCCGTGATGA 650  
 35 AGGTCGTGAC GTTCTGCTGT TCGTCGACAA CATCTACCGT TATACCCTCG 700  
 CCGGTACGGA AGTATCCGCA CTGCTGGGTC GTATGCCTTC CGCGGTAGGT 750  
 TAYCASCCGA CTCTGGCGGA AGAGATGGGC GTTCTGCAGG AACGTATCAC 800  
 CTCCACCAAAA ACCGGTTCTA TCAC 824

40

## 2) INFORMATION FOR SEQ ID NO: 343

## (i) SEQUENCE CHARACTERISTICS:

- 45 (A) LENGTH: 820 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

50

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Salmonella choleraesuis* subsp. *choleraesuis*  
 serotype *Choleraesuis*  
 55 (B) STRAIN: ATCC 7001

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 343

GATGCCGTAC CACGCGTGTA CGATGCCCTT GAGGTGCAGA ATGGTAATGA 50  
 60 GAAGCTGGTG CTGGAAGTTC AGCAGCAGCT TGGCGGCGGT ATCGTGCGTA 100

	CCATCGCGAT	GGGGTCTTCT	GACGGTCTGC	GTCGCGGTCT	GGATGTAAAA	150
	GATCTCGAAC	ACCCGATCGA	AGTCCCGGTA	GGTAAAGCCA	CGCTGGGTCG	200
	TATCATGAAC	GTCCTGGGCG	AACCGGTCGA	CATGAAAGGC	GAGATCGGCG	250
	AAGAAGAGCG	TTGGGCGATT	CACCGCGCAG	CACCTTCCTA	CGAAGAGTTG	300
5	TCAAACCTCTC	AGGAACTGCT	GGAAACCGGT	ATCAAAGTTA	TCGACCTGAT	350
	GTGTCCGTTT	GCGAAGGGCG	GTAAAGTCCG	TCTGTTCCGG	GGTGCGGGTG	400
	TAGGTAAAC	CGTAAACATG	ATGGAGCTTA	TTCGTAACAT	CGCGATCGAG	450
	CACTCCGGTT	ACTCAGTGTT	TGCGGGCGTA	GGGGAACGTA	CTCGTGAGGG	500
	TAACGACTTC	TACCACGAAA	TGACCGACTC	CAACGTTATC	GATAAAGTAT	550
10	CCCTGGTGTA	TGGCCAGATG	AACGAGCCGC	CGGGAAACCG	TCTGCGCGTT	600
	GCACTGACCG	GCCTGACCAT	GGCGGAGAAA	TTCCGTGACG	AAGGTCGTGA	650
	TGTACTGCTG	TTCGTCGATA	ACATCTATCG	TTACACCCTG	GCCGGTACGG	700
	AAGTATCCGC	ACTGCTGGGC	CGTATGCCTT	CCGCAGTAGG	TTACCAGCCG	750
	ACTCTGGCGG	AAGAGATGGG	CGTTCTGCAG	GAACGTATCA	CCTCCACCAA	800
15	AACCGGTTCT	ATCACCTCCG				820

## 2) INFORMATION FOR SEQ ID NO: 344

20

## (i) SEQUENCE CHARACTERISTICS:

25

- (A) LENGTH: 831 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

30

- (A) ORGANISM: *Salmonella choleraesuis* subsp. *diarizonae*
- (B) STRAIN: ATCC 43973

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 344

35	TTCCCTCAGG	ATGCCGTACC	ACGCGTGTAC	GATGCTCTTG	AGGTGCAGAA	50
	TGGTAATGAG	AAGCTGGTGC	TGGAAGTTCA	GCAGCAGCTT	GGCGGCGGTA	100
	TCGTGCGTAC	CATCGCGATG	GGGTCTTCTG	ACGGTCTGCG	TCGCGGTCTT	150
	GATGTAAAAG	ATCTCGAACA	CCCGATCGAA	GTCCCGGTAG	GTAAAGCAAC	200
	GCTGGGTCGT	ATCATGAACG	TCCTGGGTGA	ACCGGTCGAT	ATGAAAGGCG	250
40	AGATCGGCCA	AGAAGAGCGT	TGGGCGATTC	ACCGCGCGGC	GCCGTCTTAC	300
	GAAGAGTTGT	CAAACCTCTCA	GAAACTGCTG	GAAACCGGTA	TCAAAGTTAT	350
	CGACCTGATG	TGTCCGTTTC	GGAAGGGCGG	TAAAGTCGGT	CTGTTCCGGTG	400
	GCGCGGGTGT	AGGTAAAACC	GTAAACATGA	TGGAGCTTAT	CCGTAACATC	450
	GCGATCGAGC	ACTCCGGTTA	CTCTGTGTTT	GCGGGCGTAG	GTGAACGTAC	500
45	TCGTGAGGGT	AACGACTTCT	ACCACGAAAT	GACCGACTCT	AACGTTATCG	550
	ATAAAGTATC	CCTGGTGTAT	GGCCAGATGA	ACGAGCCACC	GGGAAACCGT	600
	CTGCGCGTTG	CATTGACCGG	CCTGACCATG	GCGGAAAAAT	TCCGTGATGA	650
	AGGTCGTGAC	GTTCTGCTGT	TCGTGACAA	CATCTACCGT	TATACCCTCG	700
	CCGGTACGGA	AGTATCCGCA	CTGCTGGGTC	GTATGCCTTC	CGCGGTAGGT	750
50	TATCAGCCGA	CTCTGGCTGA	AGAAATGGGC	GTTCTGCAGG	AACGTATCAC	800
	CTCCACCAAA	ACCGGTTCTA	TCACCTCCGT	A		831

## 55 2) INFORMATION FOR SEQ ID NO: 345

## (i) SEQUENCE CHARACTERISTICS:

60

- (A) LENGTH: 831 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Salmonella choleraesuis* subsp. *houtenae*  
 (B) STRAIN: ATCC 43974

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 345

```

10  TTCCCTCAGG ATGCCGTACC ACGCGTGTAC GATGCTCTTG AGGTGCAGAA      50
    TGGTAATGAG AAGCTGGTGC TGGAAGTTCA GCAGCAGCTT GGCGGCGGTA      100
    TCGTACGTAC CATCGCGATG GGGTCTTCTG ACGGTCTGCG TCGCGGTCTG      150
    GATGTAAAAG ATCTCGAACA CCCGATCGAA GTCCCGGTAG GTAAAGCTAC      200
15  GCTGGGTCGT ATCATGAACG TCCTGGGCGA ACCGGTCGAT ATGAAAGGCG      250
    AGATCGGCGA AGAAGAGCGT TGGGCGATTG ACCGCGCTGC GCCGTCCTAC      300
    GAAGAGTTGT CAAACTCTCA GGAAGTGTCT GAAACCGGTA TCAAAGTTAT      350
    CGACCTGATG TGTCCGTTCT CGAAGGGCGG TAAAGTCGGT CTGTTTCGGTG      400
    GCGCGGGTGT AGGTAAAACC GTAAACATGA TGGAGCTTAT CCGTAACATC      450
20  GCGATCGAGC ACTCCGGTTA CTCCGTGTTT GCGGGCGTAG GTGAACGTAC      500
    TCGTGAGGGT AACGACTTCT ACCACGAAAT GACCGACTCC AACGTTATCG      550
    ATAAAGTATC CCTGGTGTAT GGTGAGATGA ACGAGCCGCC GGGAAACCGT      600
    CTGCGCGTTG CATTGACCGG CCTGACCATG GCGGAAAAT TCCGTGACGA      650
    AGGTCGTGAC GTTCTGCTGT TCGTCGATAA CATCTATCGT TACACCCTGG      700
25  CCGGTACGGA AGTATCCGCA CTGCTGGGTC GTATGCCTTC CGCGGTAGGT      750
    TATCAGCCGA CGCTGGCGGA AGAGATGGGC GTTCTGCAGG AACGTATCAC      800
    CTCCACCAAG ACCGGTTCTA TCACCTCCGT A                          831
  
```

2) INFORMATION FOR SEQ ID NO: 346

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 829 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Salmonella choleraesuis* subsp. *indica*  
 (B) STRAIN: ATCC 43974

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 346

```

50  TTCCCTCAGG ATGCCGTACC ACGCGTGTAC GATGCCCTTG AGGTGCAGAA      50
    TGGTAATGAG AAGCTCGTGC TGGAAGTTCA GCAGCAGCTT GGCGGCGGTA      100
    TCGTGCGTAC CATCGCGATG GGGTCTTCTG ACGGTCTGCG TCGCGGTCTG      150
    GATGTAAAAG ATCTCGAACA CCCGATCGAA GTCCCGGTAG GTAAAGCCAC      200
    GCTGGGTCGT ATCATGAACG TCCTGGGCGA ACCGGTCGAT ATGAAAGGCG      250
    AGATCGGCGA AGAAGAGCGT TGGGCGATTG ACCGCGCGGC GCCGTCCTAT      300
    GAAGAGTTGT CAAACTCTCA GGAAGTGTCT GAAACCGGTA TCAAAGTTAT      350
    CGACCTGATG TGTCCGTTCT CGAAGGGCGG TAAAGTCGGT CTGTTTCGGTG      400
55  GTGCGGGCGT AGGTAAAACC GTAAACATGA TGGAGCTTAT CCGTAACATC      450
    GCGATCGAGC ACTCCGGTTA CTCTGTGTTT GCGGGCGTAG GTGAACGTAC      500
    TCGTGAGGGT AACGACTTCT ACCACGAAAT GACCGACTCC AACGTTATCG      550
    ACAAAGTATC CCTGGTGTAT GGCCAGATGA ACGAGCCGCC GGGAAACCGT      600
    CTGCGCGTTG CACTGACCGG CCTGACCATG GCGGAGAAGT TCCGTGACGA      650
60  AGGTCGTGAC GTACTGCTGT TCGTCGATAA CATCTATCGT TATACCCTGG      700
  
```



CCGGTACGGA	AGTTTCCGCA	CTGCTGGGTC	GTATGCCTTC	CGCGGTAGGT	750
TATCAGCCAA	CTCTGGCGGA	AGAGATGGGC	GTTCTGCAGG	AACGTATCAC	800
CTCCACCAAA	ACCGGTTCTA	TCACCTCCG			829

5

## 2) INFORMATION FOR SEQ ID NO: 347

## (i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 817 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

15 (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Salmonella choleraesuis* subsp. *choleraesuis*  
 serotype Paratyphi A  
 20 (B) STRAIN: ATCC 9150

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 347

GCCGTACCAC	GCGTGTACGA	TGCCCTTGAG	GTGCAGAATG	GTAATGAGAA	50
GCTGGTGCTG	GAAGTTCAGC	AGCAGCTTGG	CGGCGGTATC	GTGCGTACCA	100
TCGCGATGGG	GTCTTCTGAC	GGTCTGCGTC	GCGGTCTGGA	TGTAAAAGAT	150
CTCGAACACC	CGATCGAAGT	CCCGGTAGGT	AAAGCTACGC	TGGGTCGTAT	200
CATGAACGTC	CTGGGCGAAC	CGGTCGACAT	GAAAGGCGAG	ATCGGCGAAG	250
AAGAGCGTTG	GGCGATTAC	CGCGCAGCGC	CTTCCTACGA	AGAGTTGTCA	300
AACTCTCAGG	AACTGCTGGA	AACCGGTATC	AAAGTTATCG	ACCTGATGTG	350
TCCGTTTCGG	AAGGGCGGTA	AAGTCGGTCT	GTTCGGTGGT	GCGGGTGTAG	400
GTAAAACCGT	AAACATGATG	GAGCTTATCC	GTAACATCGC	GATCGAGCAC	450
TCCGGTTACT	CTGTGTTTGC	GGGCGTAGGT	GAACGTACTC	GTGAGGGTAA	500
CGACTTCTAC	CATGAAATGA	CCGACTCCAA	CGTTATCGAT	AAAGTATCCC	550
TGGTGTATGG	CCAGATGAAC	GAGCCGCCGG	GAAACCGTCT	GCGCGTTGCA	600
CTGACCGGCC	TGACCATGGC	GGAGAAATTC	CGTGACGAAG	GTCGTGACGT	650
ACTGCTGTTC	GTCGATAACA	TCTATCGTTA	CACCCTGGCC	GGTACGGAAG	700
TATCCGCACT	GCTGGGTCGT	ATGCCTTCCG	CGGTAGGTTA	CCAGCCGACT	750
CTGGCGGAAG	AGATGGGCGT	TCTGCAGGAA	CGTATCACCT	CCACCAAGAC	800
CGGTTCTATC	ACCTCCG				817

## 2) INFORMATION FOR SEQ ID NO: 348

45

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 806 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 50 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Salmonella choleraesuis* subsp. *choleraesuis*  
 serotype Paratyphi B  
 55 (B) STRAIN: ATCC 8759

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 348

60

	GCCGTACCAC	GCGTGTACGA	TGCCCTTGAG	GTGCAGAATG	GTAATGAGAA	50
	GCTGGTGCTG	GAAGTTCAGC	AGCAGCTTGG	CGGCGGTATT	GTGCGTACCA	100
	TCGCGATGGG	GTCTTCTGAC	GGTCTGCGTC	GCGGTCTGGA	TGTAAAAGAT	150
	CTCGAACACC	CGATCGAAGT	CCCGGTAGGT	AAAGCCACGC	TGGGTCTGTAT	200
5	CATGAACGTC	CTGGGCGAAC	CGGTCGACAT	GAAAGGCGAG	ATCGGCGAAG	250
	AAGAGCGTTG	GGCGATTAC	CGCGCAGCGC	CTTCCTACGA	AGAGTTGTCA	300
	AACTCTCAGG	AACTGCTGGA	AACCGGTATC	AAAGTTATCG	ACCTGATGTG	350
	TCCGTTTCGG	AAGGGCGGTA	AAGTCGGTCT	GTTTCGGTGGT	GCGGGTGTGG	400
	GTAAAACCGT	AAACATGATG	GAGCTTATCC	GTAACATCGC	GATCGAGCAC	450
10	TCCGGTTACT	CTGTGTTTGC	GGGCGTAGGT	GAACGTACTC	GTGAGGGTAA	500
	CGACTTCTAC	CACGAAATGA	CCGACTCCAA	CGTTATCGAT	AAAGTATCCC	550
	TGGTGTATGG	CCAGATGAAC	GAGCCGCCGG	GAAACCGTCT	GCGCGTTGCA	600
	TTGACCGGTC	TGACCATGGC	GGAGAAATTC	CGTGACGAAG	GTCGTGACGT	650
	ACTGCTGTTC	GTCGATAACA	TCTATCGTTA	CACCTGGCC	GGTACGGAAG	700
15	TATCCGCACT	GCTGGGCCGT	ATGCCTTCCG	CAGTAGGTTA	CCAGCCGACT	750
	CTGGCGGAAG	AGATGGGCGT	TCTGCAGGAA	CGTATCACCT	CCACCAAAC	800
	CGGTTC					806

20

## 2) INFORMATION FOR SEQ ID NO: 349

## (i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 831 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

30

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Salmonella choleraesuis* subsp. *salamae*  
 (B) STRAIN: ATCC 43972

35

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 349

	TTCCCTCAGG	ATGCCGTACC	ACGCGTGTAC	GATGCCCTTG	AGGTGCAGAA	50
	TGGTAATGAG	AAGCTGGTGC	TGGAAGTTCA	GCAGCAGCTT	GGCGGCGGTA	100
	TCGTGCGTAC	CATCGCGATG	GGGTCTTCTG	ACGGTCTGCG	TCGKGGTCTG	150
40	GATGTAAAAG	ATCTCGAACA	CCCGATCGAA	GTCCCGGTAG	GTAAAGCAAC	200
	GCTGGGCCGT	ATCATGAACG	TACTGGGCGA	ACCGGTCGAC	ATGAAAGGCG	250
	AGATTGGTGA	AGAAGAGCGT	TGGGCTATTC	ACCGTGCTGC	GCCGTCCTAC	300
	GAAGAGTTGT	CAAACCTCTCA	GGAAGTGTG	GAAACCGGTA	TCAAAGTTAT	350
	CGACCTGATG	TGTCCGTTCG	CGAAGGCGCG	TAAAGTCGGT	CTGTTCCGGTG	400
45	GCGCGGGTGT	AGGTAAAACC	GTAAACATGA	TGGAGCTCAT	CCGTAACATC	450
	GCGATCGAGC	ACTCCGGTTA	CTCCGTGTTT	GCGGGCGTAG	GTGAACGTAC	500
	TCGTGAGGGT	AACGACTTCT	ACCACGAAAT	GACCGACTCC	AACGTTATCG	550
	ATAAAGTATC	CCTGGTGTAT	GGCCAGATGA	ACGAGCCGCC	GGGAAACCGT	600
	CTGCGCGTTG	CACTGACCGG	CCTGACCATG	GCGGAAAAAT	TCCGTGACGA	650
50	AGGTCGTGAC	GTAAGTGTGT	TCGTGATAA	CATCTATCGT	TATACCCTGG	700
	CCGGTACGGA	AGTATCCGCA	CTGCTGGGTC	GTATGCCTTC	CGCGGTAGGT	750
	TATCAGCCGA	CGCTGGCGGA	AGAGATGGGC	GTTCTGCAGG	AACGTATCAC	800
	CTCCACTAAA	ACCGGTTCTA	TCACCTCCGT	A		831

55

## 2) INFORMATION FOR SEQ ID NO: 350

## (i) SEQUENCE CHARACTERISTICS:

- 60 (A) LENGTH: 823 bases

(B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

5 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Salmonella choleraesuis* subsp. *choleraesuis*  
 serotype Typhi  
 10 (B) STRAIN: ATCC 10749

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 350

	TTCCCTCAGG	ATGCCGTACC	ACGCGTGTAC	GATGCCCTTG	AGGTGCAGAA	50
15	TGGTAATGAG	AAGCTGGTGC	TGGAAGTTCA	GCAGCAGCTT	GGCGGCGGTA	100
	TCGTGCGTAC	CATCGCGATG	GGGTCTTCTG	ACGGTCTGCG	TCGCGGTCTG	150
	GATGTAAAAG	ATCTCGAACA	CCCGATCGAA	GTCCCGGTAG	GTAAAGCTAC	200
	GCTGGGTCGT	ATCATGAACG	TCCTGGGCGA	ACCGGTCGAC	ATGAAAGGCG	250
	AGATCGGCCGA	AGAAGAGCGT	TGGGCGATTG	ACCGCGCAGC	GCCTTCCTAC	300
20	GAAGAGTTAT	CAAACCTCTCA	GGAAGTGTCTG	GAAACCGGTA	TCAAAGTTAT	350
	CGACCTGATG	TGTCCGTTTCG	CGAAGGGCGG	TAAAGTCGGT	CTGTTCCGGTG	400
	GTGCGGGTGT	AGGTAAAACC	GTAAACATGA	TGGAGCTTAT	CCGTAACATC	450
	GCGATCGAGC	ACTCCGGTTA	CTCTGTGTTT	GCGGGCGTAG	GTGAACGTAC	500
	TCGTGAGGGT	AACGACTTCT	ACCATGAAAT	GACCGACTCC	AACGTTATCG	550
25	ATAAAGTATC	CCTGGTGTAT	GGCCAGATGA	ACGAGCCGCC	GGGAAACCGT	600
	CTGCGCGTTG	CACTGACCGG	CCTGACCATG	GCGGAGAAAT	TCCGTGACGA	650
	AGGTCGTGAC	GTAAGTGTCTG	TCGTGATAAA	CATCTATCGT	TACACCCTGG	700
	CCGGTACGGA	AGTATCCGCA	CTGCTGGGTC	GTATGCCTTC	CGCGGTAGGT	750
	TACCAGCCGA	CTCTGGCGGA	AGAGATGGGC	GTTCTGCAGG	AACGTATCAC	800
30	CTCCACCAAG	ACCGGTTCTA	TCA			823

2) INFORMATION FOR SEQ ID NO: 351

35

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 831 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 40 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

45 (A) ORGANISM: *Salmonella choleraesuis* subsp. *choleraesuis*  
 serotype Typhimurium  
 (B) STRAIN: ATCC 14028

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 351

50

	TTCCCTCAGG	ATGCCGTACC	ACGCGTGTAC	GATGCCCTTG	AGGTGCAGAA	50
	TGGTAATGAG	AAGCTGGTGC	TGGAAGTTCA	GCAGCAGCTT	GGCGGCGGTA	100
	TTGTGCGTAC	CATCGCGATG	GGGTCTTCTG	ACGGTCTGCG	TCGCGGTCTG	150
	GATGTAAAAG	ATCTCGAACA	CCCGATCGAA	GTCCCGGTAG	GTAAAGCTAC	200
55	GCTGGGTCGT	ATCATGAACG	TCCTGGGCGA	ACCGGTCGAC	ATGAAAGGCG	250
	AGATCGGCCGA	AGAAGAGCGT	TGGGCGATTG	ACCGCGCAGC	GCCTTCCTAC	300
	GAAGAGTTGT	CAAACCTCTCA	GGAAGTGTCTG	GAAACCGGTA	TCAAAGTTAT	350
	CGACCTGATG	TGTCCGTTTCG	CGAAGGGCGG	TAAAGTCGGT	CTGTTCCGGTG	400
	GTGCGGGTGT	AGGTAAAACC	GTAAACATGA	TGGAGCTTAT	CCGTAACATC	450
60	GCGATCGAGC	ACTCCGGTTA	CTCAGTGTTT	GCGGGCGTAG	GGGAACGTAC	500

	TCGTGAGGGT	AACGACTTCT	ACCACGAAAT	GACCGACTCC	<del>AACGTTATCG</del>	560
	ATAAAGTATC	CCTGGTGTAT	GGCCAGATGA	ACGAGCCGCC	GGGAAACCGT	600
	CTGCGCGTTG	CATTGACCGG	TCTGACCATG	GCGGAGAAAT	TCCGTGACGA	650
	AGGTCGTGAC	GTACTGCTGT	TCGTCGATAA	CATCTATCGT	TACACCCTGG	700
5	CCGGTACGGA	AGTATCCGCA	CTGCTGGGCC	GTATGCCTTC	CGCAGTAGGT	750
	TACCAGCCGA	CTCTGGCGGA	AGAGATGGGC	GTTCTGCAGG	AACGTATCAC	800
	CTCCACCAAA	ACCGGTTCTA	TCACCTCCGT	A		831

10

## 2) INFORMATION FOR SEQ ID NO: 352

## (i) SEQUENCE CHARACTERISTICS:

15

- (A) LENGTH: 810 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

20

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Salmonella choleraesuis* subsp. *choleraesuis*  
serotype Virchow
- (B) STRAIN: ATCC 51955

25

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 352

	GCCGTACCAC	GCGTGTACGA	TGCCCTTGAG	GTGCAGAATG	GTAATGAGAA	50
	GCTGGTGCTG	GAAGTTCAGC	AGCAGCTTGG	CGGCGGTATC	GTGCGTACCA	100
30	TCGCGATGGG	GTCTTCTGAC	GGTCTGCGTC	GCGGTCTGGA	TGTAAAAGAT	150
	CTCGAACACC	CGATCGAAGT	CCCGGTAGGT	AAAGCCACGC	TGGGTCGTAT	200
	CATGAACGTC	CTGGGCGAAC	CGGTGACAT	GAAAGGCGAG	ATCGGCGAAG	250
	AAGAGCGTTG	GGCGATTAC	CGCGCAGCAC	CTTCCTACGA	AGAGTTGTCA	300
	AACTCTCAGG	AACTGCTGGA	AACCGGTATC	AAAGTTATCG	ACCTGATGTG	350
35	TCCGTTTCGCG	AAGGGCGGTA	AAGTCGGTCT	GTTCGGTGGT	GCGGGTGTAG	400
	GTAAAACCGT	AAACATGATG	GAGCTTATTC	GTAACATCGC	GATCGAGCAC	450
	TCCGGTACT	CTGTGTTTGC	GGGCGTAGGG	GAACGTACTC	GTGAGGGTAA	500
	CGACTTCTAC	CACGAAATGA	CCGACTCCAA	CGTTATCGAT	AAAGTCTCCC	550
	TGGTGTATGG	CCAGATGAAC	GAGCCGCCGG	GAAACCGTCT	GCGCGTTGCA	600
40	TTGACCGGTC	TGACCATGGC	GGAGAAATTC	CGTGACGAAG	GTCGTGACGT	650
	ACTGCTGTTC	GTCGATAACA	TCTATCGTTA	CACCTGGCC	GGTACGGAAG	700
	TATCCGCACT	GCTGGGCCGT	ATGCCTTCCG	CAGTAGGTTA	CCAGCCGACT	750
	CTGGCGGAAG	AGATGGGCGT	TCTGCAGGAA	CGTATCACCT	CCACCAAAC	800
45	CGGTTCTATC					810

## 2) INFORMATION FOR SEQ ID NO: 353

## 50 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 820 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

55

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Serratia ficaria*
- (B) STRAIN: ATCC 33105

60

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 353

	GATGCCGTAC	CAAAAGTGTA	CGATGCCCTT	GAGGTAGAAA	ACGGTACCGA	50
5	GAAACTGGTG	CTGGAAGTTC	AGCAGCAGCT	GGGCGGTGGC	GTCGTTCGCT	100
	GTATCGCAAT	GGGGACCTCT	GACGGTCTGC	GTCGCGGTCT	GAAAGTGAAC	150
	AACCTGGAAC	ACCCGATTGA	AGTGCCGGTG	GGTAAAGCTA	CCCTGGGCCG	200
	TATCATGAAC	GTATTGGGCG	AACCAATCGA	CATGAAAGGC	GAGATCGGCG	250
	AAGAAGAGCG	TTGGGCGATT	CACCGTCCTG	CGCCAAGCTA	CGAAGAGCTG	300
10	TCCAACCTCCC	AGGACCTGCT	GGAAACCGGT	ATCAAGGTAA	TGGACCTGAT	350
	TTGTCCGTTT	GCCAAGGGCG	GTAAAGTCGG	TCTGTTCGGT	GGTGCGGGCG	400
	TGGGCAAAAC	CGTAAACATG	ATGGAGCTGA	TCCGTAAACAT	CGCGATCGAG	450
	CACTCCGGTT	ATTCCGTGTT	TGCGGGCGTG	GGCGAGCGTA	CTCGTGAGGG	500
	TAACGACTTC	TACCACGAAA	TGAACGACTC	CAACGTTCTG	GACAAAGTAT	550
15	CCCTGGTTTA	CGGCCAGATG	AACGAGCCGC	CGGGTAACCG	TCTGCGCGTT	600
	GCATTGACCG	GCCTGACCAT	GGCGGAGAAA	TTCCGTGACG	AAGGCCGCGA	650
	CGTTCTGCTG	TTCGTTGACA	ACATTTACCG	TTACACCCTG	GCCGGTACCG	700
	AAGTGTCCGC	ACTTCTGGGC	CGTATGCCAT	CCGCGGTAGG	TTATCAGCCA	750
	ACGCTGGCGG	AAGAGATGGG	CGTTCTGCAA	GAACGTATCA	CCTCGACCAA	800
20	GACCGGTTCC	ATCACCTCCG				820

## 2) INFORMATION FOR SEQ ID NO: 354

25

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 816 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

30

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Serratia fonticola*  
 (B) STRAIN: ATCC 29844

35

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 354

40	GATGCCGTAC	CGAAAGTGTA	CAACGCTCTT	GAGGTTGCAA	ACGGCACCGA	50
	GAAATTGGTG	CTGGAAGTTC	AGCAACAGCT	GGGTGGCGGC	GTGGTTTCGCT	100
	GTATCGCAAT	GGGGACCTCA	GACGGTCTGC	GTCGTGGTCT	GGCCGTAACC	150
	GACCTGCAGC	ACCCAATTGA	AGTACCGGTA	GGTAAAGCTA	CCCTGGGCCG	200
	TATCATGAAC	GTATTGGGTG	AACCAATCGA	CATGAAGGGC	GACATCGGCG	250
45	AAGAAGAACG	TTGGGCTATT	CACCGCCCTG	CGCCAAGCTA	CGAAGAGCTG	300
	TCCAGCTCCC	AGGATCTGCT	GGAAACCGGT	ATCAAGGTAA	TGGACCTGAT	350
	CTGCCCCTTC	GCCAAGGGTG	GTAAAGTTGG	TCTGTTCGGT	GGTGCTGGTG	400
	TAGGTAAAAC	CGTAAACATG	ATGGAGCTGA	TCCGTAAACAT	CGCGATCGAG	450
	CACTCCGGTT	ATTCTGTGTT	TGCGGGCGTG	GGTGAACGTA	CTCGTGAGGG	500
50	TAACGACTTC	TACCACGAAA	TGACCGATTC	CAACGTACTG	GACAAAGTTT	550
	CCCTGGTTTA	CGGCCAGATG	AACGAGCCAC	CAGGTAACCG	TCTGCGCGTT	600
	GCGCTGACCG	GCCTGACCAT	GGCTGAGAAG	TTCCGTGACG	AAGGTCGTGA	650
	CGTACTGCTG	TTCGTCGATA	ACATCTACCG	TTATACCCTG	GCCGGTACCG	700
	AAGTGTCCGC	ACTTCTGGGC	CGTATGCCAT	CGGCGGTAGG	TTATCAGCCA	750
55	ACGCTGGCGG	AAGAGATGGG	TGTTCTGCAA	GAACGTATCA	CCTCTACCAA	800
	GACTGGTTCA	ATCACC				816

## 60 2) INFORMATION FOR SEQ ID NO: 355

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 822 bases  
 (B) TYPE: Nucleic acid  
 5 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Serratia grimesii*  
 10 (B) STRAIN: ATCC 14460

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 355

15 GATGCCGTAC CAAAAGTGTA CAACGCTCTT GAGGTAGAAA ACGGTGCCAA 50  
 TAAGCTGGTG CTGGAAGTTC AGCAACAGTT GGGCGGTGGC GTGGTTCGCT 100  
 GTATCGCAAT GGGGACCTCT GATGGTCTGC GTCGCGGTCT GAAAGTCACA 150  
 GACCTGGACC ACCCAATTGA AGTACCGGTA GGTAAAGCTA CTCTGGGCCG 200  
 20 TATCATGAAC GTATTGGGTG AACCAATCGA CATGAAGGGC GATATCGGCG 250  
 AAGAAGAACG TTGGGCGATT CACCGTCCGG CGCCAAGCTA CGAAGATTTG 300  
 GCCAACTCCC AGGATCTGCT GGAAACCGGT ATCAAGGTAA TGGACCTGAT 350  
 CTGCCCCGTT GCCAAGGGTG GTAAAGTCGG TCTGTTCGGT GGTGCGGGTG 400  
 TTGGTAAAC CGTAAACATG ATGGAGCTGA TCCGTAACAT CGCGATCGAG 450  
 25 CACTCCGGTT ATTCTGTGTT TGCGGGCGTG GGTGAGCGTA CTCGTGAGGG 500  
 TAACGACTTC TACCACGAAA TGAACGACTC CAACGTACTG GACAAAGTAT 550  
 CCCTGGTTTA CGGCCAGATG AACGAGCCAC CGGGTAACCG TCTGCGCGTT 600  
 GCTCTGACCG GTCTGACCAT GGCTGAGAAA TTCCGTGACG AAGGCCGTGA 650  
 CGTTCTGCTG TTCGTTGATA ACATCTACCG TTATACCCTG GCCGGTACCG 700  
 30 AAGTGTCCGC ACTTCTGGGC CGTATGCCAT CGGCGGTAGG TTATCAGCCA 750  
 ACGCTGGCGG AAGAGATGGG TGTTCTGCAA GAACGTATCA CCTCTACCAA 800  
 GACTGGTTCA ATCACCTCCG TA 822

## 2) INFORMATION FOR SEQ ID NO: 356

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 819 bases  
 40 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Serratia liquefaciens*  
 45 (B) STRAIN: ATCC 27592

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 356

50 ATGCCGTACC AAAAGTGTAC AATGCTCTTG AGGTAGAAAA CCGTACCGAG 50  
 AAGCTGGTGC TGGAAGTTCA GCAGCAGTTG GGCGGTGGCG TAGTTCGCTG 100  
 TATCGCGATG GGGACCTCAG ATGGTCTGCG CCGCGGTCTG AAAGTGAACG 150  
 55 ATCTGGAACA CCAATTGAA GTACCGGTAG GTAAAGCTAC CCTGGGCCGT 200  
 ATCATGAACG TATTGGGTGA ACCAATCGAC ATGAAAGGCG ACATCGGCCG 250  
 AGAAGAACGT TGGGCGATT CACGTCCAGC GCCAAGCTAC GAAGATTTGT 300  
 CAAACTCCCA GGATCTGCTG GAAACCGGTA TCAAGGTTAT GGACCTGATT 350  
 TGTCCGTTTC CTAAGGGCGG TAAAGTTGGT CTGTTCCGGT GTGCTGGTGT 400  
 60 TGGTAAACC GTAAACATGA TGGAGCTGAT CCGTAACATC GCGATCGAGC 450

	ACTCCGGTTA	TTCCGTGTTT	GCAGGCGTGG	GTGAGCGTAC	TCGTGAGGGT	500
	AACGACTTCT	ACCACGAAAT	GAACGACTCC	AACGTACTGG	ACAAAGTATC	550
	CCTGGTTTAC	GGCCAGATGA	ACGAGCCACC	GGGTAACCGT	CTGCGCGTTG	600
	CTCTGACCGG	TCTGACCATG	GCGGAGAAAT	TCCGTGACGA	AGGCCGCGAC	650
5	GTTCTGCTGT	TCGTTGATAA	CATTTACCGT	TATACCCTGG	CCGGTACCGA	700
	AGTGTCCGCA	CTTCTGGGCC	GTATGCCATC	TGCGGTAGGT	TATCAGCCAA	750
	CGCTGGCGGA	AGAGATGGGC	GTTCTGCAAG	AACGTATCAC	CTCTACCAAG	800
	ACCGGTTCTA	TCACTTCCG				819

10

## 2) INFORMATION FOR SEQ ID NO: 357

## (i) SEQUENCE CHARACTERISTICS:

- 15 (A) LENGTH: 805 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

## 20 (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Serratia marcescens*  
 (B) STRAIN: ATCC 13880

25

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 357

	TCAGGATGCC	GTACCGAAAG	TGTACGACGC	CCTTGAGGTA	GAAAACGGCA	50
	CCGAAAAACT	GGTGTGGA	GTTTACGCAAC	AGCTGGGCGG	TGGCGTGGTT	100
30	CGCTGTATCG	CAATGGGGAC	CTCCGACGGT	CTGCGTCGCG	GTCTGAAAGT	150
	GAACAACCTG	GACCACCCGA	TTGAAGTGCC	GGTGGGTAAA	GCTACCCTGG	200
	GTCGTATCAT	GAACGTATTG	GGTCAACCGA	TCGACATGAA	AGGCGACATC	250
	GGCGAAGAAG	AGCGTTGGGC	GATTCACCGC	GCGGCGCCAA	GCTACGAAGA	300
	GCTGTCAAGC	TCTCAGGAAC	TGCTGGAAAC	CGGTATCAAG	GTAATGGACC	350
35	TGATTTGTCC	GTTTCGCCAAG	GGCGGTAAAG	TCGGTCTGTT	CGGCGGTGCG	400
	GGCGTAGGTA	AAACCGTAAA	CATGATGGAG	CTGATCCGTA	ACATCGCGAT	450
	CGAGCACTCC	GGTTATTCCG	TGTTTGCGGG	CGTGGGCGAG	CGTACTCGTG	500
	AGGGTAACGA	CTTCTACCAC	GAAATGACCG	ACTCCAACGT	TCTGGACAAA	550
	GTATCCCTGG	TTTACGGCCA	GATGAACGAG	CCACCAGGTA	ACCGTCTGCG	600
40	CGTTGCGCTG	ACCGGTCTGA	CCATGGCGGA	GAAATTCCGT	GACGAAGGCC	650
	GTGACGTTCT	GCTGTTTCGT	GACAACATCT	ACCGTTACAC	CCTGGCCGGT	700
	ACCGAAGTGT	CCGCACTTCT	GGGCCGTATG	CCATCCGCGG	TAGGTTATCA	750
	GCCAACGCTG	GCGGAAGAGA	TGGGCGTTCT	GCAAGAACGT	ATCACCTCGA	800
	CCAAG					805

45

## 2) INFORMATION FOR SEQ ID NO: 358

## (i) SEQUENCE CHARACTERISTICS:

- 50 (A) LENGTH: 822 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

55

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- 60 (A) ORGANISM: *Serratia odorifera*  
 (B) STRAIN: ATCC 33077

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 358

```

5  GATGCCGTAC CAAAAGTGTA CGATGCCCTT GAGGTAGAAA ACGGTACCGA      50
   AACTCTGGTG CTGGAAGTTC AGCAGCAGCT GGGCGGTGGC GTGGTTTCGTT      100
   GTATCGCTAT GGGCACCTCC GACGGTTTGC GTCGCGGCCT GAAAGTGAAC      150
   GATCTGCAAC ACCCAATCGA AGTCCC GGTT GGCAAGGCAA CGCTGGGTCG      200
   TATCATGAAC GTATTGGGTC AACCAATCGA CATGAAAGGC GACATCGGCG      250
   AAGAAGAGCG TTGGGCGATT CACCGCGCGG CGCCAAGCTA CGAAGAAGTG      300
10  TCCAAC TCC AGGATCTGCT GGAAACCGGT ATCAAGGTTA TGGACCTGAT      350
   CTGCCC GTT GCCAAGGGTG GTAAAGTCGG TCTGTTTCGGT GGTGCGGGTG      400
   TTGGTAA AAC CGTAAACATG ATGGAGCTGA TCCGTAACAT CGCGATCGAG      450
   CACTCCGGTT ATTCAGTGTT TCGGGGCGTG GGTGAGCGTA CTCGTGAGGG      500
   TAACGACTTC TACCACGAAA TGACCGACTC CAACGTA CTG GACAAGGTTT      550
15  CCCTGGTTTA CGGCCAGATG AGCCGAGCAC CGGGTAACCG TCTGCGCGTT      600
   GCGCTGACCG GTCTGACCAT GGCCGAGAAA TTCCGTGACG AAGGTCGTGA      650
   CGTTCTGCTG TTCGTTGACA ACATTTACCG TTACACCCTG GCCGGTACCG      700
   AAGTGTCTGC ACTTCTGGGC CGTATGCCAT CGGCGGTAGG TTATCAGCCA      750
   ACGCTGGCGG AAGAGATGGG CGTTCTGCAA GAACGTATCA CCTCGACCAA      800
20  GACCGGTTCT ATCACCTCCG TA                                     822

```

## 2) INFORMATION FOR SEQ ID NO: 359

25

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 805 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

30

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Serratia plymuthica*  
 (B) STRAIN: ATCC 183

35

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 359

```

40  GTGTACAACG CTCTTGAGGT AGAAAACGGT GCCAATAAGC TGGTGCTGGA      50
   AGTTCAGCAA CAGCTGGGCG GTGGCGTGTT TCGCTGTATC GCGATGGGGA      100
   CCTCTGATGG TCTGCGTCGC GGTCTGAAAG TGATCGACCT GGATCACCCG      150
   ATTGAAGTAC CGGTAGGTAA AGCTACCCTG GGCCGTATCA TGAACGTATT      200
   GGGTGAACCA ATCGACATGA AAGGCGACAT CGGCGAAGAA GAACGTTGGG      250
45  CAATTCACCG TCCAGCGCCA AGCTACGAAG ATTTGGCCAA CTCCCAGGAT      300
   CTGCTGGAAA CCGGTATCAA GGTATGGAC CTGATCTGTC CGTTCGCTAA      350
   GGGCGGTAAA GTGGGTCTGT TCGGCGGTGC GGGCGTGGGT AAAACCGTAA      400
   ACATGATGGA GCTGATCCGT AACATCGCGA TCGAACACTC CGGTTATTCC      450
   GTGTTTGCGG GCGTGGGTGA GCGTACTCGT GAGGGTAACG ACTTCTACCA      500
50  CGAAATGAAC GACTCCAACG TACTGGACAA AGTATCCCTG GTTTACGGCC      550
   AGATGAACGA GCCACCGGGT AACCGTCTGC GCGTTGCTCT GACCGGTCTG      600
   ACCATGGCGG AGAAATTCCG TGACGAAGGC CGCGACGTTT TGCTGTTTCG      650
   TGATAACATC TACCGTTATA CCCTGGCCGG TACCGAAGTG TCCGCACTTC      700
   TGGGCCGTAT GCCATCTGCG GTAGGTTATC AGCCAACGCT GGCGGAAGAG      750
55  ATGGGCGTTC TGCAAGAACG TATCACCTCT ACCAAGACCG GTTCTATCAC      800
   CTCCG                                     805

```

## 60 2) INFORMATION FOR SEQ ID NO: 360



## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 831 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Serratia rubidaea*  
 (B) STRAIN: ATCC 27593

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 360

```

15 TTCCCTCAGG ATGCCGTACC AAAAGTGTAC GATGCCCTTG AGGTAGAGAA      50
   CCGTAACGAA AAACTGGTGC TGGAAGTTCA GCAGCAGCTG GGCGGCGGCG      100
   TTGTACGCTG TATCGCCATG GGTACTTCCG ACGGTCTGCG TCGCGGTCTG      150
   AAAGTTAACG ACCTCGAGCA CCAATCGAA GTGCCAGTTG GTAAAGCAAC      200
20 GCTGGGTCGT ATCATGAACG TATTGGGTCA GCCAATCGAC ATGAAAGGCG      250
   ACATCGGCGA AGAAGAGCGT TGGGCGATTG ACCGCGCGGC GCCAAGCTAC      300
   GAAGAGCTGT CCAGCTCCCA AGAGCTGCTG GAAACCGGTA TCAAGGTAAT      350
   GGACCTGATC TGCCCGTTTC CCAAGGGTGG TAAAGTTGGT CTGTTTCGGTG      400
   GTGCGGGCGT AGGTAAAACC GTAAACATGA TGGAGCTGAT CCGTAACATC      450
25 GCGATCGAGC ACTCCGGTTA CTCTGTGTTT GCGGGCGTGG GTGAGCGTAC      500
   TCGTGAGGGT AACGACTTCT ACCACGAAAT GACCGACTCC AACGTACTGG      550
   ACAAAGTATC CCTGGTTTAC GGCCAGATGA ACGAGCCGCC GGGTAACCGT      600
   CTGCGCGTTG CACTGACCGG CCTGACCATG GCGGAAAAAT TCCGTGATGA      650
   AGGCCGCGAC GTTCTGCTGT TCGTGGATAA CATCTACCGT TACACCCTGG      700
30 CCGGTACCGA AGTGTCGCA CTGCTCGGCC GTATGCCATC TCGGGTAGGT      750
   TATCAGCCAA CGCTGGCGGA AGAGATGGGC GTTCTGCAAG AACGTATCAC      800
   CTCGACCAAG ACCGGTTCAA TCACCTCCGT A                        831

```

## 2) INFORMATION FOR SEQ ID NO: 361

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 406 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Pseudomonas putida*  
 (B) STRAIN: LCDC D7172

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 361

```

55 CCGTAAACAT GATGGAAGT ATCCGTAAACA TCGCCATCGA GCACAGCGGT      50
   TATTCCGTGT TCGCCGGTGT GGGTGAGCGT ACTCGTGAGG GTAACGACTT      100
   CTACCACGAG ATGAAGGACT CCAACGTTCT CGACAAGGTA GCGCTGGTCT      150
   ACGGTCAGAT GAACGAGCCA CCAGGAAACC GTCTGCGCGT AGCGCTGACC      200
   GGCCTGACCA TGGCCGAGAA GTTCCGTGAC GAAGGTAACG ACGTTCTGCT      250
   GTTCGTCGAC AACATCTATC GTTACACCCT GGCCGGTACC GAAGTATCCG      300
   CACTGCTGGG CCGTATGCCT TCGGCGGTAG GTTACCAGCC GACCCTGGCT      350
   GAAGAGATGG GCGTTCTGCA AGAACGTATC ACTTCGACCA AGGAAGGTTC      400
60 GATCAC                                           406

```

## 2) INFORMATION FOR SEQ ID NO: 362

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 831 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Shigella boydii*  
 (B) STRAIN: ATCC 9207

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 362

20	TTCCCTCAGG	ATGCCGTACC	GCGCGTGTAC	GATGCTCTTG	AGGTGCAAAA	50
	TGGTAATGAG	CGTCTGGTGC	TGGAAGTTCA	GCAGCAGCTC	GGCGGCGGTA	100
	TCGTGCGTAC	CATCGCAATG	GGTTCCTCCG	ACGGTCTGCG	TCGCGGTCTG	150
	GATGTAAAAG	ACCTCGAACA	CCCGATCGAA	GTCCCGGTAG	GTAAAGCGAC	200
	TCTGGGCCGT	ATCATGAACG	TACTGGGTGA	ACCGGTCGAC	ATGAAAGGCG	250
25	AGATCGGTGA	AGAAGAGCGT	TGGGCGATTC	ACCGCGCAGC	ACCTTCCTAC	300
	GAAGAGCTGT	CAAACCTCTCA	GGAACCTGCTG	GAAACCGGTA	TCAAAGTTAT	350
	CGACCTGATG	TGTCCGTTTCG	CTAAGGGCGG	TAAAGTTGGT	CTGTTCCGGTG	400
	GTGCGGGTGT	AGGTAAAACC	GTAAACATGA	TGGAGCTCAT	TCGTAACATC	450
	GCGATCGAGC	ACTCCGGTTA	CTCTGTGTTT	GCGGGCGTAG	GTGAACGTAC	500
30	TCGTGAGGGT	AACGACTTCT	ACCACGAAAT	GACCGACTCC	AACGTTATCG	550
	ACAAAGTATC	CCTGGTGTAT	GGCCAGATGA	ACGAGCCGCC	GGGAAACCGT	600
	CTGCGCGTTG	CTCTGACCGG	TCTGACCATG	GCTGAGAAAT	TCCGTGACGA	650
	AGGTCGTGAC	GTTCTGCTGT	TCGTTGACAA	CATCTATCGT	TACACCCTGG	700
	CCGGTACGGA	AGTATCCGCA	CTGCTGGGCC	GTATGCCTTC	AGCGGTAGGT	750
35	TATCAGCCGA	CCCTGGCGGA	AGAGATGGGC	GTTCTGCAGG	AACGTATCAC	800
	CTCCACCAAA	ACTGGTTCTA	TCACCTCCGT	A		831

## 2) INFORMATION FOR SEQ ID NO: 363

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 802 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Shigella dysenteriae*  
 (B) STRAIN: ATCC 11835

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 363

55	GCCGTACCGC	GCGTGTACGA	TGCTCTTGCG	GTGCAAAATG	GTAATGAGCG	50
	TCTGGTGCTG	GAAGTTCAGC	AGCAGCTCGG	CGGCGGTATC	GTGCGTACCA	100
	TCGCAATGGG	TTCCTCCGAC	GGTCTGCGTC	GCGGTCTGGA	TGTAAAAGAC	150
	CTCGAACACC	CGATCGAAGT	CCCGGTAGGT	AAAGCGACTC	TGGGCCGTAT	200
60	CATGAACGTA	CTGGGTGAAC	CGGTCGACAT	GAAAGGCGAG	ATCGGTGAAG	250

	AAGAGCGTTG	GGCTATTCAC	CGCGCAGCAC	CTTCCTACGA	AGAGCTGTCA	300
	AACTCTCAGG	AACTGCTGGA	AACCGGTATC	AAAGTTATCG	ACCTGATGTG	350
	TCCGTTTCGCT	AAGGGCGGTA	AAGTTGGTCT	GTTTCGGTGGT	GCGGGTGTAG	400
	GTAACACCGT	AAACATGATG	GAGCTCATTC	GTAACATCGC	GATCGAGCAC	450
5	TCCGGTTACT	CTGTGTTTGC	GGGCGTAGGT	GAACGTA	GTGAGGGTAA	500
	CGACTTCTAC	CACGAAATGA	CCGACTCCAA	CGTTATCGAC	AAAGTATCCC	550
	TGGTGTATGG	CCAGATGAAC	GAGCCGCCGG	GAAACCGTCT	GCGCGTTGCT	600
	CTGACCGGTC	TGACCATGGC	TGAGAAATTC	CGTGACGAAG	GTCGTGACGT	650
	TCTGCTGTTT	GTTGACAACA	TCTATCGTTA	CACCTGGCC	GGTACGGAAG	700
10	TATCCGCACT	GCTGGGCCGT	ATGCCTTCAG	CGGTAGGTTA	TCAGCCGACC	750
	CTGGCGGAAG	AGATGGGCGT	TCTGCAGGAA	CGTATCACCT	CCACCAAAAC	800
	CG					802

15

## 2) INFORMATION FOR SEQ ID NO: 364

## (i) SEQUENCE CHARACTERISTICS:

- 20 (A) LENGTH: 819 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

25

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Shigella flexneri*  
 (B) STRAIN: ATCC 12022

30

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 364

	ATGCCGTACC	GCGCGTGTAC	GATGCTCTTG	AGGTGCAAAA	TGGTAATGAG	50													
	CGTCTGGTGC	TGGAAGTTCA	GCAGCAGCTC	GGCGGCGGTA	TCGTGCGTAC	100													
	CATCGCAATG	GGTTCCTCCG	ACGGTCTGCG	TCGCGGTCTG	GATGTAAAAG	150													
35	ACCTCGAACA	CCCGATCGAA	GTCCCGGTAG	GTAAGCGAC	TCTGGGCCGT	200													
	ATCATGAACG	TACTGGGTGA	ACCGGTCGAC	ATGAAAGGCG	AGATCGGTGA	250													
	AGAAGAGCGT	TGGGCGATTC	ACCGCGCAGC	ACCTTCCTAC	GAAGAGCTGT	300													
	CAA	ACTCTCA	GGA	ACTGCTG	GAA	ACCGGTA	TCAA	AGTTAT	CG	ACCT	GATG	350							
	TGT	CCGTT	CG	CTA	AGGG	CGG	TAA	AGTT	GGT	CT	GTT	CGGT	G	GT	GCGGG	TGT	400		
40	AGGT	AAA	ACC	GTA	AAC	ATGA	TGG	AGCT	CAT	TCG	TAA	CATC	GCG	ATC	GAG	C	450		
	ACT	CCG	GTTA	CT	CT	GTT	GTT	GCG	GGC	GTA	G	TGA	AC	GTA	C	TCG	TGAGGGT	500	
	AAC	GACT	TCT	ACC	AC	GAA	AAT	GAC	CG	ACT	CC	AAC	GTT	ATCG	AC	AA	AGTATC	550	
	CCT	GGT	GTAT	GG	CC	CAG	ATGA	AC	GAG	CC	GC	GG	AA	ACCGT	CT	GCG	CGTTG	600	
	CT	CT	GAC	CGG	TCT	GAC	CATG	GCT	GAG	AA	TCC	GT	GAC	G	AGG	TC	GTGAC	650	
45	GTT	CT	GCT	GT	TC	GT	TGAC	AA	CAT	CT	AT	CGT	TAC	ACC	CT	G	CCGGT	ACGGA	700
	AGT	AT	CCG	CA	CT	GCT	GGG	CC	GTAT	GC	CTTC	AG	CGG	TAG	GT	TAT	CAG	CCGA	750
	CC	CT	GGC	GGA	AG	AG	ATGG	GCG	GTT	CT	G	CAGG	AAC	G	TAT	CAC	CT	CCACCAAA	800
	ACT	G	GTT	TCTA	TC	AC	CTCCG											819	

50

## 2) INFORMATION FOR SEQ ID NO: 365

## (i) SEQUENCE CHARACTERISTICS:

- 55 (A) LENGTH: 802 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

60

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Shigella sonnei*

(B) STRAIN: ATCC 29930

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 365

	GTACCGCGCG	TGTACGATGC	TCTTGAGGTG	CAAAATGGTA	ATGAGCGTCT	50
	GGTGCTGGAA	G TTCAGCAGC	AGCTCGGCGG	CGGTATCGTG	CGTACCATCG	100
10	CAATGGGTTC	CTCCGACGGT	CTGCGTCGCG	GTCTGGATGT	AAAAGACCTC	150
	GAACACCCGA	TCGAAGTCCC	GGTAGGTAAA	GCGACTCTGG	GCCGTATCAT	200
	GAACGTACTG	GGTGAACCGG	TCGACATGAA	AGGCGAGATC	GGTGAAGAAG	250
	AGCGTTGGGC	GATTCACCGC	GCAGCACCTT	CCTACGAAGA	GCTGTCAAAC	300
	TCTCAGGAAC	TGCTGGAAAC	CGGTATCAAA	GTTATCGACC	TGATGTGTCC	350
15	GTTCGCTAAG	GGCGGTAAAG	TTGGTCTGTT	CGGTGGTGCG	GGTGTAGGTA	400
	AAACCGTAAA	CATGATGGAG	CTCATTCGTA	ACATCGCGAT	CGAGCACTCC	450
	GGTTACTCTG	TGTTTGCGGG	CGTAGGTGAA	CGTACTCGTG	AGGGTAACGA	500
	CTTCTACCAC	GAAATGACCG	ACTCCAACGT	TATCGACAAA	GTATCCCTGG	550
	TGTATGGCCA	GATGAACGAG	CCGCCGGGAA	ACCGTCTGCG	CGTTGCTCTG	600
20	ACCGGTCTGA	CCATGGCTGA	GAAATTCCGT	GACGAAGGTC	GTGACGTTCT	650
	GCTGTTTCGT	GACAACATCT	ATCGTTACAC	CCTGGCCGGT	ACGGAAGTAT	700
	CCGCACTGCT	GGGCCGTATG	CCTTCAGCGG	TAGGTTATCA	GCCGACCCTG	750
	GCGGAAGAGA	TGGGCGTTCT	GCAGGAACGT	ATCACCTCCA	CCAAAACCTGG	800
	TT					802

## 2) INFORMATION FOR SEQ ID NO: 366

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 785 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Staphylococcus aureus*

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 366

	TAACGCCTTG	GTTATTGATG	TGCCTAAAGA	AGAAGGTACA	ATACAACTAA	50
	CATTAGAAGT	TGCGCTGCAA	TTAGGTGACG	ACGTTGTTCG	TACAATTGCG	100
45	ATGGATTCAA	CTGATGGTGT	CCAAAGAGGC	ATGGATGTAA	AAGATACAGG	150
	CAAAGAAATT	AGTGTACCTG	TTGGTGATGA	AACATTAGGT	CGTGTATTTA	200
	ATGTACTAGG	TGAAACAATT	GACCTTAAAG	AAGAAATTAG	TGATTCTGTT	250
	CGCCGCGATC	CTATCCATCG	TCAAGCACCA	GCATTGATG	AACTTCAAC	300
	AGAAGTTCAA	ATTTTAGAAA	CAGGTATTAA	AGTAGTAGAT	TTACTAGCAC	350
50	CTTATATTAA	AGGTGGTAAA	ATCGGATTGT	TCGGTGGTGC	CGGTGTAGGT	400
	AAAACAGTAT	TAATCCAAGA	ATTAATTAAC	AACATCGCTC	AAGAGCACGG	450
	TGGTATTTCT	GTATTCGCCG	GTGTAGGTGA	ACGTACTCGT	GAAGGTAACG	500
	ATTTATACTT	CGAAATGAGT	GATAGTGGTG	TAATTAAGAA	AACAGCCATG	550
	GTATTCGGGC	AAATGAATGA	GCCACCTGGT	GCACGTATGC	GTGTTGCATT	600
55	ATCTGGTTTA	ACAATGGCTG	AATATTTCCG	TGACGAACAA	GGTCAAGACG	650
	TATTATTATT	CATCGATAAC	ATTTTCAGAT	TTACACAAGC	TGGTTCTGAG	700
	GTATCTGCAT	TATTAGGTCG	TATGCCTTCT	GCAGTAGGTT	ACCAACCAAC	750
	ACTTGCTACT	GAAATGGGAC	AATTACAAGA	ACGTA		785

## 2) INFORMATION FOR SEQ ID NO: 367

## (i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 843 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus auricularis*  
 (B) STRAIN: ATCC 33753

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 367

GAACATAACG AAGTGCCTAA TATTAATAAC GCCTTAGTAC TCGATGTTGA 50  
 AAGAGAAGAC GGAACAGTGT CTTTAACTTT AGAAGTAGCT TTACAATTAG 100  
 20 GCGATGACGT TGTTCTGTACC ATTGCAATGG ATTCAACTGA TGGTGTTTAAA 150  
 CGTGGAACG AAGTCAAAGA TACTGGTAAT AGCATTAGCG TACCAAGTCGG 200  
 AGACGAACT TTAGGACGTG TCTTCAACGT TCTAGGTGAA ACAATTGATT 250  
 TAGAAGATAA ACTTGATGAT TCTGCGCGAC GTGACCCTAT ACATAGAGAA 300  
 GCGCCAGCGT TTGATCAATT ATCAACTCAA GTTGAAATTT TAGAAACAGG 350  
 25 AATTAAAGTT GTTGACTTAT TAGCACCTTA TATTAAAGGT GGTAAAGTTG 400  
 GACTCTTCGG TGGTGCCGGT GTTGGTAAAA CCGTTTTAAT CCAAGAATTA 450  
 ATCAACAACA TCGCTCAAGA ACACGGTGGT ATTTTCAGTCT TTGCCGGTGT 500  
 AGGTGAACGT ACACGTGAAG GTAACGACTT GTACTATGAA ATGAGCGACA 550  
 GTGGTGTAAT CAAGAAAACA GCCATGGTCT TCGGACAAAT GAACGAACCA 600  
 30 CCTGGCGCAC GTATGCGTGT TGCTTTATCT GGTTTAACAA TGGCTGAATA 650  
 TTTCCGTGAT GAACAAGGAC AAGACGTATT GTTATTCATC GACAATATTT 700  
 TCCGTTTCAC ACAAGCCGGT TCAGAAGTTT CTGCCTTACT AGGTCGTTTA 750  
 CCATCAGCCG TTGGTTATCA ACCTACATTA GCAACAGAAA TGGGACAATT 800  
 35 ACAAGAACGT ATTACTTCAA CAACAAAAGG ATCAGTTACT TCA 843

## 2) INFORMATION FOR SEQ ID NO: 368

## (i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 849 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- 50 (A) ORGANISM: *Staphylococcus capitis* subsp. *capitis*  
 (B) STRAIN: ATCC 27840

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 368

GCTTTGAACA TAATGAAGTT CCTGATATTA ACAATGCCTT ACACATCGAA 50  
 55 GTTCCTAAAG AAGATAGCAC ACTTCATTTA ACTTTAGAAG TTGCACTTCA 100  
 ATTAGGTGAC GATGTAGTAC GTACAATCGC AATGGACTCA ACTGACGGCG 150  
 TTCAAAGAGG TATGGAAGTT AAAGATACAG GTAAAGATAT TAGCGTACCT 200  
 GTTGGTGATG CAACCTTAGG AAGAGTATTT AACGTATTAG GAGAAACAAT 250  
 CGATTTAGAT GAAAAGATTG ATGATTCAGT ACGTCGTGAT CCTATTCTA 300  
 60 GACAGGCACC TGGCTTCGAT GAATTATCTA CTAAAGTAGA AATCTTAGAA 350

	ACAGGTATCA	AAGTAGTAGA	CTTATTAGCA	CCTTACATTA	AAGGTGGTAA	400
	AATTGGATTA	TTCGGTGGTG	CCGGTGTGG	TAAGACAGTT	TTAATCCAAG	450
	AACTTATCAA	TAATATCGCT	CAAGAGCATG	GTGGTATTTC	AGTATTCGCC	500
	GGTGTTGGTG	AACGTACACG	TGAAGGTAAC	GACCTTTACT	ATGAAATGAG	550
5	CGATAGTGGT	GTAATTAAGA	AAACAGCGAT	GGTATTCGGT	CAGATGAACG	600
	AGCCACCTGG	TGCTCGTATG	CGTGTTGCAT	TATCAGGTTT	AACAATGGCA	650
	GAATATTTCC	GTGATGAAGA	AGGCCAAGAC	GTATTATTAT	TCATTGATAA	700
	TATCTTCAGA	TTCACACAAG	CTGGTTCTGA	AGTTTCAGCA	TTACTTGGAC	750
	GTATGCCTTC	AGCCGTTGGT	TATCAACCAA	CACTTGCTAC	TGAAATGGGT	800
10	CAATTACAAG	AACGTATTAG	TTCAACTAAT	AAAGGTTCTG	TTACTTCAA	849

## 2) INFORMATION FOR SEQ ID NO: 369

15

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 830 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 20 (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- 25 (A) ORGANISM: *Staphylococcus cohnii*  
 (B) STRAIN: DSM 20260

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 369

30	GAAGTTCCAG	AAATTAATAA	TGCCTTAGTT	CTCGATATAG	AAAGAGAAGA	50
	AGGTACTGTT	GAATTAACGT	TAGAAGTTGC	ATTACAACCTT	GGTGATGACG	100
	TAGTACGAAC	AATCGCAATG	GATTCAACTG	ATGGTGTTAA	ACGTGGTACA	150
	GAAGTTAGAG	ATAGCGGAAA	TAGTATCAGC	GTACCAGTTG	GTAATGAAAC	200
	ATTAGGTAGA	GTATTTAATG	TATTAGGTGA	TACGATAGAT	TTAGATGAAG	250
35	ACATAGATGA	CTCAGTGCGT	CGTGACCCAA	TTCATAGAGA	AGCACCTGCA	300
	TTTGATCAGT	TATCTACTAA	AGTTGAAATT	TTAGAAACAG	GTATCAAAGT	350
	CATTGATTTA	TTAGCACCAT	ATATCAAAGG	TGGTAAAGTT	GGATTATTCG	400
	GTGGTGCCGG	TGTTGGTAAA	ACTGTATTAA	TTCAAGAATT	AATCAATAAT	450
	ATCGCTCAAG	AGCATGGTGG	TATATCCGTA	TTTGCTGGTG	TAGGTGAGCG	500
40	TACGCGTGAA	GGTAATGACC	TATACTTTGA	AATGAGTGAT	AGTGGTGTTA	550
	TTAAAAAGAC	AGCTATGGTA	TTTGGACAAA	TGAACGAACC	ACCTGGTGCG	600
	CGTATGCGAG	TAGCACTTTC	TGGTTTAAAC	ATGGCTGAAT	ATTTCCGGGA	650
	TGAACAAGGA	CAAGATGTTC	TATTATTCAT	AGATAACATC	TTTAGATTTA	700
	CTCAAGCTGG	TTCAGAAGTT	TCTGCGTTAT	TAGGTCGTAT	GCCTTCAGCT	750
45	GTTGGTTACC	AACCAACGTT	AGCAACTGAA	ATGGGACAAT	TACAAGAACG	800
	TATTACTTCT	ACAATAAAG	GTTCAAGTAA			830

## 50 2) INFORMATION FOR SEQ ID NO: 370

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 787 bases  
 (B) TYPE: Nucleic acid  
 55 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

## 60 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Staphylococcus epidermidis*  
 (B) STRAIN: ATCC 14990

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 370

5  
 AATAATGCAT TACACATCGA AGTTCCTAAA GAAGATGGAG CGCTTCAATT 50  
 AACATTAGAA GTTGCACTTC AACTAGGTGA CGATGTAGTT CGTACAATTG 100  
 CAATGGACTC AACTGACGGC GTTCAAAGAG GAATGGAAGT TAAAGATACA 150  
 GGTAGAGACA TAAGTGTACC TGTCGGTGAC GTAACCTCTAG GAAGAGTGTT 200  
 10 TAACGTACTA GGAGAAACTA TTGACTTAGA TGAAAAAATT GATGATTGAG 250  
 TACGACGTGA CCCTATCCAT AGACAAGCTC CAGGATTCTGA CGAATTATCA 300  
 ACAAAAGTAG AAATCTTAGA AACTGGTATT AAAGTAGTAG ACTTATTAGC 350  
 ACCTTACATA AAAGGTGGTA AAATTGGATT ATTTGGTGGT GCCGGTGTAG 400  
 GTAAAACCGT ACTAATCCAA GAACTTATTA ATAACATCGC TCAAGAACAC 450  
 15 GGTGGTATCT CAGTATTCGC TGGTGTGGT GAACGTACAC GTGAAGGTAA 500  
 TGATCTTTAC TATGAAATGA GTGACAGTGG TGTATCAAG AAAACTGCAA 550  
 TGGTCTTTGG TCAAATGAAT GAGCCACCTG GTGCACGTAT GCGTGTAGCA 600  
 TTATCCGGAT TAACAATGGC CGAATATTTT CGAGATGAAG AAGGCCAAGA 650  
 TGTGTTATTA TTCATTGATA ACATTTTCAG ATTCACTCAA GCTGGTTCAG 700  
 20 AAGTTTCTGC GTTATTAGGT CGTATGCCAT CAGCTGTTGG TTATCAACCT 750  
 ACACCTTGCTA CAGAAATGGG TCAATTACAA GAACGTA 787

## 25 2) INFORMATION FOR SEQ ID NO: 371

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 830 bases  
 (B) TYPE: Nucleic acid  
 30 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

## 35 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Staphylococcus haemolyticus*  
 (B) STRAIN: ATCC 29970

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 371

40  
 GAAGTACCTG AAATTAATAA CGCCTTAATC ATCGAAGTTC CCAAAGAAGA 50  
 TGGTACTTTT GAATTAACGC TTGAAGTTGC ATTACAATA GGTGATGACG 100  
 TTGTTCTGAC AATTGCTATG GATTCAACAG ATGGTGTTC ACGTGGTATG 150  
 GAAGTTTCTA AACTGGAAG AGACATTTCA GTACCAGTTG GCGAAGTAAC 200  
 45 TTTAGGACGT GTATTTAACG TATTAGGTGA CACAATTGAT TTAGAAGATA 250  
 AATTAGATGG TTCAGTAAGA CGTGATCCAA TTCATAGACA ATCACCTAAC 300  
 TTTGACGAAT TATCTACTGA AGTAGAAATT CTTGAAACTG GAATCAAAGT 350  
 TGTAGACTTA TTAGCACCAT ACATCAAAGG TGGTAAAATC GGTCTATTTG 400  
 GTGGTGCCGG TGTGTTGTAAG ACCGTTTAA TCCAAGAATT GATTAATAAT 450  
 50 ATCGCACAAAG AACATGGTGG TATCTCAGTA TTTGCTGGTG TAGGTGAACG 500  
 TACACGTGAA GGTAACGACC TATATTATGA AATGAGAGAT AGTGGTGTGA 550  
 TTAAGAAAAC AGCAATGGTA TTTGGTCAAA TGAACGAGCC ACCTGGTGCA 600  
 CGTATGCGTG TGGCACTTTC TGCATTGACA ATGGCTGAGT ATTTCCGTGA 650  
 TGAACAAGGA CAAGACGTTT TGTATTTCAT CGATAACATT TTCAGATTTA 700  
 55 CTCAAGCAGG TTCAGAAGTA TCAGCATTAT TGGGACGTAT GCCTTCAGCT 750  
 GTAGGTTATC AACCTACTTT AGCTACAGAA ATGGGTCAAT TACAAGAACG 800  
 TATTACATCA ACGAATAAAG GTTCAGTAAC 830

## 2) INFORMATION FOR SEQ ID NO: 372

## (i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 846 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus hominis* subsp. *hominis*  
 (B) STRAIN: ATCC 27844

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 372

TCGAACATAA TGAAGTCCCT GAAATTAATA ATGCCCTAAT TATTGAAGTA 50  
 CCCAAAAATG ATGGCACATT TAAATTAACA TTAGAAGTTG CATTGCAACT 100  
 AGGTGATGAT GTTGTTTCGTA CTATTGCAAT GGATTCAACT GATGGTGTTC 150  
 20 AACGTGGTAT GCAAGTTGTG AATACTGGTA AAGATATTAG TGTTCTGTGA 200  
 GGTGAAGAAA CACTTGGACG TGTGTTTAAC GTTTTAGGAG AAACAATAGA 250  
 TTAAACGAA AAAATAGATA GTTCTGTTAG ACGTGATCCA ATTCATCGTC 300  
 GTCAACCTAA TTTTGATGAA TTATCTACTG AAGTAGAAAT TCTTGAAACA 350  
 GGTATTAAAG TTGTAGACTT ATTAGCACCT TATATTAAAG GTGGTAAGAT 400  
 25 TGGTTTATTC GGTGGTGCCG GCGTAGGTAA AACTGTATTA ATTCAGAAT 450  
 TAATCAATAA TATCGCTCAA GAACATGGTG GTATTTCTGT ATTCGCTGGT 500  
 TAGGTGAAC GTACTCGTGA AGGTAACGAT TTATACTATG AAATGAGCGA 550  
 TAGTGGCGTT ATCAATAAAA CAGCCATGGT ATTTGGGCAA ATGAATGAGC 600  
 CGCCAGGTGC GCGTATGCGT GTTGCTTTAT CAGCATTGAC AATGGCTGAA 650  
 30 TATTTCCGTG ATGAACAAGG TCAAGATGTA CTTTTATTCA TTGACAATAT 700  
 TTTCCGCTTT ACTCAAGCTG GTTCTGAAGT TTCAGCATTA TTAGGACGTA 750  
 TGCCTTCAGC TGTAGGTTAT CAACCTACAT TAGCAACTGA AATGGGTCAA 800  
 TTACAAGAAC GTATTACATC TACTAATAAA GGTTCAGTCA CTTCAA 846

## 2) INFORMATION FOR SEQ ID NO: 373

## (i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 846 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus hominis*  
 (B) STRAIN: CSG 175

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 373

TCGAACATAA TGAAGTCCCT GAAATTAATA ATGCCCTAAT TATTGAAGTA 50  
 CCCAAAAATG ATGGCACATT CAAATTAACA TTAGAAGTTG CATTGCAACT 100  
 55 AGGTGATGAT GTTGTTTCGTA CTATTGCAAT GGATTCAACT GATGGTGTTC 150  
 AACGTGGTAT GCAAGTTGTG AATACTGGTA AAGATATTAG TGTTCTGTGA 200  
 GGTGAAGAAA CACTTGGACG TGTGTTTAAC GTTTTAGGAG AAACAATAGA 250  
 TTAAACGAA AAAATAGATA GTTCTGTTAG ACGTGATCCA ATTCATCGTC 300  
 GTCAACCTAA TTTTGATGAA TTATCTACTG AAGTAGAAAT TCTTGAAACA 350  
 60 GGTATTAAAG TTGTAGACTT ATTAGCACCT TATATTAAAG GTGGTAAGAT 400



	TGGTTTATTC	GGTGGTGCCG	GCGTAGGTAA	AACTGTATTA	ATTCAAGAAT	450
	TAATCAATAA	TATCGCTCAA	GAACATGGTG	GTATTTCTGT	ATTCGCTGGT	500
	GTAGGTGAAC	GTACTCGTGA	AGGTAACGAT	TTATACTATG	AAATGAGCGA	550
	TAGTGGCGTT	ATCAATAAAA	CAGCCATGGT	ATTTGGGCAA	ATGAATGAGC	600
5	CGCCAGGTGC	GCGTATGCGT	GTTGCTTTAT	CAGCATTGAC	AATGGCTGAA	650
	TATTTCCGTG	ATGAACAAGG	TCAAGATGTA	CTTTTATTCA	TTGACAATAT	700
	TTTCCGCTTT	ACTCAAGCTG	GTTCTGAAGT	TTCAGCATT	TTAGGACGTA	750
	TGCCTTCAGC	TGTAGGTTAT	CAACCTACAT	TAGCAACTGA	AATGGGTCAA	800
10	TTACAAGAAC	GTATTACATC	TACTAATAAA	GGTTCAGTCA	CTTCAA	846

## 2) INFORMATION FOR SEQ ID NO: 374

## 15 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 835 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

20

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus lugdunensis*  
 (B) STRAIN: ATCC 43809

25

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 374

	ATAATGAAGT	GCCTGAAATA	AATAATGCGC	TCATTGTTGA	AATTCCTAAA	50
30	AGTGATACAA	CAATCAGTTT	AACACTTGAA	GTTGCTTTGC	AATTAGGTGA	100
	CGATGTTGTA	CGTACTATTG	CAATGGATTTC	AACTGATGGC	GTTCAACGTG	150
	GTATGGAAGT	TCAAAACACA	GGTAAAGACA	TCAGTGTACC	TGTTGGAGAT	200
	GAAACATTAG	GAAGAGTATT	TAACGTTTTA	GGAGAATCTA	TTGATTTAGA	250
	AGAAAAGCTA	GATGACTCTG	TGCGTAGAGA	TCCAATTCAT	AGACTAGCAC	300
35	CTAAATTTGA	TGAATTATCT	ACAGAAGTAG	AAATTCTTGA	AACTGGTATT	350
	AAAGTTGTTG	ATTTATTAGC	ACCATATATT	AAAGGTGGTA	AAGTTGGATT	400
	GTTTGGTGGT	GCCGGAGTAG	GTAAAACGGT	ATTAATTCAA	GAATTAATCA	450
	ACAATATTGC	TCAAGAACAT	GGTGGTATTT	CTGTGTTTGC	CGGAGTAGGT	500
	GAACGTACAC	GTGAAGGTAA	TGACTTATAT	TATGAAATGA	GCGATAGTGG	550
40	CGTAATTAAG	AAAACAGCGA	TGGTATTTGG	CCAAATGAAT	GAACCACCTG	600
	GTGCACGTAT	GAGAGTTGCG	TTATCTGCCT	TAACAATGGC	TGAATATTTT	650
	CGTGACGAGC	AAGGACAAGA	CGTATTGCTG	TTTATCGATA	ATATATTCCT	700
	TTTTACACAA	GCAGGTTTCAG	AAGTATCTGC	ATTACTTGGA	CGTATGCCAT	750
	CTGCCGTTGG	TTATCAACCA	ACATTGGCTA	CAGAAATGGG	ACAATTGCAA	800
45	GAAAGAATTA	CATCTACAAA	TAAAGGTTCT	GTAAC		835

## 2) INFORMATION FOR SEQ ID NO: 375

50

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 842 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

55

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus saprophyticus*

60

(B) STRAIN: ATCC 15305

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 375

5	GAGCACAATG	AAGTTCCAGA	AATTAACAAT	GCCTTAGTCTG	TAGACGTTGA	50
	AAGAGATGAA	GGTACAGTAT	CTCTTACATT	AGAAGTGGCA	TTACAACCTTG	100
	GCGATGATGT	CGTACGTACA	ATTGCAATGG	ATTCTACTGA	TGGTGTTAAA	150
	CGTGGTACAG	AAGTTTCGAGA	TAGCGGAGAT	AGCATCAGTG	TTCCAGTTGG	200
	TGATGCTACG	TTAGGACGTG	TGTTTAATGT	TCTTGGTGAT	ACAATTGACT	250
10	TAGACGAGAA	GCTTGATACT	TCTGTCAAAC	GTGATCCAAT	TCATAGAGAA	300
	GCACCTGCAT	TCGATCAATT	ATCAACAAAA	GTTGAAATCT	TAGAAACAGG	350
	TATTAAAGTA	ATTGATTAC	TTGCACCATA	TATTAAAGGT	GGTAAAATCG	400
	GTTTATTTCGG	TGGCGCTGGT	GTAGGTAAAA	CAGTATTAAT	TCAAGAATTA	450
	ATTAATAATA	TAGCTCAAGA	ACATGGTGGT	ATTTTCAGTAT	TTGCCCGCGT	500
15	AGGTGAACGT	ACGCGTGAAG	GTAATGACTT	ATACTACGAA	ATGAGTGATA	550
	GTGGTGTTAT	TAAGAAAACA	GCTATGGTCT	TCGGACAAAT	GAATGAGCCA	600
	CCTGGTGCGC	GTATGCGTGT	TGCTTTATCA	GGCTTAACAA	TGGCTGAACA	650
	CTTCCGTGAT	GTACAAGGAC	AAGATGTTTT	ACTATTTATT	GATAACATAT	700
	TCAGATTTAC	GCAAGCTGGT	TCAGAAGTAT	CAGCACTATT	AGGTCGTATG	750
20	CCATCAGCCG	TTGGTTATCA	ACCTACCCTT	GCTACTGAAA	TGGGTCAATT	800
	ACAAGAACGT	ATTACATCAA	CAACTAAAGG	ATCTGTAACG	TC	842

## 25 2) INFORMATION FOR SEQ ID NO: 376

## (i) SEQUENCE CHARACTERISTICS:

	(A)	LENGTH: 842 bases
	(B)	TYPE: Nucleic acid
30	(C)	STRANDEDNESS: Double
	(D)	TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

## 35 (vi) ORIGINAL SOURCE:

	(A)	ORGANISM: <i>Staphylococcus simulans</i>
	(B)	STRAIN: ATCC 27848

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 376

40	TGATGAACTG	CCTAAGATTA	ATAACGCATT	AGTGCTAGAT	GTACCTAAGA	50
	AAGATGGCAC	GACTGAATCT	CTTACATTAG	AAGTAGCACT	TGAATTAGGC	100
	GACGACGTAG	TTAGAACTAT	CGCCATGGAC	TCTACAGACG	GAATTAAACG	150
	TGGTGACGAC	GTAAAGACA	CTGGTCGTCC	AATCAGTGTA	CCTGTCGGTG	200
45	AAGATACGTT	AGGAAGAGTA	TTTAACGTTT	TAGGTGATCC	AATCGATAAT	250
	GATGGACCGA	TTTCTGAATC	AGTTCCACGT	GAACCAATTC	ATAGACAACC	300
	ACCTAAATTT	GATGAATTAT	CAACAAAAGT	TGAACACTTT	GAAACTGGTA	350
	TCAAAGTAGT	AGACTTATTA	GCACCATATA	TCAAAGGTGG	TAAAGTTGGT	400
	TTATTCGGTG	GTGCCGGAGT	AGGTAAAACT	GTATTAATCC	AAGAATTAAT	450
50	TAATAACATC	GCTCAAGAAC	ACGGCGGTAT	TTCAGTATTC	GCAGGTGTTG	500
	GTGAACGTAC	ACGTGAAGGT	AACGACTTGT	ACTTCGAAAT	GAGCGACAGT	550
	GGTGTTATCA	AGAAAACAGC	GATGGTATTC	GGACAAATGA	ACGAACCACC	600
	TGGTGACCGT	ATGCGTGTAG	CTTTATCAGG	TTTAACAATG	GCTGAATACT	650
	TCCGTGATGT	TAAAGGACAA	GACGTTCTTT	TATTCATCGA	TAACATTTTC	700
55	CGCTTCACAC	AAGCAGGTTT	TGAGGTATCA	GCATTGCTTG	GCCGTATGCC	750
	ATCAGCCGTT	GGTTACCAAC	CAACATTGGC	AACAGAAATG	GGTCAATTAC	800
	AAGAACGTAT	CACTTCTACA	ATGAAAGGTT	CTATCACATC	TA	842

60

## 2) INFORMATION FOR SEQ ID NO: 377

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 841 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus warneri*  
 (B) STRAIN: ATCC 27836

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 377

CATAACGAAG	TCCCTGATAT	TAATAATGCC	CTTATTATTG	AAGTTCCAAA	50
AGAAGATGGA	ACGTTAAACT	TAACATTAGA	AGTTGCACTA	CAATTAGGTG	100
ATGATGTTGT	ACGTACAATT	GCAATGGATT	CAACTGATGG	TGTTCAAAGA	150
GGCATGGATG	TTAAAGACAC	AGGTAAAGAT	ATTAGTGTAC	CTGTAGGCGA	200
TGAAACGCTT	GGAAGAGTGT	TTAATGTACT	AGGTGAAACA	ATTGACTTGG	250
AAGAGAAAAT	TGATGATTCC	GTACGTCGTG	ATCCAATCCA	TAGACAATCA	300
CCAGGTTTCG	ATGAATTATC	TACTGAAGTA	GAAATCTTAG	AAACAGGTAT	350
TAAAGTAGTA	GACTTATTAG	CACCTTACAT	TAAAGGTGGT	AAAGTTGGAC	400
TATTCGGTGG	TGCCGGAGTA	GGTAAAACCG	TTTAAATCCA	AGAATTAATT	450
AACAATATTG	CACAAGAACA	TGGTGGTATT	TCAGTATTCG	CGGGTGTAGG	500
TGAACGTACT	CGTGAAGGTA	ATGATTTATA	CTATGAAATG	AGTGATAGTG	550
GTGTAATTAA	GAAAACAGCG	ATGGTATTTG	GACAAATGAA	TGAACCACT	600
GGCGCACGTA	TGCGTGTAGC	TTTATCTGGT	TTAACTATGG	CTGAATACTT	650
CCGTGATGAA	CAAGGACAAG	ACGTACTTTT	ATTCATCGAT	AATATTTTCA	700
GATTTACACA	AGCTGGTTCT	GAAGTTTCTG	CATTACTTGG	TCGTATGCCT	750
TCAGCCGTTG	GTTACCAACC	AACATTAGCA	ACTGAAATGG	GTCAATTACA	800
AGAACGAATT	ACATCTACAA	ATAAAGGTTC	TGTAACATCT	A	841

## 2) INFORMATION FOR SEQ ID NO: 378

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 846 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus acidominimus*  
 (B) STRAIN: ATCC 51726

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 378

TTTAACACGA	ATGAACCGCT	TCCTGAGATA	AATAATGCAC	TTGTTGTTTA	50
CAAAGACAGT	GAGAAAAAAC	ATAAAATCGT	TCTTGAAGTA	GCTCTTGAAC	100
TTGGTGAAGG	CCTCGTTCGT	ACCATTGCTA	TGGAATCAAC	TGATGGTTTG	150
ACACGTGGTC	TAGAAGTTCT	TGATACAGGC	CGTGCAATCA	GTGTACCAGT	200
TGGTAAAGAA	ACGCTTGAC	GTGTCTTCAA	CGTTCTTGGT	GATGCTATCG	250
ATCTTGAAGA	ACCATTGGA	GAAGATGCAG	AACGTCACCC	CATTCATAAG	300
AGTGCCCCAA	CTTTTGATGA	ATTATCAACG	TCAACAGAAA	TCCTTGAAAC	350
AGGGATTAAA	GTTATCGACC	TACTTGCCCC	TTACTTAAAA	GGAGGGAAGG	400

	TTGGACTTTT	CGGTGGTGCC	GGAGTTGGTA	AGACCGTTCT	TATCCAAGAG	450
	TTGATTCATA	ACATTGCTCA	AGAGCATGGT	GGTATTTTCAG	TATTTACCGG	500
	AGTTGGTGAA	CGTACACGTG	AAGGTAATGA	CCTCTATTGG	GAAATGAAAG	550
	AATCAGGCGT	TATTGAAAAA	ACAGCTATGG	TATTTGGTCA	GATGAATGAG	600
5	CCACCTGGTG	CACGTATGCG	TGTAGCCCTT	ACTGGTTTGA	CAATCGCTGA	650
	ATATTTCCGT	GATGTTGAAG	GACAGGACGT	GCTTCTCTTT	ATTGATAACA	700
	TTTTTCGTTT	CACACAAGCA	GGTTCTGAAG	TTTCAGCTCT	TCTTGGACGT	750
	ATGCCATCAG	CCGTTGGTTA	TCAACCAACC	TTGGCAACTG	AAATGGGTCA	800
10	ATTGCAAGAA	CGTATCACGT	CAACTAAAAA	AGGTTCTGTT	ACATCA	846

## 2) INFORMATION FOR SEQ ID NO: 379

15 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 846 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

20 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus agalactiae*
- (B) STRAIN: ATCC 12403

25

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 379

	TTGCAAGTGG	CGACAAACTT	CCTGAGATTA	ATAATGCATT	GATTGTCTAT	50
30	AAAAATGGCG	ATAAGTCACA	AAAAGTAGTA	CTTGAAGTTA	CTCTTGAAC	100
	TGGTGACGGC	CTCGTTCGTA	CAATCGCTAT	GGAATCAACT	GATGGGCTTA	150
	CACGTGGTTT	GGAAGTATTA	GATACTGGTC	GCGCAATTAG	TGTGCCGGTT	200
	GGTAAGGATA	CTTTGGGTCG	TGTCTTCAAC	GTTCTTGGAG	ATGCTATTGA	250
	CCTTGAAGAG	CCTTTTGCAG	AAGATGCAGA	ACGTCAACCA	ATCCATAAAA	300
35	AAGCACCATC	GTTTGATGAA	TTATCAACAT	CATCAGAAAT	CTTAGAAACA	350
	GGTATTAAAG	TTATTGACTT	ATTAGCACCT	TACTTAAAAG	GTGGTAAAGT	400
	TGGACTTTTC	GGTGGTGCA	GTGTTGGTAA	AACCGTTCTT	ATTCAAGAAT	450
	TAATCCACAA	CATCGCCCAA	GAACATGGTG	GTATTTTCAGT	ATTTACTGGT	500
	GTAGGAGAAC	GTAATCGTGA	AGGGAATGAC	CTTTATTGGG	AAATGAAAGA	550
40	ATCTGGCGTT	ATTGAAAAAA	CGGCTATGGT	CTTTGGTCAA	ATGAATGAAC	600
	CACCAGGAGC	ACGTATGCGT	GTGGCACTTA	CTGGTCTTAC	AATAGCTGAG	650
	TACTTCCGTG	ATGTAGAAGG	ACAAGATGTG	CTTCTCTTCA	TTGATAATAT	700
	CTTCCGTTTC	ACACAAGCTG	GGTCAGAAGT	GTCAGCGCTT	TTAGGTCGTA	750
	TGCCTTCAGC	CGTTGGTTAT	CAACCAACAC	TTGCTACAGA	AATGGGACAA	800
45	TTACAAGAGC	GTATCACTTC	AACTAAAAAA	GGTTCTGTTA	CCTCAA	846

## 2) INFORMATION FOR SEQ ID NO: 380

50 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 846 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

55 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus agalactiae*

60

(B) STRAIN: ATCC 13813

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 380

5	TTGCAAGTGG	CGACAAACTT	CCTGAGATTA	ATAATGCATT	GATTGTCTAT	50
	AAAAATGGCG	ATAAGTCACA	AAAAGTAGTA	CTTGAAGTTG	CTCTTGAACT	100
	TGGTGACGGC	CTCGTTCGTA	CAATCGCTAT	GGAATCAACT	GATGGGCTTA	150
	CACGTGGTTT	GGAAGTATTA	GATACTGGTC	GCGCAATTAG	TGTGCCGGTT	200
	GGTAAGGATA	CTTTGGGTCG	TGTCTTCAAC	GTTCTTGGAG	ATGCTATTGA	250
10	TCTTGAAGAG	CCTTTTGCAG	AAGATGCAGA	ACGTCAACCA	ATCCATAAAA	300
	AAGCACCATC	GTTTGATGAA	TTATCAACAT	CATCAGAAAT	CTTAGAAACT	350
	GGTATTAAAG	TTATTGACTT	ATTAGCACCT	TACTTAAAAG	GTGGTAAAGT	400
	TGGACTTTTC	GGTGGTGCGG	GTGTTGGTAA	AACCGTTCTT	ATTCAAGAAT	450
	TAATCCACAA	CATCGCCCAA	GAACATGGTG	GTATTTTCAGT	ATTTACTGGT	500
15	GTAGGAGAAC	GTACTCGTGA	AGGGAATGAC	CTTTATTGGG	AAATGAAAGA	550
	ATCTGGCGTT	ATTGAAAAAA	CGGCTATGGT	CTTTGGTCAA	ATGAATGAAC	600
	CACCAGGAGC	ACGTATGCGT	GTGGCACTTA	CTGGTCTTAC	AATAGCTGAG	650
	TACTTCCGTG	ATGTAGAAGG	ACAAGATGTG	CTTCTCTTCA	TTGATAATAT	700
	CTTCCGTTTC	ACACAAGCTG	GGTCAGAAGT	GTCAGCGCTT	TTAGGTCGTA	750
20	TGCCTTCAGC	CGTTGGTTAT	CAACCAACAC	TTGCTACAGA	AATGGGACAA	800
	TTACAAGAGC	GTATCACTTC	AACTAAAAAA	GGTTCTGTTA	CCTCAA	846

25 2) INFORMATION FOR SEQ ID NO: 381

(i) SEQUENCE CHARACTERISTICS:

	(A)	LENGTH: 845 bases
	(B)	TYPE: Nucleic acid
30	(C)	STRANDEDNESS: Double
	(D)	TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

35 (vi) ORIGINAL SOURCE:

	(A)	ORGANISM: <i>Streptococcus agalactiae</i>
	(B)	STRAIN: ATCC 12973

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 381

40	TTGCAAGTGG	CGACAAACTT	CCTGAGATTA	ATAATGCATT	GATTGTCTAT	50
	AAAAATGGCG	ATAAGTCACA	AAAAGTAGTA	CTTGAAGTTG	CTCTTGAACT	100
	TGGTGACGGC	CTCGTTCGTA	CAATCGCTAT	GGAATCAACT	GATGGGCTTA	150
	CACGTGGTTT	GGAAGTATTA	GATACTGGTC	GTGCAATTAG	TGTGCCGGTT	200
45	GGTAAGGATA	CTTTGGGTCG	TGTCTTCAAC	GTTCTTGGAG	ATGCTATTGA	250
	CCTTGAAGAG	CCTTTTGCAG	AAGATGCAGA	ACGTCAACCA	ATCCATAAAA	300
	AAGCACCATC	ATTTGATGAA	TTATCAACAT	CATCAGAAAT	CTTAGAAACA	350
	GGTATTAAAG	TTATTGACTT	ATTAGCACCT	TACTTAAAAG	GTGGTAAAGT	400
	TGGACTTTTC	GGTGGTGCGG	GTGTTGGTAA	AACCGTTCTT	ATTCAAGAAT	450
50	TAATCCACAA	CATCGCCCAA	GAACATGGTG	GTATTTTCAGT	ATTTACTGGT	500
	GTAGGAGAAC	GTACTCGTGA	AGGGAATGAC	CTTTATTGGG	AAATGAAAGA	550
	ATCTGGCGTT	ATTGAAAAAA	CGGCTATGGT	CTTTGGTCAA	ATGAATGAAC	600
	CACCAGGAGC	ACGTATGCGT	GTGGCACTTA	CTGGTCTTAC	AATAGCTGAG	650
	TACTTCCGTG	ATGTAGAAGG	ACAAGATGTG	CTTCTCTTCA	TTGATAATAT	700
55	CTTCCGTTTC	ACACAAGCTG	GGTCAGAAGT	GTCAGCGCTT	TTAGGTCGTA	750
	TGCCTTCAGC	CGTTGGTTAT	CAACCAACAC	TTGCTACAGA	AATGGGACAA	800
	TTACAAGAGC	GTATCACTTC	AACTAAAAAA	GGTTCTGTTA	CCTCA	845

60

## 2) INFORMATION FOR SEQ ID NO: 382

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 845 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus agalactiae*  
 (B) STRAIN: ATCC 27591

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 382

```

TTGCAAGTGG CGACAAACTT CCTGAGATTA ATAATGCATT GATTGTCTAT      50
AAAAATGGCG ATAAGTCACA AAAAGTAGTA CTTGAAGTTG CTCTTGAACT      100
TGGTGACGGC CTCGTTTCGTA CAATCGCTAT GGAATCAACT GATGGGCTTA      150
CACGTGGTTT GGAAGTATTA GATACTGGTC GCGCAATTAG TGTGCCGGTT      200
GGTAAGGATA CTTTGGGTCG TGTCTTCAAC GTTCTTGGAG ATGCTATTGA      250
CCTTGAAGAG CCTTTTGCAG AAGATGCAGA ACGTCAACCA ATCCATAAAA      300
AAGCACCATC GTTTGTATGAA TTATCAACAT CATCAGAAAT CTTAGAAACT      350
GGTATTAAAG TTATTGACTT ATTAGCACCT TACTTAAAAG GTGGTAAAGT      400
TGGACTTTTC GGTGGTGCAG GTGTTGGTAA AACCGTTCTT ATTCAAGAAT      450
TAATCCACAA CATCGCCCAA GAACATGGTG GTATTTTCAGT ATTTACTGGT      500
GTAGGAGAAC GTACTCGTGA AGGGAATGAC CTTTATTGGG AAATGAAAGA      550
ATCTGGCGTT ATTGAAAAAA CGGCTATGGT CTTTGGTCAA ATGAATGAAC      600
CACCAGGAGC ACGTATGCGT GTGGCACTTA CTGGTCTTAC AATAGCTGAG      650
TACTTCCGTG ATGTAGAAGG ACAAGATGTG CTTCTCTTCA TTGATAATAT      700
CTTCCGTTTC ACACAAGCTG GGTGAGAAGT GTCAGCGCTT TTAGGTCGTA      750
TGCCTTCAGC CGTTGGTTAT CAACCAACAC TTGCTACAGA AATGGGACAA      800
TTACAAGAGC GTATCACTTC AACTAAAAAA GGTTCCTGTTA CATCA          845

```

## 2) INFORMATION FOR SEQ ID NO: 383

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 845 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus agalactiae*  
 (B) STRAIN: CDC ss1073

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 383

```

TTGCAAGTGG CGACAAACTT CCTGAGATTA ATAATGCATT GATTGTCTAT      50
AAAAATGGCG ATAAGTCACA AAAAGTAGTA CTTGAAGTTG CTCTTGAACT      100
TGGTGACGGC CTCGTTTCGTA CAATCGCTAT GGAATCAACT GATGGGCTTA      150
CACGTGGTTT GGAAGTATTA GATACTGGTC GCGCAATTAG TGTGCCGGTT      200
GGTAAGGATA CTTTGGGTCG TGTCTTCAAC GTTCTTGGAG ATGCTATTGA      250
CCTTGAAGAG CCTTTTGCAG AAGATGCAGA ACGTCAACCA ATCCATAAAA      300
AAGCACCATC GTTTGTATGAA TTATCAACAT CATCAGAAAT CTTAGAAACT      350
GGTATTAAAG TTATTGACTT ATTAGCACCT TACTTAAAAG GTGGTAAAGT      400

```

```

TGGACTTTTC GGTGGTGCAG GTGTTGGTAA AACCGTTCTT ATTCAAGAAT 450
TAATCCACAA CATCGCCCAA GAACATGGTG GTATTTTCAGT ATTTACTGGT 500
GTAGGAGAAC GTACTCGTGA AGGGAATGAC CTTTATTGGG AAATGAAAGA 550
ATCTGGCGTT ATTGAAAAAA CGGCTATGGT CTTTGGTCAA ATGAATGAAC 600
5 CACCAGGAGC ACGTATGCGT GTGGCACTTA CTGGTCTTAC AATAGCTGAG 650
TACTTCCGTG ATGTAGAAGG ACAAGATGTG CTTCTCTTCA TTGATAATAT 700
CTTCCGTTTC ACACAAGCTG GGTCAGAAAGT GTCAGCGCTT TTAGGTCGTA 750
TGCCTTCAGC CGTTGGTTAT CAACCAACAC TTGCTACAGA AATGGGACAA 800
TTACAAGAGC GTATCACTTC AACTAAAAAA GGTTCTGTTA CATCA 845
10

```

## 2) INFORMATION FOR SEQ ID NO: 384

## 15 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 845 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

20

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus dysgalactiae*  
 25 (B) STRAIN: ATCC 43078

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 384

```

TTGCTAGTGG GGACAAACTT CCAGAGATTA ATAATGCATT GATTGTTTAT 50
30 AAAGATAGTG ATAAAAAGCA AAAAATCGTC CTTGAAGTTG CTCTGGAACT 100
TGGTGACGGT ATGGTGCGAA CAATCGCTAT GGAATCAACT GATGGGCTTA 150
CACGTGGGTT AGAAGTTCTT GACACTGGTC GTGCGATTAG TGTACCAGTA 200
GGTAAAGAAA CTTTGGGACG CGTCTTTAAT GTACTTGGAG AAACCATTGA 250
CTTGGAAGAA CCATTTGCAG AAGACGTTGA CCGTCAGCCA ATCCATAAAA 300
35 AAGCACCATC GTTTGATGAA TTATCAACAT CATCAGAAAT TCTTGAAACT 350
GGTATCAAGG TAATTGACCT TCTTGCCCCT TACCTTAAAG GTGGTAAAGT 400
TGGACTTTTC GGGGGTGCCG GAGTTGGTAA GACTGTCCTT ATCCAAGAAT 450
TAATCCACAA TATCGCCCAA GAACACGGAG GTATTTTCAGT ATTTACCGGT 500
GTTGGTGAGC GAACACGTGA AGGAAATGAC CTTTACTGGG AAATGAAAGA 550
40 ATCAGGCGTT ATTGAGAAAA CTGCCATGGT TTTTGGTCAG ATGAATGAGC 600
CGCCTGGGGC ACGTATGCGT GTAGCCCTTA CTGGTTTAAAC CATTGCTGAG 650
TATTTCCGTG ATGTAGAAGG CCAAGATGTT TTGCTCTTTA TTGATAATAT 700
CTTCCGTTTC ACTCAGGCAG GTTCAGAAAGT ATCAGCCCTC TTAGGCCGTA 750
TGCCTTCTGC TGTGTTGTTAC CAACCGACCC TTGCTACTGA AATGGGACAA 800
45 TTGCAAGAAC GTATTACGTC AACTCAAAAA GGATCTGTTA CTTCT 845

```

## 2) INFORMATION FOR SEQ ID NO: 385

50

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 846 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 55 (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus equi* subsp. *equi*

(B) STRAIN: ATCC 9528

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 385

5	TTGCGAGTGG	GGACAAACTA	CCAGAGATTA	ATAATGCGTT	GATAGTTTAT	50
	AAAGATGGCG	ATAAAAAGCA	AAAAATCGTT	CTCGAGGTTG	CCCTAGAGCT	100
	TGGAGACGGT	ATGGTACGTA	CAATTGCTAT	GGAATCAACC	GATGGGCTTA	150
	CACGTGGATT	AGAGGTTCTT	GATACTGGTC	GTGCCATTAG	TGTACCAGTT	200
	GGTAAAGAGA	CTCTAGGTCG	TGTTTTCAAC	GTTCTTGGTG	AAACCATCGA	250
10	CCTAGAAGCA	CCATTTGCAG	ATGATGTTAA	TCGTGAACCG	ATCCATAAAA	300
	AAGCACCAGC	CTTTGATGAA	TTGTCAACAT	CATCAGAAAT	TCTTGAAACA	350
	GGTATCAAGG	TTATTGACCT	GCTTGCCCCCT	TACTTAAAGG	GTGGTAAGGT	400
	CGGTCTTTTC	GGTGGTGCCG	GAGTTGGTAA	AACCGTTCTT	ATCCAAGAAT	450
	TAATCCACAA	TATCGCTCAA	GAGCATGGTG	GGATCTCGGT	ATTTACCGGT	500
15	GTTGGTGAGC	GTACGCGTGA	AGGAAATGAC	CTTTACTGGG	AAATGAAGGA	550
	ATCAGGCGTT	ATTGAAAAAA	CAGCCATGGT	TTTTGGTCAG	ATGAATGAAC	600
	CACCAGGAGC	CCGTATGCGT	GTTGCCTTGA	CCGGCTTGAC	AATTGCTGAA	650
	TATTTCCGCG	ATGTTGAAGG	CCAAGACGTC	CTGCTCTTCA	TTGACAATAT	700
	TTTCCGCTTT	ACTCAAGCAG	GCTCAGAGGT	ATCAGCCCTT	CTAGGTCGTA	750
20	TGCCTTCAGC	CGTTGGTTAC	CAGCCAACAC	TTGCCACTGA	AATGGGACAA	800
	TTGCAAGAGC	GTATCACCTC	AACGAAAAAA	GGCTCTGTTA	CCTCTA	846

## 25 2) INFORMATION FOR SEQ ID NO: 386

## (i) SEQUENCE CHARACTERISTICS:

	(A)	LENGTH: 846 bases
	(B)	TYPE: Nucleic acid
30	(C)	STRANDEDNESS: Double
	(D)	TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

## 35 (vi) ORIGINAL SOURCE:

	(A)	ORGANISM: <i>Streptococcus anginosus</i>
	(B)	STRAIN: ATCC 27335

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 386

40	TTGCAGCTGG	TGATAAATTA	CCTGAGATAA	ATAATGCACT	TGTAGTCTAT	50
	AAAAATGACG	AAAATAAATC	AAAAATCGTC	CTTGAAGTAG	CTCTTGAGCT	100
	TGGTGATGGA	GTGGTTCGAA	CTATTGCCAT	GGAATCCACT	GATGGGTTGA	150
	CTCGTGGCAT	GGAAGTTCTA	GATACTGGTC	GACCAATTTT	TGTTCCAGTT	200
45	GGGAAAGAAA	CACTTGGTTC	CGTCTTTAAC	GTTTTAGGCG	ATACCATTGA	250
	TTTGATACT	CCATTCGGCG	AAGATGCAGA	ACGTCAACCA	ATCCATAAAA	300
	AAGCTCCAAC	TTTTGATGAG	TTATCTACTT	CATCAGAAAT	CTTAGAAACA	350
	GGAATAAAGG	TTATTGACCT	TTTAGCCCCC	TACCTCAAAG	GTGGGAAAGT	400
	CGGCCTCTTC	GGTGGTGCTG	GCGTTGGGAA	AACTGTCTTG	ATTCAAGAGT	450
50	TGATTCATAA	TATCGCCCAA	GAACACGGCG	GGATTTCAGT	CTTTACTGGT	500
	GTTGGGGAAC	GAAGTCGTGA	AGGGAATGAC	CTGTACTGGG	AAATGAAAGA	550
	ATCTGGTGTT	ATCGAAAAGA	CGGCTATGGT	CTTTGGGCAA	ATGAATGAAC	600
	CGCCTGGAGC	ACGTATGCGT	GTAGCTTTGA	CTGGGTTAAC	GATTGCAGAG	650
	TATTTCCGTG	ATGTGGAAGG	TCAAGATGTT	CTTTTGTTTA	TTGATAATAT	700
55	TTTCCGTTTC	ACTCAAGCTG	GTTCTGAAGT	GTCAGCCCTT	CTTGGTCGTA	750
	TGCCATCAGC	TGTTGGTTAC	CAACCAACCT	TGGCTACTGA	AATGGGGCAA	800
	TTACAAGAAC	GTATTACATC	AACGAAAAAA	GGTTCTGTTA	CCTCAA	846



## 2) INFORMATION FOR SEQ ID NO: 387

## (i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 843 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- 10 (A) ORGANISM: *Streptococcus salivarius*  
 (B) STRAIN: ATCC 7073

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 387

15 GCAGCTGGTG ATAAACTTCC TGAGATTAAC AATGCATTGG TCGTTTATAC 50  
 TGATGAACAA AAGTCTAAAC GTATCGTGCT CGAAGTAGCT CTTGAACTTG 100  
 GAGAAGGTGT GGTTCGTACC ATTGCCATGG AATCTACTGA TGGATTGACT 150  
 20 CGTGGACTAG AAGTTCTGGA CACTGGTCGT CCAATCAGCG TTCCTGTTGG 200  
 TAAAGATACC CTTGGACGTG TCTTTAACGT TCTTGGTGAT ACCATTGACT 250  
 TGGAAGCACC TTTTGCAGAC GATGCAGAGC GTGAACCAAT TCACAAAAAA 300  
 GCACCAACTT TCGATGAATT GTCAACATCT ACTGAAATCC TTGAAACAGG 350  
 GATTAAAGTT ATCGACTTGC TAGCCCCTTA CCTTAAGGGT GGTAAGTCG 400  
 25 GACTCTTCGG TGGTGCCGGT GTTGGTAAAA CCGTTCTTAT TCAAGAGTTG 450  
 ATTCACAACA TTGCCAAGA GCACGGTGGT ATTTCCGTGT TTACAGGTGT 500  
 TGGTGAACGT ACACGTGAAG GTAATGACCT TTACTGGGAA ATGAAAGAAT 550  
 CTGGCGTTAT CGAGAAAACA GCCATGGTCT TCGGTCAAAT GAACGAACCA 600  
 CCTGGAGCAC GTATGCGTGT TGCCCTTACT GGTTTGACAA TTGCGGAATA 650  
 30 CTTCCGTGAT GTCGAGGGTC AAGACGTTCT TCTCTTCATC GATAACATCT 700  
 TCCGTTTCAC TCAAGCAGGT TCTGAGGTTT CTGCCCTTCT TGGTCGTATG 750  
 CCATCAGCCG TTGGTTACCA ACCTACACTT GCTACTGAAA TGGGTCAATT 800  
 GCAAGAACGT ATCACATCAA CTAAAAAAGG TTCTGTTACA TCT 843

## 2) INFORMATION FOR SEQ ID NO: 388

## (i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 841 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- 45 (A) ORGANISM: *Streptococcus suis*  
 (B) STRAIN: ATCC 43765

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 388

55 TTGCAGCAGA AGATAAACTT CCTGAGATTA ACAACGCACT CGTTGTATAT 50  
 AAAAATGATG ATTCCAAACA AAAAGTCGTG CTTGAAGTGG CTTTGGAAGT 100  
 TGGTGATGGC GTTGACGGA CCATTGCCAT GGAATCAACG GATGGATTGA 150  
 CACGTGGGAT GGAAGTTCTC GATACAGGTC GTCCCATCTC TGTTCCAGTC 200  
 GGTAAAGAAA CGCTGGGTCTG TGTCTTCAAT GTGTTGGGAG ATACCATTGA 250  
 CTTGAAGAG TCTTTTCCGG CAGATTTTGA ACGTGAGCCT ATCCATAAGA 300  
 AAGCGCCGGC TTTTGACGAA TTATCTACTT CAAGCGAAAT TTTGGAAACA 350  
 60 GGGATTAAGG TTATCGACCT CTTAGCACCT TATCTAAAAG GTGGTAAGGT 400

	TGGTCTCTTC	GGTGGTGCTG	GTGTTGGTAA	AACCGTTCTT	ATCCAAGAAT	450
	TGATTCACAA	TATTGCCCAA	GAACACGGTG	GTATCTCTGT	ATTTACCGGA	500
	GTTGGCGAGC	GTACCCGTGA	AGGGAACGAT	CTTTACTGGG	AAATGAAAGA	550
	ATCAGGTGTT	ATTGAAAAAA	CGGCCATGGT	ATTTGGTCAG	ATGAATGAGC	600
5	CACCAGGAGC	CCGTATGCGT	GTTGCTCTTA	CTGGTTTGAC	TATTGCGGAA	650
	TACTTCCGTG	ATGTGGAAGG	GCAGGATGTT	CTTCTGTTCA	TCGATAATAT	700
	CTTCCGTTTC	ACACAGGCTG	GTTCAGAAGT	GTCTGCCCTC	TTGGGTCGTA	750
	TGCCATCAGC	CGTTGGTTAT	CAGCCAACAC	TTGCGACGGA	GATGGGACAA	800
	TTGCAGGAGC	GTATTACCTC	AACCAAGAAG	GGTTCTGTTA	C	841

## 2) INFORMATION FOR SEQ ID NO: 389

## 15 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 844 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

## 20 (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus uberis*  
 (B) STRAIN: ATCC 19436

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 389

	GCAAACGGTG	AAAAATTACC	AGAGATTAAT	AATGCATTGA	TAGTTTATAA	50
30	AGGTAGCGAT	AAAAAACAAA	AGATTGTTCT	TGAAGTTGCT	TTGGAACCTG	100
	GGGACGGAAT	GGTTCGTACA	ATCGCTATGG	AATCAACTGA	TGGGCTTACA	150
	CGTGGATTAG	AAGTTTTAGA	TACTGGCCGT	GCCATTAGTG	TACCAGTCGG	200
	AAAAGAAACT	TTGGGTCGTG	TTTTCAATGT	GCTTGGTGAA	ACCATTGATT	250
	TGGATGAACC	ATTTGCCGCT	GATGCTGCAA	GAGAACCCAT	CCATAAAAAA	300
35	GCCCCAGCAT	TTGATGAACT	ATCAACGTCT	TCAGAAATTC	TTGAAACCGG	350
	AATAAAAGTT	ATTGACTTAT	TAGCCCCTTA	TCTCAAAGGT	GGTAAAGTTG	400
	GTTTATTTGG	TGGTGCCGGA	GTAGGTAAAA	CGGTTTTAAT	TCAAGAATTA	450
	ATTCATAATA	TTGCACAAGA	ACATGGTGGT	ATTTTCAGTAT	TTACCGGTGT	500
	TGGTGAAAGA	ACTCGTGAAG	GTAATGACCT	TTATTGGGAA	ATGAAAGAAT	550
40	CTGGCGTTAT	TGAAAAAACA	GCCATGGTAT	TTGGACAAAT	GAACGAACCA	600
	CCAGGAGCAC	GTATGCGCGT	TGCTTTAACA	GGTTTAACCA	TTGCTGAATA	650
	TTTCCGGGAT	GTTGAAGGTC	AAGATGTTTT	GCTCTTTATT	GACAACATTT	700
	TCCGTTTCAC	GCAAGCTGGT	TCAGAAGTTT	CAGCCCTATT	GGGTCGTATG	750
	CCTTCAGCGG	TAGGATACCA	ACCAACACTT	GCTACCGAAA	TGGGACAATT	800
45	GCAAGAAAGA	ATTACCTCAA	CTAACAAGGG	ATCTGTACT	TCTA	844

## 2) INFORMATION FOR SEQ ID NO: 390

## 50 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 896 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Tatumella ptyseos*

(B) STRAIN: ATCC 33301

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 390

5	TTCCCTCAGG	ACGCTGTACC	ACAGGTGTAC	AACGCTCTTG	AGGTTGAAAA	50
	TGGTGATACC	CGTCTGGTGC	TGGAAGTTCA	GCAGCAGCTG	GGCGGTGGTG	100
	TCGTTCTGAC	GATTGCAATG	GGAACCTCTG	ACGGCCTGAA	ACGTGGCCTT	150
	AAGGTGACCG	ATCTGCAAAA	ACCGATTCTG	GTACCGGTCTG	GTAAAGCGAC	200
	GCTGGGCCGT	ATCATGAACG	TACTGGGTCA	GCCAATCGAT	ATGAAAGGCG	250
10	ACCTGAAGAA	CGAAGATGGT	AGCAATGTTG	AGGTGAACTC	TATTCACCGT	300
	GCAGCGCCAA	GCTACGAAGA	ACTGGCTAAC	TCTACTGAGC	TGCTGGAAAC	350
	GGGTATCAAG	GTTATCGACC	TGATCTGTCC	GTTTGCAAAA	GGCGGTAAAG	400
	TGGGTCTGTT	CGGTGGTGCG	GGTGTAGGTA	AGACCGTCAA	CATGATGGAA	450
	CTGATCCGTA	ACATCGCTAT	CGAGCACTCT	GGTACTCTG	TATTTGCAGG	500
15	GGTGGGTGAG	CGTACCCGTG	AAGGTAACGA	CTTCTACCAC	GAAATGACCG	550
	AGTCTAACGT	TCTGGATAAA	GTTGCTCTGG	TTTATGGCCA	GATGAACGAG	600
	CCACCAGGAA	ACCGTCTGCG	CGTTGCGCTG	ACCGGTCTGA	CTATGGCTGA	650
	AAAATTCCGT	GACGAAGGCC	GTGACGTACT	GCTGTTTCGT	GATAACATCT	700
	ATCGTTATAC	CCTGGCCCGT	ACTGAAGTTT	CAGCACTGCT	GGGTCGTATG	750
20	CCTTCTGCGG	TAGGTTATCA	GCCAACACTG	GCCGAAGAAA	TGGGTGTTCT	800
	TCAGGAACGT	ATCACGTCAA	CCAAAACCGG	TTCAATCACT	TCCGTA	896

25 2) INFORMATION FOR SEQ ID NO: 391

(i) SEQUENCE CHARACTERISTICS:

	(A)	LENGTH: 829 bases
	(B)	TYPE: Nucleic acid
30	(C)	STRANDEDNESS: Double
	(D)	TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

35 (vi) ORIGINAL SOURCE:

	(A)	ORGANISM: <i>Trabulsiella guamensis</i>
	(B)	STRAIN: ATCC 49490

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 391

40	TTCCCTCAGG	ATGCCGTACC	GCGCGTGTAC	GATGCTCTTG	AGGTTATGAA	50
	TGGTAGTGAG	CGTCTGGTGC	TGGAAGTTCA	GCAGCAGCTC	GGTGGTGGTA	100
	TCGTACGTAC	TATCGCCATG	GGTTCTTCCG	ACGGTCTGCG	TCGTGGTCTG	150
	GATGTAAAAG	ATCTCGAGCA	TCCGATCGAA	GTCCCAGGTAG	GTAAAGCAAC	200
45	GCTGGGTCGT	ATCATGAACG	TGCTGGGTCA	GCCGATCGAT	ATGAAAGGCG	250
	ACATCGGCGA	AGAAGAGCGT	TGGGCTATCC	ACCGCGCAGC	ACCGTCTTAC	300
	GAAGAGCTGT	CCAGCTCTCA	GGAAGTGTCTG	GAAACCGGCA	TCAAAGTTAT	350
	CGACCTGATG	TGTCCGTTCG	CGAAGGGCGG	TAAAGTCGGT	CTGTTTCGGTG	400
	GTGCGGGTGT	AGGTAAAACC	GTAAACATGA	TGGAGCTGAT	TCGTAAACATC	450
50	GCGATCGAGC	ACTCCGGTTA	CTCTGTGTTT	GCGGGCGTGG	GTGAACGTAC	500
	TCGTGAGGGT	AACGACTTCT	ACCACGAAAT	GACCGACTCC	AACGTTCTGG	550
	ACAAAGTATC	CCTGGTGTAT	GGACAGATGA	ACGAGCCGCC	GGGAAACCGT	600
	CTGCGCGTTG	CACTGACCGG	TCTGACCATG	GCTGAGAAGT	TCCGTGACGA	650
	AGGTCGTGAC	GTTCTGCTGT	TCGTGATAAA	CATCTACCGT	TACACCCTGG	700
55	CGGGTACTGA	AGTATCTGCA	CTGCTGGGCC	GTATGCCTTC	AGCGGTAGGT	750
	TACCAGCCGA	CCCTGGCGGA	AGAGATGGGT	GTTCTTCAGG	AACGTATCAC	800
	CTCAACCAA	ACCGGTTCTA	TCACCTCCG			829

60

## 2) INFORMATION FOR SEQ ID NO: 392

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 835 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Yersinia bercovieri*  
 (B) STRAIN: ATCC 43970

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 392

	CGAATTCCCC	CAAGACGCTG	TACCAAAAGT	GTACAACGCC	CTTGAGGTTG	50
	AAGGCACAGC	TCAGAAGCTG	GTGCTGGAAG	TTCAGCAACA	GCTGGGCGGT	100
	GGTGTGTGTC	GTTGTATCGC	AATGGGCTCT	TCCGATGGTC	TGAGCCGCGG	150
20	GTTGAAAGTC	ATCAACCTGG	AACACCCAAT	TGAAGTGCCG	GTGGGTAAAT	200
	CAACTCTGGG	CCGTATCATG	AACGTATTGG	GTGACCCAAT	CGACATGAAA	250
	GGTCCTATCG	GTGAAGAAGA	GCGTTGGGCA	ATCCACCGCG	AAGCGCCTTC	300
	TTACGAAGAG	CTTGCCAGCT	CGCAAGATCT	GTTAGAAACC	GGTATCAAGG	350
	TAATGGATCT	GATTTGTCCG	TTCGCTAAGG	GCGGTAAAGT	CGGTCTGTTC	400
25	GGTGGTGCGG	GTGTGGGTAA	AACAGTCAAC	ATGATGGAGC	TGATTCGTAA	450
	TATTGCGATT	GAGCACTCAG	GTTATTCTGT	ATTTGCCGGT	GTGGGTGAGC	500
	GTACTCGTGA	GGGTAACGAC	TTCTACCACG	AGATGACTGA	CTCCAACGTT	550
	CTGGACAAAG	TATCCTTGGT	TTATGGCCAG	ATGAATGAGC	CACCAGGTAA	600
	CCGTCTGCGC	GTTGCACTGA	CCGGCTTGAC	CATGGCGGAG	AAATTCCGTG	650
30	ATGAAGGTCTG	TGATGTACTG	TTATTCATCG	ATAACATCTA	TCGTTATAACC	700
	CTGGCCGGTA	CAGAGGTATC	TGCACGTGCTA	GGTCGTATGC	CATCAGCGGT	750
	AGGCTATCAG	CCAACGCTGG	CAGAAGAGAT	GGGTGTGTTG	CAGGAACGTA	800
	TCACTTCCAC	CAAGACGGGT	TCAATCACCT	CCGTA		835

## 2) INFORMATION FOR SEQ ID NO: 393

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 812 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Yersinia enterocolitica*  
 (B) STRAIN: ATCC 9610

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 393

	GCTGTACCAA	AAGTGTACAA	CGCCCTTGAG	GTTGAAGGCG	CAGCTGAGAA	50
	GCTGGTGCTG	GAAGTTCAGC	AACAGCTGGG	CGGTGGTGTT	GTTCGTTGTA	100
55	TCGCAATGGG	CTCTTCCGAT	GGTCTGAGCC	GTGGGTTGAA	AGTCATCAAC	150
	CTGGAACACC	CAATTGAAGT	GCCTGTGGGC	AAGTCAACTC	TGGGCCGTAT	200
	CATGAACGTA	TTGGGTGACC	CAATCGACAT	GAAAGGTCCT	ATCGGCGAAG	250
	AAGAGCGTTG	GGCAATCCAT	CGTGAAGCGC	CTTCTTACGA	AGATCTTGCC	300
	AGCTCGCAAG	ACTTGTTAGA	AACCGGTATC	AAGGTAATGG	ACTTGATTTG	350
60	TCCGTTGCT	AAGGGCGGTA	AAGTCGGTCT	GTTCGGTGGT	GCGGGTGTAG	400

	GTAAAACGGT	AAACATGATG	GAGCTTATTC	GTAACATTGC	GATTGAGCAC	450
	TCAGGTTATT	CCGTATTTGC	TGGCGTGGGT	GAGCGTACTC	GTGAGGGTAA	500
	CGACTTCTAC	CACGAGATGA	CTGACTCCAA	CGTTCTGGAC	AAAGTATCCT	550
	TGGTTTATGG	CCAAATGAAT	GAGCCACCAG	GTAACCGTCT	GCGCGTTGCA	600
5	CTGACCGGCT	TGACCATGGC	GGAGAAATTC	CGTGATGAAG	GTCGTGACGT	650
	ATTGCTGTTT	ATCGATAACA	TCTATCGCTA	TACCTTAGCC	GGTACGGAAG	700
	TTTCCGCACT	GCTGGGTCGT	ATGCCATCTG	CCGTAGGTTA	CCAGCCAACG	750
	CTGGCAGAAAG	AGATGGGTGT	GTTGCAGGAA	CGTATTACTT	CCACCAAGAC	800
	GGGTTCAATC	AC				812

10

## 2) INFORMATION FOR SEQ ID NO: 394

## 15 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 802 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

20

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Yersinia frederiksenii*  
 (B) STRAIN: ATCC 33641

25

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 394

	AAAGTGTACA	ACGCCCTTGA	GGTTGAAGGT	ACTGCTGAGA	AGTTAGTACT	50
30	GGAAGTTCAG	CAACAGCTGG	GCGGTGGTGT	TGCTCGTTGT	ATCGCCATGG	100
	GCTCTTCCGA	TGGTTTGAGC	CGCGGGTTGA	AAGTTGTCAA	CCTGGAACAC	150
	CCAATTGAAG	TACCGGTTGG	TAAATCAACT	CTGGGCCGTA	TCATGAACGT	200
	ATTGGGTGAC	CCAATCGACA	TGAAAGGTCC	TATCGGTGAA	GAAGAGCGTT	250
	GGGCAATCCA	CCGCGAAGCG	CCTTCTTACG	AAGAGCTTGC	CAGCTCGCAA	300
35	GATCTGTTAG	AAACCGGTAT	CAAGGTAATG	GATCTGATTT	GCCCGTTTCGC	350
	TAAAGGCGGT	AAAGTCGGTC	TGTTTCGGTGG	TGCGGGTGTA	GGTAAAACGG	400
	TAAACATGAT	GGAGCTGATC	CGTAATATCG	CGATCGAGCA	CTCAGGTTAT	450
	TCCGTATTTG	CGGGTGTTGG	TGAACGTACC	CGTGAGGGTA	ACGACTTCTA	500
	CCACGAGATG	ACTGACTCCA	ACGTTCTGGA	CAAAGTATCC	TTGGTTTATG	550
40	GCCAGATGAA	TGAGCCACCA	GGTAACCGTC	TTCGCGTTGC	ACTGACCGGT	600
	CTGACCATGG	CGGAGAAATT	CCGTGATGAA	GGTCGTGACG	TATTGCTGTT	650
	CATCGATAAC	ATCTATCGTT	ATACCTTGGC	CGGTACGGAA	GTATCCGCAC	700
	TGCTGGGTCG	TATGCCATCT	GCGGTAGGCT	ATCAGCCAAC	GCTGGCAGAA	750
	GAGATGGGTG	TGTTGCAGGA	ACGTATTACT	TCCACCAAGA	CGGGTTCAAT	800
45	CA					802

## 2) INFORMATION FOR SEQ ID NO: 395

50

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 806 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

55

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Yersinia intermedia*  
 236

60

(B) STRAIN: ATCC 29909

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 395

5	GCTGTACCAA	GAGTGTACAA	CGCCCTTGAG	GTTGAAGGCA	CTGCTGAGAA	50
	GCTGGTGCTG	GAAGTTCAGC	AACAGCTAGG	CGGTGGTGTT	GTTCGTTGTA	100
	TCGCAATGGG	CTCTTCCGAT	GGTCTGAGCC	GCGGGTTGAA	AGTCATCAAC	150
	CTGGAACACC	CAATTGAAGT	GCCGGTTGGT	AAATCAACTC	TGGGCCGTAT	200
	CATGAACGTA	TTGGGTGACC	CAATCGACAT	GAAAGGTCCT	ATCGGTGAAG	250
10	AAGAGCGTTG	GGCAATCCAC	CGCGAAGCGC	CTTCTTACGA	AGAGCTTGCC	300
	AGCTCACAAG	ATTTGTTAGA	AACCGGTATC	AAAGTAATGG	ACTTGATTTG	350
	CCCGTTTCGT	AAGGGCGGTA	AAGTGGGTCT	GTTTCGGTGGT	GCGGGTGTAG	400
	GTAAACAGT	AAACATGATG	GAGCTTATTC	GTAACATCGC	GATTGAGCAC	450
	TCAGGTTATT	CTGTATTTGC	TGGTGTGGGT	GAGCGTACTC	GTGAGGGTAA	500
15	CGACTTCTAC	CACGAGATGA	CTGACTCCAA	CGTTCTGGAC	AAAGTATCCT	550
	TGGTGTATGG	CCAGATGAAT	GAGCCACCAG	GTAACCGTCT	GCGCGTTGCA	600
	CTGACCGGCC	TGACCATGGC	GGAGAAATTC	CGTGATGAAG	GTCGTGACGT	650
	ACTGTTGTTT	ATCGATAACA	TCTATCGCTA	TACCTTGGCC	GGTACGGAAG	700
	TATCCGCACT	GCTGGGTCGT	ATGCCATCAG	CGGTAGGCTA	CCAGCCAACG	750
20	CTGGCAGAAG	AGATGGGTGT	GTTGCAGGAA	CGTATTACGT	CCACCAAGAC	800
	GGGTTC					806

## 25 2) INFORMATION FOR SEQ ID NO: 396

## (i) SEQUENCE CHARACTERISTICS:

	(A)	LENGTH: 806 bases
	(B)	TYPE: Nucleic acid
30	(C)	STRANDEDNESS: Double
	(D)	TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

## 35 (vi) ORIGINAL SOURCE:

	(A)	ORGANISM: <i>Yersinia pseudotuberculosis</i>
	(B)	STRAIN: ATCC 29833

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 396

40	GCTGTACCAA	AAGTGTACAA	CGCCCTTGAG	GTAGAAGGCA	CAACTGAAAA	50
	GTTAGTGCTG	GAAGTTCAGC	AACAGTTGGG	CGGTGGTGTT	GTTCGTTGTA	100
	TCGCAATGGG	CTCTTCCGAT	GGTCTGAGCC	GTGGGTGAA	AGTAACCAAC	150
	CTGGAACACC	CGATCGAAGT	ACCGGTTGGT	AAAGCGACCC	TTGGCCGTAT	200
45	CATGAACGTA	TTGGGTGAAC	CAATCGACAT	GAAAGGTCCT	ATCGGTGAAG	250
	AAGAGCGTTG	GGCAATCCAT	CGCGAAGCGC	CTTCTTATGA	AGAGCTTGCT	300
	AGCTCACAAG	ATCTGTTAGA	AACCGGTATC	AAGGTTATGG	ACCTGATTTG	350
	TCCGTTTGCT	AAGGGCGGTA	AAGTCGGTCT	GTTTCGGTGGT	GCGGGTGTAG	400
	GTAAACAGT	AAACATGATG	GAGCTGATCC	GTAACATCGC	GATCGAGCAC	450
50	TCTGGGTATT	CTGTATTTGC	CGGTGTAGGT	GAGCGTACCC	GTGAGGGTAA	500
	TGACTTCTAC	CATGAAATGA	CTGACTCCAA	CGTTTTGGAC	AAAGTATCCT	550
	TGGTTTACGG	CCAGATGAAT	GAGCCACCAG	GTAACCGTCT	ACGCGTTGCA	600
	CTGACCGGCC	TGACCATGGC	GGAGAAATTC	CGTGATGAAG	GTCGTGACGT	650
	ACTGCTGTTT	ATCGATAATA	TCTATCGTTA	TACCCTAGCT	GGTACGGAAG	700
55	TATCCGCATT	GCTGGGTCGT	ATGCCATCAG	CGGTAGGTTA	TCAGCCAACA	750
	CTGGCTGAAG	AGATGGGTGT	GTTGCAGGAA	CGTATTACTT	CCACTAAGAC	800
	GGGTTC					806

60

## 2) INFORMATION FOR SEQ ID NO: 397

## (i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 829 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- 10 (A) ORGANISM: *Yersinia rohdei*  
 (B) STRAIN: ATCC 43380

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 397

15 TTCCCCCAAG ACGCTGTACC AAAAGTGTAC AACGCCCTTG AGGTTGAAGG 50  
 TGCAGCTGAG AAGCTTGTGC TGGAAAGTTCA GCAGCAGCTG GGCGGTGGTG 100  
 TTGTTTCGTTG TATCGCAATG GGCTCTTCCG ATGGTTTGAG CCGTGGGTTG 150  
 20 AAAGTTATCA ACCTGGAACA CCCAATTGAA GTGCCAGTTG GTAAATCAAC 200  
 TCTGGGCCGT ATCATGAACG TATTGGGTGA CCCAATCGAC ATGAAAGGCC 250  
 CTATCGGTGA AGAAGAGCGT TGGGCAATCC ACCGTGAAGC GCCTTCTTAC 300  
 GAAGAGCTTG CCAGCTCGCA AGATCTGTTA GAAACCGGTA TCAAGGTAAT 350  
 GGATCTGATT TGTCCGTTTCG CTAAGGGCGG TAAAGTCGGT CTGTTCCGGT 400  
 25 GTGCGGGTGT TGGTAAAACA GTAAACATGA TGGAGCTTAT TCGTAACATC 450  
 GCGATTGAGC ACTCAGGTTA TTCTGTATTT GCCGGGGTAG GTGAACGTAC 500  
 TCGTGAGGGT AACGACTTCT ACCACGAGAT GACTGACTCC AACGTTCTGG 550  
 ACAAAGTATC CTTGGTTTAT GGCCAGATGA ATGAGCCACC AGGTAACCGT 600  
 CTGCGCGTTG CACTGACCGG CTTGACCATG GCGGAAAAAT TCCGTGATGA 650  
 30 AGGCCGTGAC GTATTGCTGT TCATCGATAA CATTTATCGT TATACCCTAG 700  
 CCGGTACGGA AGTATCCGCA CTGCTGGGTC GTATGCCATC TCGGGTAGGC 750  
 TATCAGCCAA CACTGGCAGA AGAGATGGGT GTGTTGCAGG AACGTATTAC 800  
 TTCCACTAAG ACGGGTTCAA TCACCTCCG 829

35

## 2) INFORMATION FOR SEQ ID NO: 398

## (i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 819 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- 45 (A) ORGANISM: *Yokenella regensburgei*  
 (B) STRAIN: ATCC 35313

50

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 398

ATGCCGTACC GCGCGTGTAC GATGCTCTTG AGGTACAAAA TGGTAACGAG 50  
 AACTGGTGC TGGAAAGCTCA GCAGCAGCTC GGCGGCGGTA TCGTGCGTAC 100  
 55 TATCGCCATG GGTTCCTTCCG ACGGTCTGCG TCGTGGTCTG GAAGTTAAAG 150  
 ACCTCGAGCA CCCGATCGAA GTCCCGGTAG GTAAAGCAAC CCTGGGCCGT 200  
 ATCATGAACG TCCTGGGTCA GCCGATCGAC ATGAAAGGCG ACATCGGTGA 250  
 AGAAGAGCGT TGGGCTATCC ACCGCGCAGC ACCTTCCTAT GAAGAGCTGT 300  
 CCAGCTCTCA GGAAGTGTG GAAACCGGTA TCAAAGTAAT GGATCTGATC 350  
 60 TGCCCGTTTCG CTAAGGGTGG TAAAGTCGGT CTGTTCCGGT GTGCGGGTGT 400

	AGGTAAAACT	GTAAACATGA	TGGAGCTTAT	CCGTAACATC	GCGATTGAGC	450
	ACTCCGGTTA	CTCTGTGTTT	GCAGGCGTGG	GTGAACGTAC	TCGTGAGGGT	500
	AACGACTTCT	ACCACGAAAT	GACCGACTCC	AACGTACTGG	ATAAAGTATC	550
	CCTGGTGTAC	GGCCAGATGA	ACGAGCCGCC	GGGAAACCGT	CTGCGCGTTG	600
5	CGCTGACCGG	CCTGACCATG	GCTGAGAAAT	TCCGTGACGA	AGGCCGTGAC	650
	GTTCTGCTGT	TCGTCGATAA	CATCTACCGT	TATACCCTGG	CCGGTACGGA	700
	AGTATCCGCA	CTGCTGGGTC	GTATGCCTTC	TGCGGTAGGT	TATCAGCCAA	750
	CTCTGGCGGA	AGAGATGGGT	GTTCTTCAGG	AACGTATCAC	CTCTACCAA	800
	ACCGGTTCTA	TCACCTCCG				819

## 2) INFORMATION FOR SEQ ID NO: 399

## 15 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1097 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

## 20 (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Yarrowia lipolytica*  
 (B) STRAIN: ATCC 38295

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 399

	AAGCTTAAGG	CTGAGCGAGA	GCGAGGTATC	ACCATTGATA	TCGCTCTCTG	50
30	GAAGTTCCAG	ACCCCTAAGT	ACTACGTCAC	CGTTATTGAT	GCTCCCGGTC	100
	ACCGAGATTT	CATCAAGAAC	ATGATTACCG	GTACTTCCCA	GGCTGACTGC	150
	GCCATCCTCA	TCATTGCTGG	TGGTGTTGGT	GAGTTCGAGG	CTGGTATCTC	200
	CAAGGATGGT	CAGACCCGAG	AGCACGCCCT	GCTCGCTTTC	ACCCTCGGTG	250
	TTAAGCAGCT	CATTGTTGCT	ATCAACAAGA	TGGACTCCGT	CAAGTGGTCT	300
35	CAGGATCGAT	ACCTCGAGAT	TTGCAAGGAG	ACTGCCAACT	TCGTCAAGAA	350
	GGTCGGTTAC	AACCCCAAGG	CTGTCCCCTT	CGTCCCCATT	TCCGGATGGA	400
	ACGGTGACAA	CATGATCGAG	CCCTCTACCA	ACTGTGACTG	GTACAAGGGA	450
	TGGACCAAGG	AGACCAAGGC	CGGCGAGATC	AAGGGTAAGA	CCCTCCTCGA	500
	GGCCATTGAT	GCCATTGAGC	CCCCCGTGCG	ACCCACGAC	AAGCCCCTCC	550
40	GACTTCCCTT	CCAGGATGTC	TACAAGATCG	GTGGTATCGG	CACAGTGCCC	600
	GTTGGCCGAG	TCGAGACCGG	TGTTATCAAG	GCCGGTATGG	KTGTTACCTT	650
	CGTCCCGGCC	AACGTGACCA	CTGAGGTCAA	GTCTGTGCGAG	ATGCACCACG	700
	AGATCCTCCC	CGATGGAGGT	TTCCCGGGTG	ACAACGTCGG	TTTCAACGTC	750
	AAGAACGTTT	CCGTCAAGGA	TATCCGACGA	GGTAACGTTG	CTGGTGACTC	800
45	CAAGAACGAC	CCCCCAAGG	GCTGCGACTC	TTTCAACGCT	CAGGTCATTG	850
	TTCTTAACCA	CCCCGGTCAG	ATCGGTGCTG	GTTACGCTCC	CGTCCTTGAT	900
	TGCCACACTG	CCCACATTGC	TTGCAAGTTC	GACACCCCTGA	TCGAGAAGAT	950
	CGACCGACGA	ACCGGTAAGA	ATGATGGAGGA	CTCCCCAAG	TTCATCAAGT	1000
	CTGGTGATGC	TGCCATTGTC	AAGATGGTTC	CCTCCAAGCC	CATGTGTGTC	1050
50	GAGGCCTTCA	CTGAGTACCC	CCCTCTTGGT	CGATTGCGCG	TCCGAGA	1097

## 2) INFORMATION FOR SEQ ID NO: 400

## 55 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1233 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

## 60



(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 5 (A) ORGANISM: *Absidia corymbifera*  
(B) STRAIN: ATCC 46775

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 400

10	CAAGCTTAAG	GCTGAACGTG	AGCGTGGTAT	CACCATCGAT	ATCGCTCTCT	50
	GGAAGTTCGA	GACTCCCAAG	TACCACGTTA	CCGTCATTGA	TGCCCCCTGGC	100
	CATCGTGATT	TCATCAAGAA	CATGATTACT	GGTACTTCCC	AAGCTGACTG	150
	CGGTATCTTG	ATTATTGCTG	CTGGTACTGG	TGAATTCGAA	GCTGGTATCT	200
	CCAAGGATGG	TCAAACCCGT	GAACACGCTT	TGCTTGCTTT	CACCCTTGGT	250
15	GTCCGTCAAT	TGATTGTCGC	TATCAACAAG	ATGGATTCCA	CCAAGTACTC	300
	TGAGGCCCGT	TACAACGAAA	TTGTCAAGGA	AGTCTCCACC	TTCATCAAGA	350
	AGATTGGTTT	CAACCCCAAG	TCCGTTCTCT	TCGTCCCTAT	CTCTGGCTGG	400
	AACGGTGACA	ACATGTTGGA	GGARTCCACC	AACATGCCTT	GGTTCAAGGG	450
	ATGGAACAAG	GAGACTAAGG	CTGGTGCCAA	GACYGGCAAG	ACCCTTCTTG	500
20	AAGCCATTGA	CAACATTGAT	CCCCCTGTTT	GTCCTTCCGA	CAAGCCCCTT	550
	CGTCTTCCCC	TTCAAGATGT	CTACAAGATC	GGTGGTATTG	GTACAGTTCC	600
	TGTCGGTTCG	GTTGAGACTG	GTGTCATCAA	GCCTGGTATG	GTTGTCACCT	650
	TCGCTCCCGC	TAACGTCACC	ACTGAAGTCA	AGTCCGTYGA	AATGCACCAC	700
	GAGCAACTTG	CTGAAGGTGT	TCCCGGTGAC	AACGTCGGTT	TCAACGTCAA	750
25	GAACGTTTCC	GTCAAGGATA	TCCGCCGTGG	TAACGTYTGC	TCTGACTCCA	800
	AGAACGACCC	CGCCAAGGAA	TCCGCTTCCT	TCACCGCTCA	AGTTATTGTC	850
	TTGAACCACC	CTGGTCARAT	TGGTGCTGGT	TACTCTCCTG	TCTTGGATTG	900
	CCACACTGCT	CACATTGCAT	GCAAGTTCTY	TKAGCTTCTT	KAGAAGATCG	950
	ATYGTCGTTC	CGGTAAGTAA	ATANTTTGGT	TTRGGATATG	GGTATTGGGC	1000
30	TTAATCTYTG	GATTTTGCTT	CAATTGCTCC	TTCTTGATC	TTTCTCGATT	1050
	ACTTTTTGAT	CATTTGCTAA	TCCAAACCCT	TTCCATTTYA	TTGAAAACAG	1100
	GTAAGAAGTT	GGAAGACTCC	CCCAAGTTCC	TCAAGWSYGG	TGACTCTGCY	1150
	ATCGTCAAGA	TGGTTCCTTC	CAAGCCCATG	TGCGTTGAAG	CCTACACTGA	1200
35	ATATCCTCCT	CTTGGTCGTT	TCGCTGTCCG	TGA		1233

## 2) INFORMATION FOR SEQ ID NO: 401

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1151 bases  
(B) TYPE: Nucleic acid  
(C) STRANDEDNESS: Double  
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 50 (A) ORGANISM: *Alternaria alternata*  
(B) STRAIN: ATCC 62099

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 401

55	CAAGTTGAAG	GCCGAGCGTG	AGCGTGGTAT	CACCATCGAC	ATTGCTCTCT	50
	GGAAGTTCGA	GACTCCCAAG	GTTAGTACCC	CTCTGCCTAC	TACATCAAGT	100
	TCTTTACAAT	GCTAACATGT	TGTACTCAGT	ACTATGTCAC	CGTCATTGAC	150
	GCCCCCGGTC	ACCGTGATTT	CATCAAGAAC	ATGATCACTG	GTACCTCCCA	200
	GGCCGACTGC	GCTATTCTCA	TCATTGCCGC	CGGTACTGGT	GAGTTCGAGG	250
	CTGGTATCTC	CAAGGATGGC	CAGACTCGTG	AGCACGCTCT	CCTCGCTTAC	300
60	ACCCTCGGTG	TCAAGCAGCT	CATCGTTGCC	ATCAACAAGA	TGGACACCAC	350

	CAAGTGGTCC	GAGGAGCGTT	ACCAGGAGAT	CATCAAGGAG	ACCTCCAAC	400
	TCATCAAGAA	GGTCGGCTAC	AACCCCAAGC	ACGTTCCCTT	CGTCCCCATC	450
	TCCGGTTTCA	ACGGTGACAA	CATGATTGAG	GCCTCATCCA	ACTGCCCCCTG	500
	GTACAAGGGT	TGGGAGAAGG	AGACCAAGGC	CAAGGCCACT	GGTAAGACCC	550
5	TCCTCGAGGC	CATCGACGCC	ATCGACCCTY	CCAGCCGTCC	CACCGACAAG	600
	CCCCCTCCGTC	TTCCCCTYCA	GGATGTTTAC	AAGATTGGTG	GTATTGGCAC	650
	GGTGCCCCGTC	GGTCGTGTCG	AGACCGGTAT	CATCAAGGCC	GGTATGGTCG	700
	TCACCTTCGC	CCCCGCTGGT	GTCACCACTG	AAGTCAAGTC	CGTCGAGATG	750
	CACCACGAGC	AGCTCACCGA	GGGTGTCCCC	GGTGACAACG	TCGGCTTCAA	800
10	CGTCAAGAAC	GTCTCCGTCA	AGGAGATCCG	TCGTGGTAAC	GTTGCCGGTG	850
	ACTCCAAGAA	CGACCCCCCC	AAGGGTGCCG	AGTCCTTCAA	CGCCCAGGTC	900
	ATCGTCTCTA	ACCACCCTGG	TCAGGTCGGT	GCTGGTTACG	CCCCAGTCCT	950
	CGACTGCCAC	ACCGCCACAC	TTGCTTGCAA	GTTCTCTGAG	CTCCTCGAGA	1000
	AGATTGACCG	CCGTACCGGA	AAGTCTGTTG	AGAACTCTCC	CAAGTTCATC	1050
15	AAGTCCGGTG	ACGCCGCCAT	CGTCAAGATG	GTTCCCTCCA	AGCCCATGTG	1100
	CGTTGAGGCT	TTCACTGACT	ACCCTCCTCT	CGGTCGTTTC	GCTGTCCGTG	1150
	A					1151

20

## 2) INFORMATION FOR SEQ ID NO: 402

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1283 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

30

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Aspergillus flavus*  
 (B) STRAIN: ATCC 26947

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 402

	CAAGCTCAAG	TCCGAGCGTG	AGCGTGGTAT	CACCATCGAT	ATCGCCCTCT	50
	GGAAGTTCCA	GACCTCCAAG	TATGAGGTCA	CCGTCATTGG	TAAGCATTTG	100
	AGTTCCAACC	TACGTTGCC	AACATTTACA	GTCATCTAAC	AAAGTTCAAT	150
40	AGATGCCCCC	GGTCACCGTG	ACTTCATCAA	GAACATGATC	ACTGGTACTT	200
	CCCAGGCTGA	CTGCGCTATC	CTCATCATTG	CCTCCGGTAC	TGGTGAATTC	250
	GAGGCTGGTA	TCTCCAAGGA	TGGTCAGACC	CGTGAGCACG	CTCTGCTCGC	300
	TTTCAACCCTC	GGTGTCGGTC	AGCTCATCGT	TGCCCTCAAC	AAGATGGACA	350
	CCTGCAAGTG	GTCTCAGGAT	CGTTACAACG	AAATCGTTAA	GGAGACTTCC	400
45	AACCTTCATCA	AGAAGGTCGG	ATACAACCCC	AAGAGCGTTC	CTTTCGTCCC	450
	CATCTCCGGT	TTCAACGGTG	ACAACATGAT	TGAGGCCTCC	ACCAACTGCC	500
	CCTGGTACAA	GGGTTGGGAG	AAGGAGACCA	AGGCTGGCAA	GTCCACCGGT	550
	AAGACCCTTC	TCGAGGCCAT	CGATGCCATC	GAGCCCCCGG	TCCGTCCCAC	600
	CGACAAGCCT	CTCCGTCTTC	CCCTYCAGGA	TGTCTACAAG	ATCTCTGGTA	650
50	TCGGTACTGT	GCCCCGTCGGT	CGTGTCGAGA	CTGGTGTGAT	CAAGCCTGGT	700
	ATGGTCGTTA	CTTTCGCTCC	TGCCAACGTG	ACCACTGAAG	TCAAGTCCGT	750
	TGAAATGCAC	CACCAGCAGC	TCCAGGCCGG	TAACCCCGGT	GACAACGTTG	800
	GTTTCAACGT	CAAGAACGTC	TCCGTCAAGG	AAGTCCGCCG	TGGTAACGTT	850
	GCCGGTGACT	CCAAGAACGA	CCCCCTGTCT	GGCTGCGATT	CCTTCAACGC	900
55	CCAGGTCATC	GTCCTTAACC	ACCCCGGTCA	GGTCGGCAAC	GGTTACGCTC	950
	CCGTCCTGGA	CTGCCACACC	GCTCACATTG	CTTGCAAGTT	CGCTGAGCTC	1000
	CTTGAGAAGA	TTGACCGCCG	TACCGGTAAA	TCTGTTGAGG	ACAAGCCCAA	1050
	GTTTCATCAAG	TCTGGTGATG	CTGCCATCGT	CAAGATGATT	CCCTCCAAGC	1100
	CCATGTGTGT	GGAGTCTTTC	ACTGACTTTC	CCCCTCTTGG	TCGTTTCGCT	1150
60	GTCCGTGACG	TAAGTTTTTC	CCTCTTGACT	ATCTTCACAA	TTTTTCACAT	1200

ATTTTCACGC CTCGTCCCAC TCTTTTTCCT CCCTTCCTCT TTGGTTCCCC 1250  
 TTTTTCCTG CAAGTTCTCT ATAGCTAACA TGA 1283

5

## 2) INFORMATION FOR SEQ ID NO: 403

## (i) SEQUENCE CHARACTERISTICS:

10

- (A) LENGTH: 1103 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

15

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Aspergillus fumigatus*  
 (B) STRAIN: DAL95

20

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 403

TCCGAGCGTG AGCGTGGTAT CACCATCGAC ATTGCCCTCT GGAAGTTCCA 50  
 GACTCCCAAG TATGAGGTCA CTGTCATCGG TAAGCTCGAC TCGCCCCGAT 100  
 ATGTTTTGGT GCTGTAGCTA ACACGATCTG AAGATGCCCC CGGTACACGT 150  
 25 GACTTCATCA AGAACATGAT CACTGGTACC TCCCAGGCTG ACTGCGCTAT 200  
 CCTCATCATT GCCTCCGGTA CTGGTGAGTT CGAGGCTGGT ATCTCCAAGG 250  
 ATGGCCAGAC CCGTGAGCAC GCTCTGCTGG CTTTCACCCT CGGTGTCAAG 300  
 CAGCTCATCG TCGCCCTCAA CAAGATGGAC ACCTGCAAGT GGTCCGAGGA 350  
 TCGTTACAAC GAAATTGTCA AGGAAACCTC CAACTTCATC AAGAAGGTCG 400  
 30 GCTACAACCC CAAGGCCGTT CCCTTCGTCC CCATCTCTGG CTTCAACGGT 450  
 GACAACATGC TTGAGCCCTC CTCCAACCTG CCCTGGTACA AGGGATGGGA 500  
 GAAGGAGACC AAGGCCGGCA AGGTCACTGG TAAGACCCTC ATCGAGGCCA 550  
 TCGACGCCAT TGAGCCCCCT GTCCGTCCCT CCAACAAGCC CCTCCGTCTT 600  
 CCCCTCCAGG ATGTCTACAA GATCTCTGGT ATCGGAACGG TCCCTGTCGG 650  
 35 CCGTGTCTGAG ACCGGTATCA TCAAGCCCGG CATGGTCGTC ACCTTCGCCC 700  
 CCGCCAACGT CACCACTGAA GTCAAGTCCG TCGAGATGCA CCACCAGCAG 750  
 CTCCAGGAGG GTGTCCCCGG TGACAACGTC GGTTC AACG TCAAGAACGT 800  
 TTCCGTCAAG GAAGTCCGCC GTGGTAACGT CTGCGGTGAC TCCAAGAACG 850  
 ATCCCCCTCA GGGTGCTGCC TCCTTCAACG CCCAGGTCAT CGTCCTCAAC 900  
 40 CACCCCGGTC AGGTCGGCGC TGGTTACGCC CCCGTCCTCG ACTGCCACAC 950  
 TGCCACATT GCTTGCAAGT TCTCTGAGCT GCTTGAGAAG ATTGACCGCC 1000  
 GTACCGGCAA GTCTGTTGAG AACAAACCCA AGTTCATCAA GTCCGGTGAT 1050  
 GCCGCCATCG TGAAGATGGT TCCTTCCAAG CCCATGTGTG TCGAGTCCTT 1100  
 CAC 1103

45

## 2) INFORMATION FOR SEQ ID NO: 404

50

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1149 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

55

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Aspergillus fumigatus*  
 (B) STRAIN: WSA-172

60

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 404

5	AAGCTCAAGT	CCGAGCGTGA	GCGTGGTATC	ACCATCGACA	TTGCCCTCTG	50
	GAAGTTCCAG	ACTCCCAAGT	ATGAGGTCAC	TGTCATCGGT	AAGCTCGACT	100
	CGCCCCGATA	TGTTTTGGTG	CTGTAGCTAA	CACGATCTGA	AGATGCCCCC	150
	GGTCACCGTG	ACTTCATCAA	GAACATGATC	ACTGGTACCT	CCCAGGCTGA	200
	CTGCGCTATC	CTCATCATTG	CCTCCGGTAC	TGGTGAGTTC	GAGGCTGGTA	250
	TCTCCAAGGA	TGGCCAGACC	CGTGAGCACG	CTCTGCTGGC	TTTCACCCCTC	300
10	GGTGTCAAGC	AGCTCATCGT	CGCCCTCAAC	AAGATGGACA	CCTGCAAGTG	350
	GTCCGAGGAT	CGTTACAACG	AAATTGTCAA	GGAAACCTCC	AACTTCATCA	400
	AGAAGGTCGG	CTACAACCCC	AAGGCCGTTT	CCTTCGTCCC	CATCTCTGGC	450
	TTCAACGGTG	ACAACATGCT	TGAGCCCTCC	TCCAAC TGCC	CCTGGTACAA	500
	GGGATGGGAG	AAGGAGACCA	AGGCCGGCAA	GGTCACTGGT	AAGACCCTCA	550
15	TCGAGGCCAT	CGACGCCATT	GAGCCCCCTG	TCCGTCCCTC	CAACAAGCCC	600
	CTCCGTCTTC	CCCTCCAGGA	TGTCTACAAG	ATCTCTGGTA	TCGGAACGGT	650
	CCCTGTCGGC	CGTGTCGAGA	CCGGTATCAT	CAAGCCC GGC	ATGGTCTGTC	700
	CCTTCGCCCC	CGCCAACGTC	ACCACTGAAG	TCAAGTCCGT	CGAGATGCAC	750
	CACCAGCAGC	TCCAGGAGGG	TGTCCCCGGT	GACAACGTCG	GTTTCAACGT	800
20	CAAGAACGTT	TCCGTCAAGG	AAGTCCGCCG	TGGTAACGTC	TGCGGTGACT	850
	CCAAGAACGA	TCCCCCTCAG	GGTGCTGCCT	CCTTCAACGC	CCAGGTCATC	900
	GTCCTCAACC	ACCCCGGTCA	GGTCGGCGCT	GGTTACGCCC	CCGTCCCTCGA	950
	CTGCCACACT	GCCCACATTG	CTTGCAAGTT	CTCTGAGCTG	CTTGAGAAGA	1000
	TTGACCGCCG	TACCGGCAAG	TCTGTTGAGA	ACAACCCCAA	GTTTCATCAAG	1050
25	TCCGGTGATG	CCGCCATCGT	GAAGATGGTT	CCTTCCAAGC	CCATGTGTGT	1100
	CGAGTCCTTC	ACTGACTACC	CCCCTCTGGG	TCGTTTCGCC	GTCCGTGAC	1149

## 30 2) INFORMATION FOR SEQ ID NO: 405

## (i) SEQUENCE CHARACTERISTICS:

- |    |     |                      |
|----|-----|----------------------|
|    | (A) | LENGTH: 1151 bases   |
|    | (B) | TYPE: Nucleic acid   |
| 35 | (C) | STRANDEDNESS: Double |
|    | (D) | TOPOLOGY: Linear     |

## (ii) MOLECULE TYPE: Genomic DNA

## 40 (vi) ORIGINAL SOURCE:

- |  |     |                                    |
|--|-----|------------------------------------|
|  | (A) | ORGANISM: <i>Aspergillus niger</i> |
|  | (B) | STRAIN: ATCC 9508                  |

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 405

45	CAAGCTCAAG	TCCGAGCGTG	AGCGTGGTAT	CACCATCGAC	ATTGCCCTCT	50
	GGAAGTTCCA	GACTGGCAAG	TATGAGGTCA	CCGTCATTGG	TATGTACTCA	100
	CAGAGTTCTC	TTTTTCATCAA	AGCAATATAC	TAACGTCCAT	CATAGACGCC	150
	CCCGGTCACC	GTGACTTCAT	CAAGAACATG	ATCACTGGTA	CCTCCCAGGC	200
50	TGACTGCGCT	ATCCTCATCA	TTGCCTCCGG	TACTGGTGAG	TTCGAGGCTG	250
	GTATCTCCAA	GGATGGCCAG	ACTCGTGAGC	ACGCTCTGCT	TGCTTTCACC	300
	CTCGGTGTCC	GCCAGCTCAT	CGTTGCCCTC	AACAAGATGG	ACACCTGCAA	350
	GTGGTCCGAG	GACCGTTACA	ACGAAATCGT	TAAGGAGACC	TCCAAC TTCA	400
	TCAAGAAGGT	CGGATACAAC	CCCAAGGGTG	TTCTTTTCGT	CCCCATCTCC	450
55	GGTTTCAACG	GTGACAACAT	GCTCGAGCCC	TCCCCCAACT	GCCCCTGGTA	500
	CAAGGGTTGG	GAGAAGGAGA	CCAAGGCCGG	CAAGGTCACC	GGTAAGACCC	550
	TCCTTGAGGC	CATCGACGCC	ATCGAGCCCC	CCGTCCGTCC	CTCCAACAAG	600
	CCCCTCCGTC	TTCCCCTCCA	GGATGTCTAC	AAGATCTCCG	GTATTGGAAC	650
	TGTTCCCGTC	GGTCGTGTCTG	AGACCGGTAT	CATTGCCCCCT	GGTATGGTCG	700
60	TGACCTTCGC	TCCCGCCAAC	GTCACCACTG	AAGTCAAGTC	CGTTGAGATG	750

	CACCACCAGC	AGCTCAAGGA	AGGTGTCCCC	GGTGACAACG	TTGGTTTCAA	800
	CGTCAAGAAC	GTTTCCGTCA	AGGAGGTTTC	CCGTGGTAAC	GTTGCCGGTG	850
	ACTCCAAGAA	CGACCCCCCT	CTTGGCTGTG	AGAGCTTCAC	CGCCCAGGTC	900
	ATCGTCCTCA	ACCACCCCGG	TCAGGTCGGC	GCTGGTTACG	CTCCCCTCCT	950
5	GGACTGCCAC	ACTGCTCACA	TTGCTTGCAA	GTTCGCTGAG	CTCCTTGAGA	1000
	AGATTGACCG	CCGTACCGGA	AAGTCTGTTG	AATCTTCCCC	CAAGTTCATC	1050
	AAGTCCGGTG	ACGCTGCCAT	CGTCAAGATG	ATTCCCTCCA	AGCCCATGTG	1100
	TGTTGAGGCT	TTCACTGACT	ACCCCCCTCT	TGGTCGTTTC	GCCGTCCGCG	1150
	A					1151

10

## 2) INFORMATION FOR SEQ ID NO: 406

## 15 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1093 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

20

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Blastoschizomyces capitatus*  
 (B) STRAIN: ATCC 10663

25

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 406

	GCTTAAAGCT	GAACGTGAAC	GTGGTATCAC	CATTGATATC	GCTCTCTGGA	50
30	AGTTCGAAAC	TCCTAAGTAC	TACGTTACTG	TTATTGATGC	TCCAGGTCAC	100
	CGTGATTTC	TCAAGAACAT	GATTACTGGT	ACTTCCCAAG	CCGATTGCGC	150
	CATTCTTATC	ATTGCTGCCG	GTGTCGGTGA	ATTCGAAGCT	GGTATCTCCA	200
	AGGAAGGTCA	AACCAGAGAA	CACGCTCTTC	TCGCTTTCAC	CCTTGGTGTC	250
	AGACAACCTA	TCATTGCCAT	CAACAAGATG	GACTCTGTCA	AGTGGGACCA	300
35	AAAGAGATAC	GAAGAAATCG	TCAAGGAGGC	TTCCAACCTC	GTCAAGAAGG	350
	TTGGTTACAA	CCCCAAGTCT	GTTCCATTTC	TTCTATCTC	TGGTTGGAAC	400
	GGTGACAACA	TGTTGGAACC	TACCACCAAC	GCCCCATGGT	ACAAGGGATG	450
	GACCAAGGAA	ACCAAGGCTG	GTGCCACTAA	GGGTATGACT	CTTATTGAAG	500
	CCATTGACGC	CATTGAACCA	CCAGTAAGAC	CATCCGACAA	GCCACTCCGT	550
40	CTCCCACTCC	AAGATGTTTA	CAAGATTGGT	GGTATCGGAA	CTGTGCCAGT	600
	CGGCCGTGTC	GAAACCGGTA	TCATCAAGGC	CGGTATGGTC	GTTACCTTTG	650
	CTCCACCAAT	GGTCACAAC	GAAGTTAAGT	CCGTTGAAAT	GCACCACGAA	700
	CAACTTGCTC	AAGGTAACCC	AGGTGACAAC	GTTGGTTTCA	ACGTCAAGAA	750
	CGTTTCCGTT	AAGGAAATCA	GACGTGGTAA	CGTCTGTGGT	GACTCCAAGA	800
45	ACGATCCACC	AAAGGGCTGC	GAATCTTTCA	ACGCTCAAGT	TATCGTCTTG	850
	AACCACCTG	GTCAAATCTC	TGCTGGTTAC	TCTCCAGTTC	TCGATTGCCA	900
	CCTGCCCAC	ATTGCCTGCA	GATTCGACGA	ACTCCTTGAA	AAGATCGACC	950
	GTCGTTCTGG	TAAGAAGATT	GAAGACTCTC	CAAAGTTTGT	CAAGTCTGGT	1000
	GATGCCGCTA	TCGTCAAGAT	GATCCCAACC	AAGCCAATGT	GCGTTGAAAC	1050
50	CTTCACTGAA	TACCCACCAC	TTGGTCGTTT	CGCCGTCCGT	GAT	1093

## 2) INFORMATION FOR SEQ ID NO: 407

55

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1101 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

60

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 5 (A) ORGANISM: *Candida albicans*  
(B) STRAIN: ATCC 10231

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 407

```

10 CTTGGACAAA TTGAAGGCTG AAAGAGAAAG AGGTATCACC ATTGATATCG      50
   CTTTGTGGAA ATTCGAAACT CCAAATATACC ACGTTACCGT CATTGATGCT      100
   CCAGGTCACA GAGATTTTCA CAAGAATATG ATCACTGGTA CTTCTCAAGC      150
   TGATTGTGCT ATTTTGATTA TTGCTGGTGG TACTGGTGAA TTCGAAGCCG      200
   GTATTTCTAA GGATGGTCAA ACCAGAGAAC ACGCTTTGTT GGCTTACACT      250
15 TTGGGTGTCA AACAATTGAT TGTGCTGTC AACAAGATGG ACTCTGTCAA      300
   ATGGGACAAA AACAGATTTG AAGAAATCAT CAAGGAAACC TCCAACCTCG      350
   TCAAGAAGGT TGGTTACAAC CCAAAGACTG TTCCATTYGT TCCAATCTCT      400
   GGTGGAATG GTGACAACAT GATTGAACCA TCCACCAACT GTCCATGGTA      450
   CAAGGGTTGG GAAAAGGAAA CCAAATCCGG TAAAGTTACT GGTAAGACCT      500
20 TGTTAGAAGC TATTGACGCT ATTGAACCAC CAACCAGACC AACCGACAAA      550
   CCATTGAGAT TGCCATTGCA AGATGTTTAC AAGATCGGTG GTATTGGTAC      600
   TGTGCCAGTC GGTAGAGTTG AAAGTGGTAT CATCAAAGCC GGTATGGTTG      650
   TTACTTTTCGC CCCAGCTGGT GTTACCACTG AAGTCAAATC CGTTGAAATG      700
   CATCACGAAC AATTGGCTGA AGGTGTTCCA GGTGACAATG TTGGTTTCAA      750
25 CGTTAAGAAC GTTTCGTTA AAGAAATTAG AAGAGGTAAC GTTTGTGGTG      800
   ACTCCAAGAA CGATCCACCA AAGGGTTGTG ACTCTTTCAA TGCCCAAGTC      850
   ATTGTTTTGA ACCATCCAGG TCAAATCTCT GCTGGTTACT CTCCAGTCTT      900
   GGATTGTCAC ACTGCCACCA TTGCTTGTA AATCGACACT TTGGTTGAAA      950
   AGATTGACAG AAGAACTGGT AAGAAATTGG AAGAAAATCC AAAATTCGTC      1000
30 AAATCCGGTG ATGCTGCTAT CGTCAAGATG GTCCCAACCA AACCAATGTG      1050
   TGTTGAAGCT TTCACTGACT ACCCACCATT AGGTAGATTC GCTGTCAGAG      1100
A                                     1101

```

2) INFORMATION FOR SEQ ID NO: 408

(i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 1089 bases  
(B) TYPE: Nucleic acid  
(C) STRANDEDNESS: Double  
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 45 (A) ORGANISM: *Candida albicans*  
(B) STRAIN: ATCC 18804

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 408

```

50 GAAGGCTGAA AGAGAAAGAG GTATCACCAT TGATATCGCT TTGTGGAAAT      50
   TCGAAACTCC AAAATACCAC GTTACCGTCA TTGATGCTCC AGGTCACAGA      100
   GATTTTCATCA AGAATATGAT CACTGGTACT TCTCAAGCTG ATTGTGCTAT      150
55 TTTGATTATT GCTGGTGGTA CTGGTGAATT CGAAGCCGGT ATTTCTAAGG      200
   ATGGTCAAAC CAGAGAACAC GCTTTGTTGG CTTACACTTT GGGTGTCAAA      250
   CAATTGATTG TTGCTGTCAA CAAGATGGAC TCTGTCAAAT GGGACAAAAA      300
   CAGATTTGAA GAAATCATCA AGGAAACCTC CAACTTCGTC AAGAAGGTTG      350
   GTTACAACCC AAAGACTGTT CCATTTCGTT CAATCTCTGG TTGGAATGGT      400
60 GACAACATGA TTGAACCATC CACCAACTGT CCATGGTACA AGGGTTGGGA      450

```

	AAAGGAAACC	AAATCCGGTA	AAGTTACTGG	TAAGACCTTG	TTAGAAGCTA	500
	TTGACGCTAT	TGAACCACCA	ACCAGACCAA	CCGACAAACC	ATTGAGATTG	550
	CCATTGCAAG	ATGTTTACAA	GATCGGTGGT	ATTGGTACTG	TGCCAGTCGG	600
	TAGAGTTGAA	ACTGGTATCA	TCAAAGCCGG	TATGGTTGTT	ACTTTCGCCC	650
5	CAGCTGGTGT	TACCACTGAA	GTCAAATCCG	TTGAAATGCA	TCACGAACAA	700
	TTGGCTGAAG	GTGTTCCAGG	TGACAAATGTT	GGTTTCAACG	TTAAGAACGT	750
	TTCCGTTAAA	GAAATTAGAA	GAGGTAACGT	TTGTGGTGAC	TCCAAGAACG	800
	ATCCACCAAA	GGGTGTGTGAC	TCTTTCAATG	CCCAAGTCAT	TGTTTTGAAC	850
	CATCCAGGTC	AAATCTCTGC	TGGTTACTCT	CCAGTCTTGG	ATTGTCACAC	900
10	TGCCCACATT	GCTTGTAAT	TCGACACTTT	GGTTGAAAAG	ATTGACAGAA	950
	GAACGTGTAA	GAAATTGGAA	GAAAATCCAA	AATTCGTCAA	ATCCGGTGAT	1000
	GCTGCTATCG	TCAAGATGGT	CCCAACCAAA	CCAATGTGTG	TTGAAGCTTT	1050
	CACTGACTAC	CCACCATTAG	GTAGATTTCG	TGTCAGAGA		1089

15

## 2) INFORMATION FOR SEQ ID NO: 409

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1101 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Candida albicans*

(B) STRAIN: ATCC 56884

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 409

	CTTGGACAAA	TTGAAGGCTG	AAAGAGAAAG	AGGTATCACC	ATTGATATCG	50
	CTTTGTGGAA	ATTCGAAACT	CCAAAATACC	ACGTTACCGT	CATTGATGCT	100
35	CCAGGTCACA	GAGATTTTCAT	CAAGAATATG	ATCACTGGTA	CTTCTCAAGC	150
	TGATTGTGCT	ATTTTGATTA	TTGCTGGTGG	TACTGGTGAA	TTCGAAGCCG	200
	GTATTTCTAA	GGATGGTCAA	ACCAGAGAAC	ACGCTTTGTT	GGCTTACACT	250
	TTGGGTGTCA	AACAATTGAT	TGTTGCTGTC	AACAAGATGG	ACTCTGTCAA	300
	ATGGGACAAA	AACAGATTTG	AAGAAATCAT	CAAGGAAACC	TCCAACCTCG	350
40	TCAAGAAGGT	TGGTTACAAC	CCAAAGACTG	TTCCATTTCG	TCCAATCTCT	400
	GGTTGGAATG	GTGACAACAT	GATTGAACCA	TCCACCAACT	GTCCATGGTA	450
	CAAGGGTTGG	GAAAAGGAAA	CCAAATCCGG	TAAAGTTACT	GGTAAGACCT	500
	TGTTAGAAGC	TATTGACGCT	ATTGAACCAC	CAACCAGACC	AACCGACAAA	550
	CCATTGAGAT	TGCCATTGCA	AGATGTTTAC	AAGATCGGTG	GTATTGGTAC	600
45	TGTGCCAGTC	GGTAGAGTTG	AAACTGGTAT	CATCAAAGCC	GGTATGGTTG	650
	TTACTTTTCGC	CCCAGCTGGT	GTTACCACTG	AAGTCAAATC	CGTTGAAATG	700
	CATCACGAAC	AATTGGCTGA	AGGTGTTCCA	GGTGACAATG	TTGGTTTCAA	750
	CGTTAAGAAC	GTTTCCGTTA	AAGAAATTAG	AAGAGGTAAC	GTTTGTGGTG	800
	ACTCCAAGAA	CGATCCACCA	AAGGGTTGTG	ACTCTTTCAA	TGCCCAAGTC	850
50	ATTGTTTTGA	ACCATCCAGG	TCAAATCTCT	GCTGGTTACT	CTCCAGTCTT	900
	GGATTGTCAC	ACTGCCACCA	TTGCTTGTA	ATTCGACACT	TTGGTTGAAA	950
	AGATTGACAG	AAGAACTGGT	AAGAAATTGG	AAGAAAATCC	AAAATTCGTC	1000
	AAATCCGGTG	ATGCTGCTAT	CGTCAAGATG	GTCCCAACCA	AACCAATGTG	1050
	TGTTGAAGCT	TTCACTGACT	ACCCACCATT	AGGTAGATTC	GCTGTCAGAG	1100
55	A					1101

## 2) INFORMATION FOR SEQ ID NO: 410

60

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1102 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Candida albicans*  
 (B) STRAIN: ATCC 60193

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 410

```

15  CTTGGACAAA TTGAAGGCTG AAAGAGAAAG AGGTATCACC ATTGATATCG      50
    CTTTGTGGAA ATTCGAAACT CCAAAATACC ACGTTACCGT CATTGATGCT      100
    CCAGGTCACA GAGATTTTCAT CAAGAATATG ATCACTGGTA CTTCTCAAGC      150
    TGATTGTGCT ATTTTGATTA TTGCTGGTGG TACTGGTGAA TTCGAAGCCG      200
    GTATTTCTAA GGATGGTCAA ACCAGAGAAC ACGCTTTGTT GGCTTACACT      250
20  TTGGGTGTCA AACAATTGAT TGTGCTGTC AACAAGATGG ACTCTGTCAA      300
    ATGGGACAAA AACAGATTG AAGAAATCAT CAAGGAAACC TCCAACCTCG      350
    TCAAGAAGGT TGGTTACAAC CCAAAGACTG TTCCATTTCGT TCCAATCTCT      400
    GGTGGAATG GTGACAACAT GATTGAACCA TCCACCAACT GTCCATGGTA      450
    CAAGGGTTGG GAAAAGGAAA CCAAATCCGG TAAAGTTACT GGTAAGACCT      500
25  TGTTAGAAGC TATTGACGCT ATTGAACCAC CAACCAGACC AACCGACAAA      550
    CCATTGAGAT TGCCATTGCA AGATGTTTAC AAGATCGGTG GTATTGGTAC      600
    TGTGCCAGTC GGTAGAGTTG AAACCTGGTAT CATCAAAGCC GGTATGGTTG      650
    TTACTTTTCGC CCCAGCTGGT GTTACCCTG AAGTCAAATC CGTTGAAATG      700
    CATCACGAAC AATTGGCTGA AGGTGTTCCA GGTGACAATG TTGGTTTCAA      750
30  CGTTAAGAAC GTTTCGGTTA AAGAAATTAG AAGAGGTAAC GTTTGTGGTG      800
    ACTCCAAGAA CGATCCACCA AAGGGTTGTG ACTCTTTCAA TGCCCAAGTC      850
    ATTGTTTTGA ACCATCCAGG TCAAATCTCT GCTGGTTACT CTCCAGTCTT      900
    GGATTGTCAC ACTGCCACA TTGCTTGTA ATTCGACACT TTGGTTGAAA      950
    AGATTGACAG AAGAACTGGT AAGAAATTGG AAGAAAATCC AAAATTTCGTC     1000
35  AAATCCGGTG ATGCTGCTAT CGTCAAGATG GTCCCAACCA AACCAATGTG     1050
    TGTGTAAGCT TTCCTGACT ACCCACCATT AGGTAGATTC GCTGTCAGAG     1100
    AT                                                                1102
  
```

## 2) INFORMATION FOR SEQ ID NO: 411

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1102 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Candida albicans*  
 (B) STRAIN: ATCC 90028

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 411

```

    CTTGGACAAA TTGAAGGCTG AAAGAGAAAG AGGTATCACC ATTGATATCG      50
    CTTTGTGGAA ATTCGAAACT CCAAAATACC ACGTTACCGT CATTGATGCT      100
    CCAGGTCACA GAGATTTTCAT CAAGAATATG ATCACTGGTA CTTCTCAAGC      150
60  TGATTGTGCT ATTTTGATTA TTGCTGGTGG TACTGGTGAA TTCGAAGCCG      200
  
```



	GTATTTCTAA	GGATGGTCAA	ACCAGAGAAC	ACGCTTTGTT	GGCTTACACT	250
	TTGGGTGTCA	AACAATTGAT	TGTTGCTGTC	AACAAGATGG	ACTCTGTCAA	300
	ATGGGACAAA	AACAGATTTG	AAGAAATCAT	CAAGGAAACC	TCCAACTTCG	350
	TCAAGAAGGT	TGGTTACAAC	CCAAAGACTG	TTCCATTTCG	TCCAATCTCT	400
5	GGTTGGAATG	GTGACAACAT	GATTGAACCA	TCCACCAACT	GTCCATGGTA	450
	CAAGGGTTGG	GAAAAGGAAA	CCAAATCCGG	TAAAGTTACT	GGTAAGACCT	500
	TGTTAGAAGC	TATTGACGCT	ATTGAACCAC	CAACCAGACC	AACCGACAAA	550
	CCATTGAGAT	TGCCATTGCA	AGATGTTTAC	AAGATCGGTG	GTATTGGTAC	600
	TGTGCCAGTC	GGTAGAGTTG	AAACTGGTAT	CATCAAAGCC	GGTATGGTTG	650
10	TTACTTTTCGC	CCCAGCTGGT	GTTACCACTG	AAGTCAAATC	CGTTGAAATG	700
	CATCACGAAC	AATTGGCTGA	AGGTGTTCCA	GGTGACAATG	TTGGTTTCAA	750
	CGTTAAGAAC	GTTTCCGTTA	AAGAAATTAG	AAGAGGTAAC	GTTTGTGGTG	800
	ACTCCAAGAA	CGATCCACCA	AAGGGTTGTG	ACTCTTTCAA	TGCCCCAAGTC	850
	ATTGTTTTGA	ACCATCCAGG	TCAAATCTCT	GCTGGTTACT	CTCCAGTCTT	900
15	GGATTGTCAC	ACTGCCCACA	TTGCTTGTA	ATTCGACACT	TTGGTTGAAA	950
	AGATTGACAG	AAGAACTGGT	AAGAAATTGG	AAGAAAATCC	AAAATTTCGTC	1000
	AAATCCGGTG	ATGCTGCTAT	CGTCAAGATG	GTCCCAACCA	AACCAATGTG	1050
	TGTTGAAGCT	TTCACTGACT	ACCCACCATT	AGGTAGATTC	GCTGTCAGAG	1100
	AT					1102
20						

## 2) INFORMATION FOR SEQ ID NO: 412

25	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 1101 bases
	(B) TYPE: Nucleic acid
	(C) STRANDEDNESS: Double
	(D) TOPOLOGY: Linear
30	(ii) MOLECULE TYPE: Genomic DNA
	(vi) ORIGINAL SOURCE:
	(A) ORGANISM: <i>Candida dubliniensis</i>
35	(B) STRAIN: NCPF 3108

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 412

	CTTGGATAAA	TTGAAGGCTG	AAAGAGAAAG	AGGTATCACC	ATTGATATCG	50
40	CTTTGTGGAA	ATTCGAAACT	CCAAAATACC	ACGTTACCGT	CATTGATGCT	100
	CCAGGTCACA	GAGATTTTCAT	CAAGAACATG	ATCACTGGTA	CTTCTCAAGC	150
	TGATTGTGCT	ATTTTGATTA	TTGCTGGTGG	TACTGGTGAA	TTCGAAGCCG	200
	GTATTTCTAA	GGATGGTCAA	ACCAGAGAAC	ACGCTTTGTT	GGCTTACACT	250
	TTGGGTGTCA	AACAATTGAT	TGTTGCTGTC	AACAAGATGG	ACTCTGTCAA	300
45	ATGGGACAAA	AACAGATTTG	AAGAAATCAT	CAAGGAAACC	TCTAACTTCG	350
	TCAAGAAGGT	TGGTTACAAC	CCAAAGACTG	TTCCATTTCG	TCCAATCTCT	400
	GGTTGGAATG	GTGACAACAT	GATTGAAGCT	TCCACCAACT	GTCCATGGTA	450
	CAAGGGTTGG	GAAAAGGAAA	CCAAATCCGG	TAAGGTTACT	GGTAAGACCT	500
	TGTTAGAAGC	TATTGATGCT	ATTGAACCAC	CAACCAGACC	AACCGACAAA	550
50	CCATTGAGAT	TGCCATTGCA	AGATGTTTAC	AAGATCGGTG	GTATTGGTAC	600
	TGTGCCAGTC	GGTAGAGTTG	AAACTGGTGT	CATTAAAGCC	GGTATGGTTG	650
	TCACTTTTGC	CCCAGCTGGT	GTTACCACTG	AAGTCAAATC	CGTTGAAATG	700
	CATCACGAAC	AATTGGCTGA	AGGTGTTCCA	GGTGACAATG	TTGGTTTCAA	750
	CGTTAAGAAT	GTTTCTGTCA	AAGAAATTAG	AAGAGGTAAC	GTTTGTGGTG	800
55	ACTCCAAGAA	CGATCCACCA	AAGGGTTGTG	ACTCTTTCAA	TGCCCCAAGTC	850
	ATTGTCTTGA	ACCATCCAGG	TCAAATCTCT	GCTGGTTACT	CTCCAGTCTT	900
	GGATTGTCAC	ACTGCCCACA	TTGCTTGTA	ATTCGACACT	TTGGTTGAAA	950
	AGATTGACAG	AAGAACTGGT	AAGAAATTGG	AAGAAAATCC	AAAATTTCGTC	1000
	AAATCCGGTG	ACGCTGCTAT	YGTCAAGATG	GTCCCAACCA	AACCAATGTG	1050
60	TGTTGAAGCT	TTCACTGACT	ACCCACCATT	AGGTAGATTC	GCTGTCAGAG	1100

A

1101

## 5 2) INFORMATION FOR SEQ ID NO: 413

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1098 bases  
 (B) TYPE: Nucleic acid  
 10 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

## 15 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Candida catenulata*  
 (B) STRAIN: ATCC 10565

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 413

20 GGACAAGCTT AAGGCTGAGC GTGAGAGAGG TATCACCATT GACATTGCCT 50  
 TGTGGAAGTT CGAGACTCCC AAGTACCACG TCACTGTCAT TGACGCCCCC 100  
 GGTCACAGAG ATTTTCATCAA GAACATGATC ACTGGTACCT CGCAGGCTGA 150  
 CTGTGCTATC TTGATCATTG CTTCCGGTGT CGGTGAGTTC GAGGCTGGTA 200  
 25 TCTCCAAGGA CGGTCAGACC CGTGAGCACG CTTTGTGGC CTACACCTTG 250  
 GGTGTCAAGC AGTTGATCGT TGCCATCAAC AAGATGGACT CCGTCAAGTG 300  
 GGACAAGAAC AGATTCGAGG AGATTGTCAA GGAGACCACC AACTTCGTCA 350  
 AGAAGGTTGG TTACAACCCC AAGGCTGTCC CTTTCGTCCC CATCTCTGGC 400  
 TGGAACGGTG ACAACATGAT TGAGGCCCTCC ACCAACTGCC CCTGGTACAA 450  
 30 GGGCTGGGAG AAGGAGACCA AGGCCGGTAA GTCTACCGGT AAGACCTTGT 500  
 TGGAGGCCAT TGACGCCATT GAGCCCCCTA CCAGACCCAC CGACAAGCCC 550  
 TTGAGATTGC CTTTGCAGGA TGTCTACAAG ATCGGTGGTA TTGGTACGGT 600  
 GCCCCGTCGGC CGTGTCGAGA CCGGTGTCAT CAAGCCCGGT ATGGTCGTCA 650  
 CCTTCGCCCC CGCTGGGTGTC ACCACTGAAG TCAAGTCCGT CGAGATGCAC 700  
 35 CACGAGCAGT TGTCCGAGGG TGTCCCCGGT GACAACGTTG GTTTCAACGT 750  
 CAAGAACGTC TCTGTTAAGG AGATCAGACG TGGTAACGTC TCGGGTGAAT 800  
 CCAAGAACGA CCCCCCATG GGTGCTCTT CTTTCAACGC CCAGGTATATC 850  
 GTGTTGAACC ACCCCGGTCA GATCTCTGCC GGTTACTCTC CCGTCTTGGA 900  
 CTGCCACACC GCCCACATTG CTTGCAAGTT CGCCGAGTTG ATCGAGAAGA 950  
 40 TTGACAGACG TACCGGTAAG TCCATGGAGG CTAACCCCAA GTTCGTCAAG 1000  
 TCTGGTGACG CCGCCATCGT CAAGATGGAG CCCACTAAGC CCATGTGTGT 1050  
 TGAGGCCTTC ACTGACTTCC CTCCTTTGGG TAGATTCGCC GTCAGAGA 1098

45

## 2) INFORMATION FOR SEQ ID NO: 414

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1102 bases  
 50 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

55

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Candida dubliniensis*  
 (B) STRAIN: NCPF 3949

## 60 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 414

249

	CTTGGATAAA	TTGAAGGCTG	AAAGAGAAAG	AGGTATCACC	ATTGATATCG	50
	CTTTGTGGAA	ATTCGAAACT	CCAAAATACC	ACGTTACCGT	CATTGATGCT	100
	CCAGGTCACA	GAGATTTCAT	CAAGAACATG	ATCACTGGTA	CTTCTCAAGC	150
5	TGATTGTGCT	ATTTTGATTA	TTGCTGGTGG	TACTGGTGAA	TTCGAAGCCG	200
	GTATTTCTAA	GGATGGTCAA	ACCAGAGAAC	ACGCTTTGTT	GGCTTACACT	250
	TTGGGTGTCA	AACAATTGAT	TGTTGCTGTC	AACAAGATGG	ACTCTGTCAA	300
	ATGGGACAAA	AACAGATTCT	AAGAAATCAT	CAAGGAAACC	TCTAACTTCG	350
	TCAAGAAGGT	TGGTTACAAC	CCAAAGACTG	TTCCATTTCG	TCCAATCTCT	400
10	GGTTGGAATG	GTGACAACAT	GATTGAAGCT	TCCACCAACT	GTCCATGGTA	450
	CAAGGGTTGG	GAAAAGGAAA	CCAAATCCGG	TAAGGTTACT	GGTAAGACCT	500
	TGTTAGAAGC	TATTGATGCT	ATTGAACCAC	CAACCAGACC	AACCGACAAA	550
	CCATTGAGAT	TGCCATTGCA	AGATGTTTAC	AAGATCGGTG	GTATTGGTAC	600
	TGTGCCAGTC	GGTAGAGTTG	AAACTGGTGT	CATTAAAGCC	GGTATGGTTG	650
15	TCACTTTTGC	CCCAGCTGGT	GTTACCACTG	AAGTCAAATC	CGTTGAAATG	700
	CATCACGAAC	AATTGGTTGA	AGGTGTTCCA	GGTGACAATG	TTGGTTTCAA	750
	CGTTAAGAAT	GTTTCTGTCA	AAGAAATTAG	AAGAGGTAAC	GTTTGTGGTG	800
	ACTCCAAGAA	CGATCCACCA	AAGGGTTGTG	ACTCTTTCAA	TGCCCCAAGTC	850
	ATTGTCTTGA	ACCATCCAGG	TCAAATCTCT	GCTGGTTAYT	CTCCAGTCTT	900
20	GGATTGTCAC	ACTGCCACCA	TTGCTTGTA	ATTCGACACT	TTGGTTGAAA	950
	AGATTGACAG	AAGAACTGGT	AAGAAATTGG	AAGAAAATCC	AAAATTCGTC	1000
	AAATCCGGTG	ACGCTGCTAT	YGTCAGATG	GTCCCAACCA	AACCAATGTG	1050
	TGTTGAAGCT	TTCATGACT	ACCCACCATT	AGGTAGATTC	GCTGTCAGAG	1100
	AT					1102
25						

## 2) INFORMATION FOR SEQ ID NO: 415

30	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 1102 bases
	(B) TYPE: Nucleic acid
	(C) STRANDEDNESS: Double
	(D) TOPOLOGY: Linear
35	(ii) MOLECULE TYPE: Genomic DNA
	(vi) ORIGINAL SOURCE:
	(A) ORGANISM: <i>Candida dubliniensis</i>
40	(B) STRAIN: CBS 7987

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 415

	CTTGGATAAA	TTGAAGGCTG	AAAGAGAAAG	AGGTATCACC	ATTGATATCG	50
	CTTTGTGGAA	ATTCGAAACT	CCAAAATACC	ACGTTACCGT	CATTGATGCT	100
	CCAGGTCACA	GAGATTTCAT	CAAGAACATG	ATCACTGGTA	CTTCTCAAGC	150
	TGATTGTGCT	ATTTTGATTA	TTGCTGGTGG	TACTGGTGAA	TTCGAAGCCG	200
	GTATTTCTAA	GGATGGTCAA	ACCAGAGAAC	ACGCTTTGTT	GGCTTACACT	250
	TTGGGTGTCA	AACAATTGAT	TGTTGCTGTC	AACAAGATGG	ACTCTGTCAA	300
50	ATGGGACAAA	AACAGATTCT	AAGAAATCAT	CAAGGAAACC	TCTAACTTCG	350
	TCAAGAAGGT	TGGTTACAAC	CCAAAGACTG	TTCCATTTCG	TCCAATCTCT	400
	GGTTGGAATG	GTGACAACAT	GATTGAAGCT	TCCACCAACT	GTCCATGGTA	450
	CAAGGGTTGG	GAAAAGGAAA	CCAAATCCGG	TAAGGTTACT	GGTAAGACCT	500
	TGTTAGAAGC	TATTGATGCT	ATTGAACCAC	CAACCAGACC	AACCGACAAA	550
55	CCATTGAGAT	TGCCATTGCA	AGATGTTTAC	AAGATCGGTG	GTATTGGTAC	600
	TGTGCCAGTC	GGTAGAGTTG	AAACTGGTGT	CATTAAAGCC	GGTATGGTTG	650
	TCACTTTTGC	CCCAGCTGGT	GTTACCACTG	AAGTCAAATC	CGTTGAAATG	700
	CATCACGAAC	AATTGGTTGA	AGGTGTTCCA	GGTGACAATG	TTGGTTTCAA	750
	CGTTAAGAAT	GTTTCTGTCA	AAGAAATTAG	AAGAGGTAAC	GTTTGTGGTG	800
60	ACTCCAAGAA	CGATCCACCA	AAGGGTTGTG	ACTCTTTCAA	TGCCCCAAGTC	850

```

ATTGTCTTGA ACCATCCAGG TCAAATCTCT GCTGGTTAYT CTCCAGTCTT      900
GGATTGTCAC ACTGCCCACA TTGCTTGTA AATCGACACT TTGGTTGAAA      950
AGATTGACAG AAGAACTGGT AAGAAATTGG AAGAAAATCC AAAATTCGTC     1000
AAATCCGGTG ACGCTGCTAT YGTCAAGATG GTCCCAACCA AACCAATGTG     1050
5  TGTGAAGCT TTCACTGACT ACCCACCATT AGGTAGATTC GCTGTCAGAG     1100
AT                                                                1102

```

10 2) INFORMATION FOR SEQ ID NO: 416

(i) SEQUENCE CHARACTERISTICS:

```

(A) LENGTH: 1094 bases
(B) TYPE: Nucleic acid
15 (C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

```

(ii) MOLECULE TYPE: Genomic DNA

20 (vi) ORIGINAL SOURCE:

```

(A) ORGANISM: Candida famata
(B) STRAIN: ATCC 62894

```

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 416

```

25 AATTGAAGGC TGAAAGAGAA AGAGGTATCA CCATTGATAT CGCTTTATGG      50
AAATTCGAAA CTCCAAAATA CCACGTTACC GTTATTGATG CTCCAGGTCA      100
CAGAGATTTT ATCAAGAACA TGATTACTGG TACTTCTCAA GCTGATTGTG      150
CTATTTTTRAT TATTGCTGGT GGTGTCGGTG AATTCGAAGC CGGTATCTCT      200
30 AAGGATGGTC AAACCAGAGA ACACGCTTTA TTGGCTTACA CCTTAGGTGT      250
TAGACAATTG ATTGTTGCCG TCAACAAGAT GGACTCTGTT AAATGGGACA      300
AGGCTAGATT CGAAGAAATC ATCAAGGAAA CCTCTAACTT CGTCAAGAAG      350
GTTGGTTACA ACCCTAAGAC TGTTCCTTTC GTYCCAATTT CTGGATGGAA      400
CGGTGACAAC ATGATTGAAG CCTCCACCAA CTGTCCATGG TACAAGGGTT      450
35 GGGAAAAGGA AACCAAGGCT GGTAATCTA CTGGTAAGAC TTTGTTAGAA      500
GCCATTGATG CCATTGAACC ACCAACCAGA CCAACCGAAA AGCCATTGAG      550
ATTACCATTA CAAGATGTCT ACAAGATCGG TGGTATTGGT ACTGTGCCAG      600
TCGGTAGAGT TGAAACCGGT GTTATCAAGG GTGGTATGGT TGTTACCTTT      650
GCCCCAGCCG GTGTCACTAC CGAAGTCAAA TCCGTTGAAA TGCACCACGA      700
40 ACAATTAGCT GAAGGTGTTT CAGGTGACAA TGTTGGTTTC AACGTCAAGA      750
ACGTTTCCGT TAAGGAAATC AGAAGAGGTA ACGTTTGTGG TGAATCCAAG      800
AACGACCCAC CAAAGGGTGC TGAATCTTTC ACCGCTCAAG TTATTGTCTT      850
GAACCACCCA GGTCCATCTT CTGCTGGTTA CTCTCCAGTC TTAGATTGTC      900
ACACCGCCCA CATTGCTTGT AAATTCGATG CTTTACTCGA AAAGATTGAC      950
45 AGAAGATCCG GTAAGAAATT AGAAGACGAA CAAAATTTCG TCAAGTCCGG     1000
TGATGCTGCT ATCGTCAAGA TGGTCCAAC CAAACCAATG TGTGTTGAAG     1050
CTTTCCTGTA ATACCCACCA TTAGGTAGAT TCGCTGTTAG AGAT           1094

```

50 2) INFORMATION FOR SEQ ID NO: 417

(i) SEQUENCE CHARACTERISTICS:

```

(A) LENGTH: 1101 bases
55 (B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

```

(ii) MOLECULE TYPE: Genomic DNA

60

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Candida glabrata*

(B) STRAIN: ATCC 66032

## 5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 417

```

TTTGGACAAG TTGAAGGCTG AAAGAGAAAG AGGTATCACT ATCGATATCG      50
CTTTGTGGAA GTTCGAAACT CCAAAGTACC ACGTYACCGT TATCGATGCT      100
CCAGGTCACA GAGATTTCAT CAAGAACATG ATTACTGGTA CTTCTCAAGC      150
10 TGA CTGTGCT ATCTTGATTA TTGCTGGTGG TGTCGGTGAA TTCGAAGCYG      200
GTATCTCCAA GGATGGTCAA ACCAGAGAAC ACGCTCTATT GGCTTTCACC      250
CTAGGTGTTA GACAATTGAT TGTYGCTGTC AACAAGATGG ACTCTGTCAA      300
GTGGGATGAA TCCAGATTTC CTGAAATCGT TAAGGAAACC TCCAACCTCA      350
TCAAGAAGGT CGGTTACAAC CCAAAGACTG TTCCATTTCGT CCCAATCTCT      400
15 GGTGGAACG GTGACAACAT GATTGAAGCC ACCACCAACG CTTCTGGTA      450
CAAGGGTTGG GAAAAGGAAA CCAAGGCTGG TGTCGTCAAG GGTAAGACCT      500
TGTTGGAAGC CATTGACGCT ATCGAACCAC CAACCAGACC AACTGACAAG      550
CCATTGAGAT TGCCATTGCA AGATGTCTAC AAGATCGGTG GTATCGGTAC      600
GGTGCCAGTC GGTAGAGTCG AAACCGGTGT CATCAAGCCA GGTATGGTTG      650
20 TTACCTTCGC CCCAGCTGGT GTTACCACTG AAGTCAAGTC CGTTGAAATG      700
CACCACGAAC AATTGACTGA AGGTTTGCCA GGTGACAACG TTGGTTTCAA      750
CGTTAAGAAC GTTTCGGTTA AGGAAATCAG AAGAGGTAAT GTCTGTGGTG      800
ACTCCAAGAA CGACCCACCA AAGGCTGCTG CTTCTTTCAA CGCTACCGTC      850
ATTGTCTTGA ACCACCCAGG TCAAATCTCT GCTGGTACT CTCCAGTTTT      900
25 GGACTGTCAC ACCGCCACA TTGCTTGTA GTTGGAAGAA TTGTTGAAA      950
AGAACGACAG AAGATCCGGT AAGAAGTTGG AAGACTCTCC AAAGTTCTTG      1000
AAGTCCGGTG ACGCTGCTTT GGTAAAGTTC GTTCCATCCA AGCCAATGTG      1050
TGTCGAAGCT TTCTCCGACT ACCCACCATT GGGTAGATTC GCTGTCAGAG      1100
A
30

```

## 2) INFORMATION FOR SEQ ID NO: 418

## 35 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1080 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

40

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Candida guilliermondii*

45

(B) STRAIN: ATCC 6260

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 418

```

AGAGAAAGAG GTATCACCAT TGACATTGCT TTGTGGAAAT TCGAGACTCC      50
50 AAAGTACCAC GTTACYGTCA TTGATGCCCC AGGTCACAGA GATTTTCATCA      100
AGAACATGAT CACTGGTACT TCTCAAGCTG ACTGTGCTAT TTTGATTATT      150
GCTGGTGGTA CCGGTGAATT CGAAGCTGGT ATCTCTAAGG ATGGTCAAAC      200
CAGAGAGCAC GCTTTGTTGG CTTACACCTT GGGTGTAGA CAATTGATTG      250
TTGCTGTCAA CAAGATGGAC TCCGTCAART GGGACAAGAA CAGATTYAGG      300
55 GAAATCATCA AGGAAACCTC TAACTTCGTC AAGAAGGTTG GTTACAACCC      350
TAAGACTGTG CCATTCGTTT CTATCTCTGG ATGGAAYGGT GACAACATGA      400
TTGAGGCTTC TACCAACTGT CCTTGGTACA AGGGATGGGA GAAGGAGACC      450
AAGGCTGGTA AGTCCACCGG TAAGACTTTG TTGGAGGCCA TTGACGCCAT      500
TGAGCCACCT CAAAGACCAA CCGACAAGCC ATTGAGATTG CCATTGCAAG      550
60 ATGTYTACAA GATTGGTGGT ATTGGAACGG TGCCAGTCGG TAGAGTTGAA      600

```

	ACCGGTATCA	TYAAGGCCGG	TATGGTTGTT	ACCTTTGCCC	CAGCTGGTGT	650
	YACCACTGAA	GTCAAGTCCG	TGGAAATGCA	CCACGAACAA	TTGGTTGAAG	700
	GTGTTCCAGG	TGACAATGTT	GGTTTCAACG	TTAAGAACGT	TTCCGTTAAG	750
	GAAATTAGAA	GAGGTAACGT	TTGTGGTGAC	TCCAAGAACG	ACCCACCAAA	800
5	GGGTTGTGAC	TCTTTCACCG	CTCAAGTTAT	TGTGTTGAAC	CACCCTGGTC	850
	AAATCTCTGC	TGGTACTCT	CCAGTTTTTG	ACTGTCACAC	CGCCCACATT	900
	GCTTGTAAT	TCGACACCTT	GTTGGAGAAG	ATTGACAGAA	GAACCGGTAA	950
	GAAGATGGAG	GACAACCCCA	AGTTTGTCAA	GTCCGGTGAC	GCTTCTATCG	1000
	TCAAGATGGT	GCCATCCAAG	CCAATGTGTG	TTGAGGCTTT	CACCGACTAC	1050
10	CCACCATTGG	GAAGATTCGC	CGTCAGAGAC			1080

## 2) INFORMATION FOR SEQ ID NO: 419

15

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 751 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 20 (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- 25 (A) ORGANISM: *Candida haemulonii*  
 (B) STRAIN: ATCC 22991

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 419

30	TCTGTCAAGT	GGGACAAGGC	CAGATACGAG	GAAATCGTCA	AGGAGACCTC	50
	TAACCTCGTC	AAGAAGGTTG	GTTACAACCC	TAAGACTGTT	CCATTCGTCC	100
	CAATCTCTGG	TTGGAACGGT	GACAACATGA	TTGAGGCTTC	TACCAACTGT	150
	GACTGGTACA	AGGGTTGGGA	GAAGGAGACC	AAGTCTGGTA	AGTCCACCGG	200
	TAAGACCTTG	TTGGAGGCCA	TTGACGCCAT	TGAGCCACCA	ACCAGACCAA	250
35	CCGACAAGCC	ATTGAGATTG	CCATTGCAGG	ATGTCTACAA	GATTGGTGGT	300
	ATCGGAAGCTG	TGCCAGTCGG	CAGAGTTGAG	ACCGGTGTTA	TCAAGGCCGG	350
	TATGGTTGTC	ACCTTCGCCC	CAGCTGGTGT	CACCACTGAA	GTCAAGTCTG	400
	TCGAGATGCA	CCACGAGCAG	TTGCCAGAGG	GTGTCCCAGG	TGACAACGTT	450
	GGTTTCAACG	TCAAGAACGT	TTCCGTTAAG	GAAATCAGAA	GAGGTAACGT	500
40	CTGTGGTGAC	TCCAAGCAGG	ACCCACCAAA	GGGCTGTGAC	TCTTTCACCG	550
	CTCAGGTTAT	TGTGTTGAAC	CACCCAGGTC	AGATCTCTTC	TGGTACTCT	600
	CCAGTTTTTG	ACTGTCACAC	TGCCCACATT	GCTTGTAAGT	TCGACACCTT	650
	GGTTGAGAAG	ATCGACAGAA	GAACCGGTAA	GAAGTTGGAA	GATGAGCCAA	700
	AGTTCATCAA	GTCCGGTGAC	GCTGCTATCG	TCAAGATGGT	CCCAACCAAG	750
45	C					751

## 2) INFORMATION FOR SEQ ID NO: 420

50

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1102 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 55 (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- 60 (A) ORGANISM: *Candida inconspicua*  
 253

(B) STRAIN: ATCC 16783

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 420

```

5  TCTTGACAAG TTAAAGGCTG AAAGAGAAAG AGGTATCACT ATTGATATTG      50
   CTTTATGGAA ATTTCGAACT CCAAAGTATC ACGTTACCGT CATTGATGCT      100
   CCAGGTCACA GAGATTTTCAT TAAGAACATG ATTACTGGTA CTTCTCAAGC      150
   AGATTGTGCT ATTTTGATTA TTGCTGGTGG TGTCGGTGAA TTCGAAGCTG      200
   GTATTTCCAA GGATGGTCAA ACTAGAGAAC ACGCTTTATT AGCATTCCACC      250
10  TTAGGTGTTA AGCAATTGAT TGTTCGTATC AACAAAGATGG ATTCTGTAA      300
   TTGGGATGAA AAGAGATTG AAGAAATTGT CAAGGAAACC CAAAACCTCA      350
   TCAAGAAGGT TGGTTACAAC CCAAAGACTG TTCCATTCTG TCCAATTTCT      400
   GGTTGGAATG GTGACAACAT GATTGAACCA TCTTCTAACT GTCCATGGTA      450
   CAAGGGTTGG ACTAAGGAAA CCAAGGCAGG TGTGTCAAG GGTAAAGACCT      500
15  TATTAGAAGC TATTGATGCT ATTGAACCAC CTGTCAGACC AACTGATAAG      550
   CCATTAAGAT TACCATTACA AGATGTTTAC AAGATTGGTG GTATTGGTAC      600
   TGTGCCAGTC GGTAGAGTTG AAACCGGTAT TATTAAGCCA GGTATGGTTG      650
   TTGTTTTTCG ACCATCTGGT GTTACCACTG AAGTCAAGTC CGTTGAAATG      700
   CACCATGAAC AATTAGAAGA AGGTGTCCCA GGTGACAATG TTGGTTTTCAA      750
20  CGTCAAGAAC GTCTCTGTTA AGGATATCAA GAGAGGTAAC GTTTGTGGTG      800
   ACTCCAAGAA TGACCCACCA CAAGGTTGTG CTTCTTCAA TGCTCAAGTC      850
   ATTGTCTTGA ACCACCCTGG TCAAATTTCT GCTGGTTACT CTCCAGTTTT      900
   AGATTGTCAC ACTGCCCACA TTGCATGTAA ATTCGATGAA TTAATTGAAA      950
   AGATTGACAG AAGAACTGGT AAGTCCGTTG AAGACCATCC AAAGTCTGTT     1000
25  AAGTCTGGTG ATGCAGCTAT CGTTAAGATG GTTCCAACCA AGCCAATGTG     1050
   TGTGAAGCT TTCACTGAAT ACCCACCATT AGGTAGATTC GCAGTCAGAG     1100
   AT                                                                1102

```

30

2) INFORMATION FOR SEQ ID NO: 421

(i) SEQUENCE CHARACTERISTICS:

```

35  (A) LENGTH: 1099 bases
   (B) TYPE: Nucleic acid
   (C) STRANDEDNESS: Double
   (D) TOPOLOGY: Linear

```

(ii) MOLECULE TYPE: Genomic DNA

40

(vi) ORIGINAL SOURCE:

```

   (A) ORGANISM: Candida kefyr
   (B) STRAIN: ATCC 28838

```

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 421

```

   TGGACAAGTT AAAGGCTGAA AGAGAAAGAG GTATCACCAT CGATATCGCT      50
   TTGTGGAAGT TCGAAACTCC AAAGTACCAA GTTACCGTTA TCGATGCTCC      100
   AGGTCACAGA GATTTTCATCA AGAACATGAT TACTGGTACT TCTCAAGCTG      150
50  ACTGTGCTAT CTTGATTATT GCTGGTGGTG TCGGTGAATT CGAAGCCGGT      200
   ATCTCCAAGG ATGGTCAAAC CAGAGAACAC GCTTTGTTGG CTTACACCTT      250
   GGGTGTTAGA CAATTGATTG TTGCTATCAA CAAGATGGAC TCTGTTAAGT      300
   GGGATGAATC TCGTTACCAA GAAATTGTTA AGGAAACCTC CAACTTCATC      350
   AAGAAGGTCG GTTACAACCC AAAGAATGTT CCATTTCGTCC CAATCTCTGG      400
55  TTGGAACGGT GACAACATGA TTGAAGCCAC CACCAACGCT CCATGGTACA      450
   AGGGTTGGGA AAAGGAAACC AAGGCTGGTA CCGTCAAGGG TAAGACCTTG      500
   TTGGAAGCTA TTGACGCTAT CGAACCACCA ACCAGACCAA CTGACAAGCC      550
   ATTGAGATTG CCATTGCAAG ATGTCTACAA GATCGGTGGT ATTGGTACTG      600
   TGCCAGTCGG TAGAGTCGAA ACCGGTGTCA TCAAGCCAGG TATGGTTGTT      650
60  ACCTTCGCCC CAGCCGGTGT CACTACCGAA GTTAAGTCCG TCGAAATGCA      700

```

	CCACGAACAA	TTGGAAGAAG	GTCTACCAGG	TGACAACGTC	GGTTTCAACG	750
	TCAAGAACGT	TTCCGTTAAG	GAAATCAGAA	GAGGTAACGT	CTGTGGTGAC	800
	TCCAAGAACG	ATCCACCAA	GGCTGCTGCT	TCTTTCAACG	CCACTGTTAT	850
	CGTCTTGAAC	CACCCAGGTC	AAATCTCTGC	TGGTTACTCT	CCAGTTTTTG	900
5	ATTGTCACAC	TGCTCACATT	GCTTGTAAGT	TCGACGAATT	GTTGGAAAAG	950
	AACGACAGAA	GATCCGGTAA	GAAGTTGGAA	GACTCTCCAA	AGTTCTTGAA	1000
	GTCTGGTGAC	GCTGCTTTGG	TTAAGTTCGT	TCCATCTAAG	CCAATGTGTG	1050
	TTGAAGCATT	CTCTGACTAC	CCACCATTGG	GTAGATTTCGC	TGTCAGAGA	1099

10

## 2) INFORMATION FOR SEQ ID NO: 422

## (i) SEQUENCE CHARACTERISTICS:

- 15 (A) LENGTH: 1095 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

## 20 (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Candida krusei*  
 (B) STRAIN: ATCC 34135

25

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 422

	AAGTTAAAGG	CAGAAAGAGA	AAGAGGTATC	ACTATTGATA	TTGCTTTATG	50
	GAAGTTYGAA	ACTCCAAART	ACCACGTTAC	CGTTATTGAT	GCTCCAGGTC	100
30	ACAGAGATT	CATCAAGAAC	ATGATTACCG	GTACTTCTCA	AGCTGATTGT	150
	GCTATTTTGA	TTATTGCTGG	TGGTGTCCGG	GAATTCGAAG	CTGGTATCTC	200
	CAAGGATGGT	CAAAC TAGAG	AACACGCTCT	ATTGGCTTTC	ACCTTAGGTG	250
	TTAGACAATT	GATTGTTGCT	ATCAACAAGA	TGGATTCCGT	TAARTGGGAT	300
	GAAAACAGAT	TTGAAGAAAT	TGTCAAGGAA	ACCCAAAAC	TCATCAAGAA	350
35	GGTTGGTTAC	AACCCAAAGA	CTGTTCCATT	CGTTCCAATY	TCTGGTTGGA	400
	ATGGTGACAA	CATGATTGAA	GCATCCACCA	ACTGTCCATG	GTACAAGGGT	450
	TGGACTAAGG	AAACCAAGGC	AGGTGTTGTT	AAGGGTAAGA	CCTTATTAGA	500
	AGCAATCGAT	GCTATTGAAC	CACCTGTCAG	ACCAACCGAA	AAGCCATTAA	550
	GATTACCATT	ACAAGATGTT	TACAAGATTG	GTGGTATTGG	TACTGTGCCA	600
40	GTCGGTAGAG	TCGAAACCGG	TGTCATTAAG	CCAGGTATGG	TTGTCACTTT	650
	TGCTCCAGCA	GGTGTCACCA	CCGAAGTCAA	GTCCGTTGAA	ATGCACCATG	700
	AACAATTAGA	ACAAGGTGTT	CCAGGTGATA	ACGTTGGTTT	CAACGTTAAG	750
	AACGTTTCTG	TCAAGGATAT	CAAGAGAGGT	AACGTTTGTG	GTGACTCCAA	800
	GAACGACCCA	CCAATGGGTG	CAGCTTCCTT	CAATGCTCAA	GTCATTGTCT	850
45	TGAACCACCC	TGGTCAAATT	TCCGCTGGTT	ACTCTCCAGT	CTTGGATTGT	900
	CACACTGCC	ACATTGCATG	TAAGTTCGAC	GAATTAATCG	AAAAGATTGA	950
	CAGAAGAACT	GGTAAGTCTG	TTGAAGACCA	TCCAAAGTCY	GTCAAGTCTG	1000
	GTGATGCAGC	TATCGTCAAG	ATGGTCCCAA	CCAAGCCAAT	GTGTGTTGAA	1050
	GCTTTCAC	TG	ACTG	CA	AG	1095

50

## 2) INFORMATION FOR SEQ ID NO: 423

## (i) SEQUENCE CHARACTERISTICS:

- 55 (A) LENGTH: 1104 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

60



(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 5 (A) ORGANISM: *Candida lambica*  
(B) STRAIN: ATCC 24750

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 423

10	CTTGGACAAG	CTTAAGGCTG	AAAGAGAAAG	AGGTATCACC	ATTGATATCG	50
	CTTTATGGAA	GTTTCGAACT	CCAAAGTACC	ACGTTACCGT	CATTGACGCT	100
	CCAGGTCACA	GAGATTTTCA	CAAGAACATG	ATTACTGGTA	CCTCTCAAGC	150
	AGATTGTGCT	ATTTTTRATYA	TTGCTGGTGG	TGTCGGTGAA	TTCGAAGCTG	200
	GTATCTCTAA	GGATGGTCAA	ACCAGAGAAC	ACGCTCTTCT	TGCATTCACT	250
	CTTGGTGTTA	GACAATTGAT	TGTTGCTATC	AACAAGATGG	ACTCTGTCAA	300
15	GTGGGACGAA	TCCAGATTTCG	ATGAAATTTG	TAAGGAAACC	GCWAACCTTCA	350
	TCAAGAAGGT	TGGTTACAAC	CCAAAGACTG	TTCCATTTCGT	CCCAATCTCT	400
	GGTTGGAACG	GTGACAACAT	GATTGAACCA	TCTGCTAACT	GTCCATGGTA	450
	CAAGGGATGG	ACTAAGGAAA	CCAAGGCTTC	CGGTGTCGTC	AAGGGTAAGA	500
	CCCTTCTTGA	AGCAATTGAT	GCTATTGAGC	CACCTGTCAG	ACCAACTGAC	550
20	AAGGCTTTGA	GATTGCCATT	RCAAGATGTC	TACAAGATTG	GTGGTATTGG	600
	TACTGTGCCA	GTCGGTAGAG	TTGAAACCGG	TATCATCAAG	CCAGGTATGA	650
	TTGTCGTTTT	CGCTCCAACC	GGTGTTACTA	CTGAAGTTAA	GTCCGTTGAA	700
	ATGCACCATG	AACAATTAGA	AGAAGGTGTC	CCAGGTGACA	ATGTTGGTTT	750
	CAACGTCAAG	AACGTCTCTG	TAAAGGATAT	TAAGAGAGGT	AACGTCTGTG	800
25	GTGACTCCAA	GAACGACCCA	CCAATGGGTT	GTGCTTCCTT	CAATGCTCAA	850
	GTCATTGTTC	TTAACCACCC	AGGTCAAATT	TCTGCTGGTT	ACTCACCAGT	900
	TCTTGACTGT	CACACTGCCC	ACATTGCATG	TAAGTTCGAY	GAATTACTCG	950
	AAAAGATTGA	CAGAAGAACC	GGTAAGGCTA	CTGAAGACCA	TCCAAAGTCT	1000
	GTCAAGTCTG	GTGATGCAGC	TATCGTCAAG	ATGGTTCCAA	CCAAGCCAAT	1050
30	GTGTGTYGAA	GCTTTCACCTG	ACTACCCACC	ATTAGGTAGA	TTCGCTGTYA	1100
	GAGA					1104

35 2) INFORMATION FOR SEQ ID NO: 424

(i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 1098 bases  
(B) TYPE: Nucleic acid  
(C) STRANDEDNESS: Double  
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

45 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Candida lusitanae*  
(B) STRAIN: ATCC 66035

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 424

50	GGACAAGTTG	AAGGCTGAGA	GAGAAAGAGG	TATCACCATC	GATATCGCTT	50
	TGTGGAAGTT	CGAGACTCCA	AAGTACCACG	TTACCGTCAT	TGACGCTCCA	100
	GGTCACAGAG	ATTTCATCAA	GAACATGATC	ACTGGTACTT	CCCAAGCTGA	150
	CTGTGCTATC	TTGATTATCG	CTGGTGGTGT	CGGTGAGTTC	GAAGCCGGTA	200
55	TCTCTAAGGA	CGGTCAAACC	AGAGAGCACG	CTTTGTTGGC	TTACACCTTG	250
	GGTGTCGAAGC	AGTTGATTGT	TGCTGTCAAC	AAGATGGACT	CCGTCAAGTG	300
	GGACCAATCT	AGATTTCGAGG	AAATCATCAA	GGAAACCTCT	AACCTTCGTCA	350
	AGAAGGTTGG	TTACAACCCT	AAGACTGTTC	CATTTCGTCCC	AATCTCTGGT	400
	TGGAACGGTG	ACAACATGAT	TGAGCCATCY	ACCAACTGCC	CATGGTACAA	450
60	GGGTTGGGAG	AAGGAGACCA	AGTCYGGTAA	GTCCACCGGT	AAGACCTTGT	500

	TGGAGGCCAT	TGACGCCATT	GAGCCACCTT	CGAGACCAAC	CGACAAAGCCA	550
	TTGAGATTGC	CATTGCAAGA	TGTCTACAAG	ATYGGTGGTA	TTGGTACTGT	600
	GCCAGTCGGT	AGAGTTGAGA	CCGGTGTCAT	CAAGGCCGGT	ATGGTTGTCA	650
	CCTTTGCTCC	AGCTGGTGTC	ACCACTGAAG	TCAAGTCCGT	GGAAATGCAC	700
5	CACGAACAAT	TGGCTGAGGG	TGTCCCAGGT	GACAACGTTG	GTTTCAACGT	750
	CAAGAACGTT	TCCGTCAAGG	AAATCAGAAG	AGGTAACGTC	TGTGGTGAAT	800
	CCAAGAACGA	CCCACCAAAG	GCTGCTGCTT	CYTTCACCTG	TCAAGTYATY	850
	GTCTTGAACC	ACCCAGGTCA	AATCTCCTCY	GGTTACTCTC	CAGTYTTGGA	900
	CTGTCACACT	GCYCACATTG	CTTGTAAGTT	CGACACCTTG	ATTGAGAAGA	950
10	TCGACAGAAG	AACYGGTAAG	AAGTTGGAAG	AAGAGCCAAA	GTTTCATCAAG	1000
	TCYGGTGACG	CTGCTATCGT	CAAGATGGTC	CCAACCAAGC	CAATGTGYGT	1050
	YGAAGCTTTC	ACCGACTACC	CACCATTGGG	TAGATTTCGCT	GTCAGAGA	1098

15

## 2) INFORMATION FOR SEQ ID NO: 425

## (i) SEQUENCE CHARACTERISTICS:

20

- (A) LENGTH: 1101 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

25

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Candida norvegensis*
- (B) STRAIN: ATCC 22977

30

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 425

	TCTTGACAAG	TTAAAGGCTG	AAAGAGAAAG	AGGTATCACT	ATTGATATTG	50
	CTTTATGGAA	ATTCGAAACT	CCAAAATACC	ACGTTACCGT	TATTGATGCT	100
	CCAGGTCACA	GAGATTTTCAT	TAAGAACATG	ATTACTGGTA	CTTCCCAAGC	150
35	TGATTGTGCT	ATCTTAATTA	TTGCTGGTGG	TGTCGGTGAA	TTCGAAGCTG	200
	GTATCTCCAA	GGATGGTCAA	ACCAGAGAAC	ACGCTTTATT	AGCATTCAAC	250
	TTAGGTGTTA	AGCAATTAAT	TGTTGCTATC	AACAAGATGG	ACTCTGTAA	300
	GTGGGATGAA	AAGAGATTTG	AAGAAATTGT	CAAGGAAACC	CAAAACTTCA	350
	TCAAGAAGGT	TGGTTACAAC	CCAAAGACTG	TTCCATTTCG	TCCAATTTCT	400
40	GGTTGGAATG	GTGACAACAT	GATTGAACCA	TCTACTAACT	GTCCATGGTA	450
	CAAGGGTTGG	ACTAAGGAAA	CCAAGGCAGG	TGTTGTTAAG	GGTAAGACCT	500
	TATTAGAAGC	TATTGATGCT	ATTGAACCAC	CTGTCAGACC	AACTGACAAG	550
	CCATTAAAGAT	TACCATTACA	AGATGTTTAC	AAGATTGGTG	GTATTGGTAC	600
	TGTGCCAGTC	GGTAGAGTTG	AAACCGGTGT	TATTAAGCCA	GGTATGGTTG	650
45	TTGTTTTTCGC	ACCATCTGGT	GTTACCACTG	AAGTCAAGTC	CGTTGAAATG	700
	CACCATGAAC	AATTAGAACA	AGGTGTCCCA	GGTGACAATG	TTGGTTTCAA	750
	CGTCAAGAAC	GTCTCTGTTA	AGGATATTAA	GAGAGGTAAC	GTTTGTGGTG	800
	ACTCCAAGAA	CGACCCACCA	CAAGGTTGTG	CTTCCTTCAA	TGCTCAAGTC	850
	ATTGTCTTGA	ACCACCCTGG	TCAAATTTCT	GCAGGTTACT	CTCCAGTTTT	900
50	AGATTGTCAC	ACTGCCACCA	TTGCATGTAA	GTTTCGATGAA	TTAATCGAAA	950
	AGATTGACAG	AAGAACTGGT	AAGTCCGTTG	AAGACCATCC	AAAGTCTGTT	1000
	AAGTCTGGTG	ATGCAGCTAT	CGTTAAGATG	GTTCCAACCA	AGCCAATGTG	1050
	TGTTGAAGCT	TTCACCTGAAT	ACCCACCATT	AGGTAGATTC	GCAGTCAGAG	1100
	A					1101

55

## 2) INFORMATION FOR SEQ ID NO: 426

60

## (i) SEQUENCE CHARACTERISTICS:

257

- (A) LENGTH: 1095 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

5

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Candida parapsilosis*  
 (B) STRAIN: ATCC 90018

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 426

	CAAATTGAAG	GCTGAAAGAG	AAAGAGGTAT	CACCATTGAT	ATCGCTTTGT	50
15	GGAAATTCTGA	AACATCCAAA	TACCATGTTA	CTGTTATTGA	TGCTCCAGGT	100
	CACAGAGATT	TCATCAAGAA	TATGATTACT	GGTACTTCTC	AAGCTGATTG	150
	TGCTATTTTG	ATTATTGCTG	GTGGTACTGG	TGAATTCGAA	GCTGGTATCT	200
	CTAAGGATGG	TCAAACCAGA	GAACACGCTT	TGTTGGCTTA	CACCTTGGGT	250
	GTTAAGCAAT	TGATTGTTGC	CATCAACAAG	ATGGACTCAG	TCAAATGGGA	300
20	CAAGAACAGA	TACGAAGAAA	TTGTCAAGGA	AACTTCCAAC	TTCGTCAAGA	350
	AGGTTGGTTA	CAACCCTAAA	GCTGTCCCAT	TCGTCCCAAT	CTCTGGTTGG	400
	AACGGTGACA	ATATGATTGA	ACCATCAACC	AACTGTCCAT	GGTACAAGGG	450
	TTGGGAAAAG	GAAACTAAAG	CTGGTAAGGT	TACCGGTAAG	ACCTTGTTGG	500
	AAGCTATCGA	TGCTATCGAA	CCACCAACCA	GACCAACTGA	CAAGCCATTG	550
25	AGATTGCCAT	TGCAAGATGT	CTACAAGATT	GGTGGTATTG	GAAGCTGTCC	600
	AGTTGGTAGA	GTTGAAACCG	GTATCATCAA	GGCTGGTATG	GTTGTTACTT	650
	TTGCCCCAGC	TGGTGTTACC	ACTGAAGTCA	AGTCCGTGTA	AATGCACCAC	700
	GAACAATTGA	CTGAAGGTGT	CCCAGGTGAC	AATGTTGGTT	TCAACGTCAA	750
	GAACGTTTCA	GTTAAGGAAA	TCAGAAGAGG	TAACGTTTGT	GGTGACTCCA	800
30	AGAACGATCC	ACCAAAGGGA	TGTGAYTCCT	TCAATGCTCA	AGTTATTGTC	850
	TTGAACCACC	CAGGTCAAAT	CTCTGCTGGT	TACTCACCAG	TCTTGGATTG	900
	TCACACTGCC	CACATTGCTT	GTAAATTCTGA	CACTTTGATT	GAAAAGATTG	950
	ACAGAAGAAC	CGGTAAGAAA	TTGGAAGATG	AACCAAAATT	CATCAAGTCC	1000
	GGTGATGCTG	CYATCGTCAA	GATGGTCCCA	ACCAAGCCAA	TGTGTGTTGA	1050
35	AGCTTTCACT	GACTACCCAC	CATTGGGAAG	ATTCGCTGTT	AGAGA	1095

2) INFORMATION FOR SEQ ID NO: 427

40

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 752 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

45

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Candida rugosa*  
 (B) STRAIN: ATCC 96275

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 427

55	CTCCGTCAAG	TGGTCTCAGT	CTCGTTTCTGA	GGAGATCGTC	AAGGAGGTTT	50
	CCAAC TTCAT	CAAGAAGGTT	GGTTACAAGC	CCGATGAGGT	TCCTTTCGTC	100
	CCCATCTCTG	GCTGGAACGG	CGACAACATG	CTTGAGCCCT	CCACCAACTG	150
	CCCCTGGTAC	AAGGGATGGA	CCAAGAAGAC	CAAGAAGGGT	GAGGTCAAGG	200
	GTAAGACTCT	TCTCGAGGCC	ATTGACGCCA	TCGAGCCCCC	CTCCCGTCCT	250
60	ACCGACAAGC	CCCTCCGCTT	GCCTCTTCAG	GATGTCTACA	AGATCGGCGG	300

	TATCGGTACG	GTACCTGTCG	GCCGTGTCGA	GACCGGTATC	ATCAAGCCCCG	350
	GCATGGTCGT	CACTTTCGCC	CCCGCTGGTG	TCACCACTGA	AGTGAAGTCC	400
	GTCGAGATGC	ACCACGAGCA	GATCCCCGAG	GGTCTCCCCG	GTGACAACGT	450
	CGGTTTCAAC	GTCAAGAACG	TTACCGTCAA	GGATATCCGC	CGTGGTAACG	500
5	TCTGCGGTGA	CTCCAAGAAC	GACCCCCCA	AGGGCTGCTC	TTCCTTCACT	550
	GCCCAGGTCA	TCGTTTTTCAA	CCACCCCGGT	CAGATCTCCA	ACGGTTACTC	600
	CCCCGTTTTG	GACTGCCACA	CCGCCACAT	TGCCTGCCGC	TTCGACGAGA	650
	TCCAGTCCAA	GATGGACCGT	CGTACTGGTA	AGACCCTTGA	GGAGAACCCC	700
	AAGTTCATCA	AGGCTGGTGA	CTCCGCTATC	GTCAAGATGG	TTCCCTCCAA	750
10	GC					752

## 2) INFORMATION FOR SEQ ID NO: 428

15

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1093 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 20 (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- 25 (A) ORGANISM: *Candida sphaerica*  
 (B) STRAIN: ATCC 2504

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 428

30	AGTTAAAGGC	TGAAAGAGAA	AGAGGTATCA	CCATCGATAT	CGCTTTGTGG	50
	AAGTTCGAAA	CTCCAAAGTA	CCAAGTTACC	GTTATCGATG	CTCCAGGTCA	100
	CAGAGATTTC	ATCAAGAACA	TGATTACTGG	TACTTCTCAA	GCTGACTGTG	150
	CTATCTTGAT	TATTGCTGGT	GGTGTCGGTG	AATTCGAAGC	CGGTATCTCC	200
	AAGGATGGTC	AAACCAGAGA	ACACGCTTTG	TTGGCTTTCA	CCTTGGGTGT	250
35	TAGACAATTG	ATTGTTGCTG	TTAACAAGAT	GGATTCCGTT	AAGTGGGATG	300
	AATCTCGTTT	CCAAGAAATT	GTCAAGGAAA	CCTCTAACTT	CATCAAGAAG	350
	GTCGGTTACA	ACCCAAAGAC	TGTTCCATTC	GTCCCAATCT	CTGGTTGGAA	400
	CGGTGACAAC	ATGATTGAAG	CCACCACCAA	TGCTTCATGG	TACAAGGGTT	450
	GGGAAAAGGA	AACCAAGTCC	GGTGTCGTCA	AGGGTAAGAC	CTTGTTGGAA	500
40	GCTATTGACG	CTATCGAACC	ACCATCCAGA	CCAAGTGAAC	AGCCATTGAG	550
	ATTGCCATTG	CAAGATGTCT	ACAAGATTGG	TGGTATCGGA	ACTGTGCCAG	600
	TCGGTAGAGT	CGAAACCGGT	GTTATCAAGC	CAGGTATGAT	TGTTACCTTT	650
	GCCCCAGCCG	GTGTTACTAC	TGAAGTTAAG	TCCGTCGAAA	TGCACCACGA	700
	ACAATTGGAA	GAAGGTCTAC	CAGGTGACAA	CGTCGGTTTC	AACGTCAAGA	750
45	ACGTTTCCGT	TAAGGAAATC	AGAAGAGGTA	ACGTCGTGG	TGACTCCAAG	800
	AACGATCCAC	CAAAGGCTGC	TGCTTCTTTC	AACGCCACTG	TTATCGTCTT	850
	GAACCATCCA	GGTCAAATCT	CTGCTGGTTA	CTCTCCAGTT	TTGGATTGTC	900
	ACACTGCTCA	CATTGCTTGT	AAGTTCGACG	AATTGTTGGA	AAAGAACGAT	950
	AGAAGATCCG	GTAAGAAGTT	GGAAGACTCT	CCAAAGTTCT	TGAAGTCCGG	1000
50	TGATGCTGCT	TTGGTTAAGT	TCGTTCCATC	TAAGCCAATG	TGTGTTGAAG	1050
	CCTTCTCTGA	CTACCCACCT	CTAGGTAGAT	TCGCTGTCAG	AGA	1093

## 55 2) INFORMATION FOR SEQ ID NO: 429

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1094 bases  
 (B) TYPE: Nucleic acid  
 60 (C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

5 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Candida tropicalis*

(B) STRAIN: ATCC 13803

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 429

10  
 AAATTGAAGG CTGAAAGAGA AAGAGGTATC ACCATTGATA TCGCTTTGTG 50  
 GAAATTTCGAA ACTCCAAAAT ACCACGTTAC CGTTATTGAT GCTCCAGGTC 100  
 ACAGAGATTT CATCAAGAAC ATGATTACTG GTACTTCCCA AGCTGATTGT 150  
 GCTATTTTGA TTATTGCTGG TGGTACTGGT GAATTCGAAG CTGGTATTTC 200  
 15 TAAAGATGGT CAAACCAGAG AACACGCTTT GTTGGCTTAC ACCTTGGGTG 250  
 TCAAACAATT GATTGTTGCT GTCAACAAGA TGGACTCTGT TAAATGGGAC 300  
 AAAAACAGAT TTGAAGAAAT TATCAAGGAA ACTTCTAACT TCGTCAAGAA 350  
 GGTGTTGTTAC AACCCTAAGG CTGTTCCATT CGTTCCAATC TCTGGTTGGA 400  
 ATGGTGACAA CATGATTGAA GCTTCTACCA ACTGTCCATG GTACAAGGGT 450  
 20 TGGGAAAAAG AAACCAAGGC TGGTAAGGTT ACCGGTAAGA CTTTGTGTTGGA 500  
 AGCCATTGAT GCTATTGAAC CACCTTCAAG ACCAACTGAC AAGCCATTGA 550  
 GATTGCCATT GCAAGATGTT TACAAGATTG GTGGTATTGG TACTGTGCCA 600  
 GTCGGTAGAG TTGAAACTGG TGTCATCAA GCGGTATGG TTGTTACTTT 650  
 CGCCCCAGCT GGTGTTACCA CTGAAGTCAA ATCCGTCGAA ATGCACCACG 700  
 25 AACAATTGGC TGAAGGTGTC CCAGGTGACA ATGTTGGTTT CAACGTTAAG 750  
 AACGTTTCTG TTAAAGAAAT TAGAAGAGGT AACGTTTGTG GTGACTCCAA 800  
 GAACGATCCA CCAAAGGGTT GTGACTCTTT CAACGCTCAA GTTATTGTCT 850  
 TGAACCAACC AGGTCAAATC TCTGCTGGTT ACTCTCCAGT CTTGGATTGT 900  
 CACACTGCTC ATATTGCTTG TAAATTCGAC ACCTTGGTTG AAAAGATTGA 950  
 30 CAGAAGAACT GGTAAGAAAT TGAAGAAAA TCCAAAATTC GTCAAATCCG 1000  
 GTGATGCTGC TATTGTCAAG ATGGTTCCAA CCAAACCAAT GTGTGTTGAA 1050  
 GCTTTCCTG ACTACCCACC ATTAGGTAGA TTCGCTGTCA GAGA 1094

35

2) INFORMATION FOR SEQ ID NO: 430

(i) SEQUENCE CHARACTERISTICS:

40 (A) LENGTH: 1095 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

45

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Candida utilis*

(B) STRAIN: Csp 388

50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 430

CAAGCTTAAA GCTGAGAGAG AGAGAGGTAT CACTATCGAC ATTGCTCTCT 50  
 GGAAGTTCGA GACTCCAAAG TACCACGTTA CTGTCATTGA TGCCCCAGGT 100  
 CACAGAGATT TCATCAAGAA CATGATTACT GGTACCTCCC AGGCTGACTG 150  
 55 TGCTATTCTT ATCATTGCCG GTGGTGTGTTG TGAGTTCGAG GCTGGTATCT 200  
 CTAAGGATGG TCAGACCAGA GAGCACGCTT TGCTCGCTTT CACCCTTGGT 250  
 GTTAGACAGA TGATTGTTGC TATCAACAAG ATGGACTCTG TCAAGTGGGA 300  
 CGAGAAGAGA TTCGAGGAGA TCGTTAAGGA GACCTCTAAC TTCATCAAGA 350  
 AGGTTGGTTA CAACCCAAAG ACTGTTCCAT TTGTCCCAAT TTCYGGTTGG 400  
 60 AACGGTGACA ACATGATTGA GGCCTCTACC AACTGTCCAT GGTACAAGGG 450

	TTGGGAGAAAG	GAGACCAAGG	CTGGTGTGTGT	CAAGGGTAAG	ACCTTGCTCG	500
	ATGCCATTGA	CGCCATTGAG	CCACCAACAA	GACCAACTGA	CAAGCCATTG	550
	AGATTGCCAC	TCCAGGATGT	CTACAAGATT	GGTGGTATCG	GAAGTGTTC	600
	AGTCGGTAGA	GTCGAGACCG	GTGTCATCAA	GCCAGGTATG	GTTGTTACCT	650
5	TTGCCCCATC	CGGTGTCACC	ACTGAGGTTA	AGTCGGTCGA	GATGCACCAC	700
	GAGCAGCTTG	CTGAGGGTAT	CCCAGGTGAC	AACGTTGGTT	TCAACGTTAA	750
	GAACGTCTCT	GTTAAGGAGA	TCAGAAGAGG	TAACGTTGCC	GGTGACTCCA	800
	AGAACGACCC	ACCACAGGGT	GCTGAGTCCT	TCAACGCTCA	GGTCATTGTC	850
	TTGAACCACC	CAGGTCAGAT	CTCTGCTGGT	TACTCTCCAG	TTTTGGACTG	900
10	TCACACCGCC	CACATTGCTT	GTAAGTTCTC	TGAGCTTTTG	GAGAAGATTG	950
	ACAGAAGATC	CGGTAAGTCC	CTTGAGGCCT	CTCCAAAGTT	CGTCAAGTCT	1000
	GGTGATGCCG	CTATCGTCAA	GATGGTTCCA	TCCAAGCCAT	TGTGTGTTGA	1050
	GGCCTTCACT	GACTACCCAC	CACTCGGTAG	ATTCGCTGTC	AGAGA	1095

15

## 2) INFORMATION FOR SEQ ID NO: 431

(i) SEQUENCE CHARACTERISTICS:

20 (A) LENGTH: 1085 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

25 (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Candida viswanathii*

(B) STRAIN: ATCC 28269

30

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 431

	GCTGAAAGAG	AAAGAGGTAT	CACCATCGAT	ATCGCTTTGT	GGAAATTCTGA	50
	AACTCCAAAR	TACCACGTTA	CCGTCATTGA	YGCTCCAGGT	CACAGAGATT	100
35	TCATCAAGAA	CATGATYACT	GGTACTTCTC	AAGCTGATTG	TGCTATYTTG	150
	ATTATCGCTG	GTGGTACTGG	TGAATTCGAA	GCTGGTATYT	CTAAGGATGG	200
	TCAAACCAGA	GAACACGCTT	TGTTGGCCTA	CACCTTGGGT	GTCAAGCAAT	250
	TGATTGTTGC	TGTCAACAAG	ATGGACTCTG	TCAAATGGGA	CAAGAACAGA	300
	TTCGAAGAAA	TCATCAAGGA	AACCTCCAAC	TTCGTCAAGA	AGGTTGGTTA	350
40	CAACCCAAAG	ACTGTTCCAT	TCGTCCCAAT	CTCTGGTTGG	AACGGTGACA	400
	ACATGATTGA	AGCCTCCACC	AACTGCCCCAT	GGTACAAGGG	TTGGGAAAAG	450
	GAAACCAAGG	CTGGTAAGGT	TACCGGTAAG	ACTTTGTTGG	AAGCCATTGA	500
	CGCTATCGAA	CCACCAACCA	GACCAACTGA	CAAGCCATTG	AGATTGCCAT	550
	TGCAAGATGT	CTACAAGATT	GGTGGTATCG	GAAGTGTGCC	AGTCGGTAGA	600
45	GTTGAAACTG	GTGTCATCAA	GGCCGGTATG	GTTGTCACTT	TYGCCCCAGC	650
	TGGTGTTACC	ACTGAAGTCA	AGTCCGTTGA	AATGCACCAC	GAACAATTGG	700
	CTGAAGGTGT	CCCAGGTGAC	AACGTTGGTT	TCAACGTCAA	GAACGTTTCC	750
	GTCAAGGAAA	TCAGAAGAGG	TAACGTCTGT	GGTGACTCCA	AGAACGACCC	800
	ACCAAAGGGT	TGTGASTCTT	TCAACGCTCA	AGTCATTGTC	TTGAACCACC	850
50	CAGGTCAAAT	CTCTGCTGGT	TACTCTCCAG	TCTTGGATTG	TCACACTGCC	900
	CACATTGCTT	GTAAGTTTGA	CACCTTGGTT	GAAAAGATTG	ACAGAAGAAC	950
	CGGTAAGAAG	TTGGAAGAAA	ACCCAAAGTT	TGTCAAGTCC	GGTGACGCTG	1000
	CTATCGTCAA	GATGGTCCCA	ACCAAGCCAA	TGTGTGTTGA	AGCYTTCCT	1050
	GACTACCCAC	CATTGGGTAG	ATTCGCTGTC	AGAGA		1085

55

## 2) INFORMATION FOR SEQ ID NO: 432

60 (i) SEQUENCE CHARACTERISTICS:

261

(A) LENGTH: 1072 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

5

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Candida zeylanoides*  
 (B) STRAIN: ATCC 7351

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 432

	AGGTATTACC	ATTGACATTG	CCTTGTGGAA	GTTTCGAGACC	CCCAAGTACC	50
15	AGGTCACCGT	CATTGACGCT	CCTGGCCACA	GAGATTTTCAT	TAAGAACATG	100
	ATCACTGGTA	CCTCCCAGGC	TGACTGTGCC	ATCTTGATCA	TTGCTGGTGG	150
	TGTTGGTGAG	TTCGAGGCTG	GTATCTCCAA	GGATGGCCAG	ACCAGAGAGC	200
	ACGCCTTGCT	TGCCTACACC	TTGGGTGTCA	AGCAATTGAT	TGTTGCTGTC	250
	AACAAGATGG	ACTCCGTCAA	GTGGGACAAG	AACAGATTCTG	AGGAGATTGT	300
20	CAAGGAGACC	TCCAACCTTCG	TCAAGAAGGT	TGGCTACAAC	CCCAAGACTG	350
	TCCCCTTCGT	TCCCATCTCC	GGTTGGAACG	GTGACAACAT	GATTGAGGCC	400
	TCCACCAACT	GCCCTTGGTA	CAAGGGTTGG	GAGAAGGAGA	CCAAGGCCGG	450
	TAAGGTCACT	GGTAAGACCT	TGTTGGAGGC	TATTGACGCC	ATTGAGCCCC	500
	CCACCAGACC	CACCGACAAG	CCCTTGAGAT	TGCCCTTGCA	GGATGTCTAC	550
25	AAGATTGGTG	GTATTGGAAC	GGTGCCCGTT	GGCAGAGTTG	AGACCGGCAT	600
	CATCAAGGCC	GGTATGGTTG	TCACCTTTGC	CCCCGCTGGT	GTCACTACTG	650
	AAGTGAAGTC	TGTCGAGATG	CACCACGAGC	AATTGGCTGA	GGGTGTCCCA	700
	GGTGACAATG	TTGGTTTCAA	CGTGAAGAAC	GTTTCCGTTA	AGGAGATCAG	750
	AAGAGGTAAC	GTTTGCGGTG	ACTCCAAGAA	CGACCCCCC	AAGGCTGCTG	800
30	CTTCTTTCAA	CGCCCAGGTT	ATCGTCTTAA	ACCACCCCGG	TCAAATCTCT	850
	GCTGGTTACT	CTCCGGTTTT	GGATTGCCAC	ACTGCCCACA	TTGCTTGCCAG	900
	ATTCGACCAG	TTGATTGAGA	AGATCGACAG	AAGAACCGGT	AAGAAGATGG	950
	AGGACGACCC	TAAGTTCATC	AAGTCCGGTG	ACGCTGCCAT	CGTCAAGATG	1000
	GTTCTTTCCA	AGCCCATGTG	TGTTGAGGCC	TTCCTGACT	ACCCTCCCTT	1050
35	GGGTCGTTTC	GCTGTCAGAG	AC			1072

2) INFORMATION FOR SEQ ID NO: 433

40

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 751 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

45

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Coccidioides immitis*  
 (B) STRAIN: Silveira

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 433

55	AGCACCAACT	GGTCCGAGCC	TCGTTTCAAC	GAAATCGTCA	AGGAAGTCTC	50
	CAACTTCATC	AAGAAGGTCG	GATACAACCC	CAAGGCTGTT	CCATTCTGTC	100
	CCATCTCTGG	TTTCGAAGGT	GACAACATGA	TTCAACCCCTC	CACCAACGCT	150
	CCTTGGTACA	AGGGCTGGAA	CAAGGAGACC	GCCTCTGGCA	AGCACACTGG	200
	CAAGACCCTC	CTCGACGCCA	TTGATGCCAT	CGACCCCCCA	ACCCGCCCCA	250
60	CCGAGAAGCC	CCTCCGTCTC	CCACTTCAGG	ATGTGTACAA	GATCTCTGGT	300

	ATCGGAACAG	TCCCAGTCGG	CCGTGTCGAA	ACCGGTGTTA	TCAAGCCTGG	350
	TATGGTTGTG	ACCTTCGCTC	CTTCCAACGT	CACCACTGAA	GTCAAGTCCG	400
	TCGAAATGCA	CCACCAGCAG	CTCACCCAGG	GTAACCCTGG	TGACAACGTT	450
	GGCTTCAACG	TCAAGAACGT	CTCTGTCAAG	GAAGTCCGCC	GCGGTAACGT	500
5	CGCTGGTGAC	TCCAAGAACG	ACCCACCAAA	GGGCTGCGAC	TCCTTCAACG	550
	CCCAGGTCAT	CGTCCTCAAC	CACCCTGGTC	AAGTCGGTGC	TGGTTATGCC	600
	CCAGTCCTTG	ACTGCCACAC	TGCCACATT	GCTTGCAAGT	TCTCCGAGCT	650
	CCTCGAGAAG	ATCGACCGCC	GTACCGGTAA	ATCCGTTGAG	AACAACCCCA	700
	AGTTCATCAA	GTCTGGTGAT	GCCGCTATCG	TCAAGATGGT	TCCATCCAAG	750
10	C					751

## 2) INFORMATION FOR SEQ ID NO: 434

15

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1146 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 20 (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- 25 (A) ORGANISM: *Cryptococcus albidus*  
 (B) STRAIN: ATCC 66030

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 434

30	AAGCTCAAGG	CCGAGCGAGA	GCGAGGTATC	ACCATCGACA	TCGCCTTGTG	50
	GAAGTTCGAG	ACCCCCAAGT	ACAATGTCAC	CGTCATTGAC	GCCCCCGGTC	100
	ACCGAGACTT	CATCAAGAAC	ATGATCACCG	GTACCTCGCA	GGCCGACTGT	150
	GCCATCCTCA	TCATCGCCTC	CGGTATCGGA	GAGTTCGAGG	CTGGTATCTC	200
	CAAGGACGGT	CAGACCCGAG	AGCACGCCCT	TTTGGCCTTC	ACCCTCGGTG	250
35	TCCGACAGCT	CATCATTGCC	ATCAACAAGA	TGGACACCTG	CAAGGTTAGT	300
	TCGCAGGTCC	TGGTCTCTGT	ACGAATCTTG	CTGACCCCTT	TTACAGTGGT	350
	CCGAAGACCG	ATACAACGAA	ATCGTCAAGG	AGGCTTCCGG	TTTCATCAAG	400
	AAGGTCGGAT	ACAACCCCAA	GACCGTTCCC	TTCGTCCCCA	TCTCCGGATG	450
	GCACGGAGAC	AACATGTTGG	AGGAGTCCAC	CAACATGCCC	TGGTACAAGG	500
40	GATGGCACAA	GGAGTCCAAG	GCCGGTGTTG	TCAAGGGAAA	GACCTTGCTC	550
	GAGGCCATCG	ACGCCATCGA	GCCCCCTACC	CGACCTTCGG	ACAAGCCCTT	600
	GCGATTGCCC	CTCCAGGATG	TCTACAAGAT	CGGTGGTATC	GGTACGGTGC	650
	CCGTGCGTCG	AGTCGAGACC	GGTGTCATCA	AGGCTGGTAT	GGTCGTCAAC	700
	TTCGCCCCTG	CCAACGTCAC	CACCGAAGTC	AAGTCCGTCG	AAATGCACCA	750
45	CGAACAGCTC	GCTGAGGGTG	TTCCCGGTGA	CAACGTCGGT	TTCAACGTCA	800
	AGAACGTTTC	CGTCAAGGAC	ATCCGACGAG	GAAACGTCTG	CTCCGACTCG	850
	AAGAACGACC	CCGCTATGGA	GTCTGCTTCC	TCAACGCTC	AGGTCATTGT	900
	CTTGAACCAC	CCGGGTCAGA	TCGGTGCCGG	CTACTCCCCC	GTTTTGGACT	950
	GCCACACCGC	TCACATTGCC	TGCAAGTTCG	CTGAGCTCGT	TGAGAAGATC	1000
50	GACCGACGAA	CCGGTAAGGT	CATGGAGGCC	GCCCCCAAGT	TCGTCAAGTC	1050
	CGGTGACGCC	GCCATCGTCA	AGTTGATCCC	GTCCAAGCCC	ATGTGTGTCTG	1100
	AGTCCTACTC	CGAGTACCCC	CCCTTGGGTC	GATTCGCCGT	CCGAGA	1146

55

## 2) INFORMATION FOR SEQ ID NO: 435

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1095 bases  
 60 (B) TYPE: Nucleic acid



(C) STRANDEDNESS: Double  
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

5

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Exophiala jeanselmei*  
(B) STRAIN: ATCC 64755

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 435

	CAAGCTGAAG	GCCGAGCGTG	AGCGTGGTAT	CACCATCGAT	ATCGCCTTGT	50
	GGAAGTTCGA	GACTCCCAAG	TACTATGTCA	CTGTCATCGA	CGCCCCTGGT	100
	CATCGTGACT	TTATCAAGAA	CATGATCACT	GGTACTTCCC	AGGCTGACTG	150
15	CGCCATTCTC	ATCATTGCCG	CCGGTACTGG	TGAATTCGAA	GCCGGTATCT	200
	CCAAGGATGG	TCAGACTCGT	GAGCACGCTC	TGCTCGCCTA	CACCCTGGGT	250
	GTCAAGCAGC	TCATTGTCGC	CATCAACAAG	ATGGACACCA	CCAAGTGGTC	300
	CGAGGATCGT	TTCAACGAAA	TCATCAAGGA	GACTTCCAGC	TTCATCAAGA	350
	AGGTCCGGCTA	CAACCCCAAG	TCCGTTCCCTT	TCGTCCCCAT	CTCCGGCTTC	400
20	AACGGTGACA	ACATGATCGA	TGTCTCCACC	AACTGCCCCCT	GGTACAAGGG	450
	CTGGGAGAAG	GAGACCAAGG	CTGGCAAGGC	CTCTGGCAAG	ACTCTCCTCG	500
	AGGCCATCGA	CGCCATCGAC	CCCCCCTC	GTCCCACCGA	CAAGCCTCTC	550
	CGTCTTCCTC	TCCAGGATGT	CTACAAGATC	TCTGGTATCG	GAACGGTGCC	600
	CGTCGGTTCGT	GTTGAGACTG	GTGTCATCAA	GGCCGGTATG	GTCGTTACCT	650
25	TCGCTCCTGC	CAACGTCACC	ACTGAAGTCA	AGTCCGTCGA	AATGCACCAC	700
	GAACAACCTCG	CCGAGGGTGT	TCCAGGTGAC	AACGTTGGTT	TCAACGTCAA	750
	GAACGTCTCC	GTCAAGGAGG	TTCGTCGTGG	AAACGTCTGC	GGTGACTCCA	800
	AGAACGACCC	ACCCAAGGGT	GCTGATTCCT	TCAACGCCCA	GGTCATCGTC	850
	TTGAACCACC	CTGGTCAAGT	CGGTGCTGGC	TACGCCCCAG	TGTTGGATTG	900
30	CCACACTGCC	CACATTGCTT	GCAAGTCTC	TGAGCTTCTC	GAGAAGATTG	950
	ACCGCCGTAC	CGGTAAATCC	ATCGAAAACA	ACCCAAGTT	CATCAAGTCT	1000
	GGTGACGCTG	CCATCGTCAA	GATGGTTCCC	AGCAAGCCCA	TGTGTGTTGA	1050
	GGCCTTCACT	GACTACCCAC	CTCTTGGTCG	TTTCGCCGTC	CGTGA	1095

35

2) INFORMATION FOR SEQ ID NO: 436

(i) SEQUENCE CHARACTERISTICS:

40 (A) LENGTH: 1113 bases  
(B) TYPE: Nucleic acid  
(C) STRANDEDNESS: Double  
(D) TOPOLOGY: Linear

45 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Fusarium oxysporum*  
(B) STRAIN: WSA-212

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 436

	AAGCTCAAGG	CCGAGCGTGA	GCGTGGTATC	ACCATCGATA	TTGCTCTCTG	50
	GAAGTTCGAG	ACTCCTCGCT	ACTATGTCAC	CGTCATTGGT	ATGTTGTTCG	100
55	TCATGCTTCA	TTCTACTTCT	CTTCGTA	CTTCACTACT	CAGACGCTCC	150
	CGGTCACCGT	GATTTCATCA	AGAACATGAT	CACTGGTACT	TCCCAGGCCG	200
	ATTGCGCCAT	TCTCATCATT	GCCGCCGGTA	CTGGTGAGTT	CGAGGCTGGT	250
	ATCTCCAAGG	ATGGCCAGAC	CCGTGAGCAC	GCTCTTCTTG	CCTACACCCT	300
	TGGTGTCAAG	AACCTCATCG	TCGCCATCAA	CAAGATGGAC	ACCACCAAGT	350
60	GGTCTGAGGC	CCGTTACCAG	GAGATCATCA	AGGAGACCTC	CTCTTTCATC	400

	AAGAAGGTCG	GCTACAACCC	CAAGGCTGTC	GCTTTCGTCC	CCATCTCCGG	450
	TTTCAACGGT	GACAACATGC	TTACCCCCTC	CACCAACTGC	CCCTGGTACA	500
	AGGGTTGGGA	GCGTGAGATC	AAGTCCGGCA	AGCTCACTGG	CAAGACCCTC	550
	CTCGAGGCCA	TTGACTCCAT	CGAGCCCCCC	AAGCGTCCCG	TTGACAAGCC	600
5	CCTTCGTCTT	CCCCTTCAGG	ATGTCTACAA	GATCGGTGGT	ATTGGAACGG	650
	TTCCCCTCGG	CCGTATCGAG	ACTGGTGTC	TCAAGCCCGG	TATGGTCGTT	700
	ACCTTCGCTC	CTTCCAACGT	CACCACTGAA	GTCAAGTCCG	TCGAGATGCA	750
	CCACGAGCAA	CTCACTGAGG	GCCAGCCCGG	TGACAACGTT	GGTTTCAACG	800
	TGAAGAACGT	CTCCGTCAAG	GACATCCGAC	GTGGTAACGT	CGCTGGTGAC	850
10	TCCAAGAACG	ACCCCCCTAT	GGGTGCCGCT	TCTTTCACCG	CCCAGGTCAT	900
	CGTCCTCAAC	CACCCCGGTC	AGGTCGGTGC	TGGTTACGCT	CCCGTCCTCG	950
	ATTGTCACAC	TGCCCACATT	GCCTGCAAGT	TCGCCGAGAT	CCAGGAGAAG	1000
	ATCGACCGCC	GAACCGGTAA	GGCTACTGAG	GCCGCCCCCA	AGTTCATCAA	1050
	GTCTGGTGAC	TCCGCCATCG	TCAAGATGGT	TCCCTCCAAG	CCCATGTGTG	1100
15	TTGAGGCTTT	CAC				1113

## 2) INFORMATION FOR SEQ ID NO: 437

20

## (i) SEQUENCE CHARACTERISTICS:

25

- (A) LENGTH: 726 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

30

- (A) ORGANISM: *Geotrichum* spp.
- (B) STRAIN: LEV-4

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 437

35	GGTCCGAGGA	CAGATTCAAC	GAGATTGTCA	AGGAGACTTC	CAACTTCATC	50
	AAGAAGGTTG	GTTAYAACCC	CAAGACTGTT	GCTTTCGTCC	CCATCTCTGG	100
	TTGGAACGGT	GACAACATGA	TTGAGCCCTC	CACCAACTGC	CCCTGGTACA	150
	AGGGATGGCA	GAAGGAGACC	AAGGCTGGTG	TCACTAAGGG	TAAGACCCTC	200
	CTTGAGGCCA	TCGATGCCAT	TGAGCCCCCT	GTCAGACCTT	CCGACAAGCC	250
40	CCTCCGTCTT	CCCCTCCAGG	ATGTCTACAA	GATCGGTGGT	ATCGGAACTG	300
	TGCCCGTCGG	CCGTGTGCGA	ACCGGTGTCA	TCAAGGCCGG	TATGGTCGTC	350
	ACCTTCGCCC	CCGCTGGTGT	CACCACTGAA	GTCAAGTCCG	TCGAGATGCA	400
	CCACGAGCTC	CTCACTGAGG	GTCTCCCCGG	TGACAACGTT	GGTTTCAACG	450
	TCAAGAACGT	CTCCGTTAAG	GATATCAGAC	GTGGTAACGT	CTGCGGTGAC	500
45	TCCAAGAACG	ATCCCCCCTA	GGCTTGCGCT	TCTTTCACCG	CCCAGGTCAT	550
	TATCTTCAAC	CACCCCTGGT	AGATCTCTGC	TGGATACTCT	CCCGTCCTTG	600
	ATTGCCACAC	CGCCCATATT	GCTTGCAAGT	TCGACACTTT	GATCGAGAAG	650
	ATTGACCGTC	GTACTGGTAA	GAAGACTGAG	GACTCCCCCA	AGTTCGTCAA	700
50	GGCCGGTGAT	GCTGCTATCG	TCAAGA			726

## 2) INFORMATION FOR SEQ ID NO: 438

55

## (i) SEQUENCE CHARACTERISTICS:

60

- (A) LENGTH: 754 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 5 (A) ORGANISM: *Histoplasma capsulatum*  
(B) STRAIN: G186A5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 438

```

10 CACCACCAAG TGGTCCGAGT CCCGTTTCAA CGAAATCATC AAGGAGGTTT      50
   CCAACTTCAT CAAGAAGGTC GGATATAACC CCAAGGCTGT TCCCTTCGTG      100
   CCAATCTCTG GTTTCGAGGG TGACAACATG ATTGAACCCT CCCCCTCTG      150
   CACATGGTAC AAGGGCTGGA ACAAGGAGAC TGCCTCTGGC AAGTCTTCTG      200
   GTAAAACCTT TCTCGATGCC ATTGACGCCA TTGAACCCCT AACCCTCTCT      250
   ACCGATAAGC CCCTCCGTCT TCCCCTCCAG GATGTGTACA AAATCTCTGG      300
15 TATTGGCACT GTTCCCGTCG GACGTGTTGA GACTGGTGTC ATCAAGCCCG      350
   GTATGGTCGT GACTTTCGCT CCCTCCAACG TCACCACTGA AGTCAAGTCC      400
   GTCGAAATGC ACCACCAACA ACTCCAGGCT GGTTACCCTG GCGACAACGT      450
   CGGCTTCAAC GTCAAGAACG TTTCAAGTCA GGAAGTCCGC CGTGGCAACG      500
   TTGCTGGCGA CTCCAAAAAT GATCCCCCTA AGGGCTGCGA ATCCTTCAAT      550
20 GCCCAGGTCA TCGTCCTTAA CCACCCCGGC CAGGTTGGCG CTGGTTATGC      600
   CCCAGTCCTC GACTGCCACA CTGCCACAT TGCTTGCAAG TTCTCTGAGC      650
   TTATTGAGAA GATCGACCGC CGTACCGGAA AGTCTGTTGA GAACAACCCC      700
   AAGTTCATCA AGTCTGGTGA TGCTGCTATC GTCAAGATGG TTCCCTCCAA      750
   GCCC
25

```

2) INFORMATION FOR SEQ ID NO: 439

(i) SEQUENCE CHARACTERISTICS:

- 30 (A) LENGTH: 743 bases  
(B) TYPE: Nucleic acid  
(C) STRANDEDNESS: Double  
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 40 (A) ORGANISM: *Issatchenkia orientalis*  
(B) STRAIN: ATCC 6258

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 439

```

45 TGGGATGAAA ACAGATTTGA AGAAATTGTC AAGGAAACCC AAAACTTCAT      50
   CAAGAAGGTT GGTTACAACC CAAAGACTGT TCCATTTCGT CCAATCTCTG      100
   GTTGGGAATGG TGACAACATG ATTGAAGCAT CCACCAACTG TCCATGGTAC      150
   AAGGGTTGGA CTAAGGAAAC CAAGGCAGGT GTTGTTAAGG GTAAGACCTT      200
   ATTAGAAGCA ATCGATGCTA TTGAACCACC TGTCAGACCA ACCGAAAAGC      250
   CATTAAGATT ACCATTACAA GATGTTTACA AGATTGGTGG TATTGGTACT      300
50 GTGCCAGTCG GTAGAGTCGA AACCGGTGTC ATTAAGCCAG GTATGGTTGT      350
   CACTTTTGCT CCAGCAGGTG TCACCACCGA AGTCAARTCC GTTGAAATGC      400
   ACCATGAACA ATTAGAACAA GGTGTTCCAG GTGATAACGT TGGTTTCAAC      450
   GTTAAGAACG TCTCTGTCAA GGATATCAAG AGAGGTAACG TTTGTGGTGA      500
   CTCCAAGAAC GACCCACCAA TGGGTGCAGC TTCYTTCAAT GCTCAAGTCA      550
55 TTGTCTTGAA CCACCCTGGT CAAATTTCCT CTGGTTACTC TCCAGTCTTG      600
   GATTGTCACA CTGCCCACAT TGCATGTAAG TTCGACGAAT TAATCGAAAA      650
   GATTGACAGA AGAACTGGTA AGTCTGTTGA AGACCATCCA AAGTCYGTCA      700
   AGTCTGGTGA TGCAGCTATC GTCAAGATGG TCCCAACCAA GCC          743

```

## 2) INFORMATION FOR SEQ ID NO: 440

## (i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 1091 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

## 10 (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Malassezia furfur*  
 (B) STRAIN: ATCC 42132

## 15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 440

	CAAGCTCAAG	GCTGAGCGTG	AGCGTGGTAT	CACCATCGAC	ATTGCTCTGT	50
	GGAAGTTCGA	GACCCCTAAG	TACCACGTTA	CCGTCATTGA	CGCTCCTGGT	100
20	CACCGTGACT	TCATCAAGAA	CATGATTACG	GGTACCTCGC	AGGCTGACTG	150
	CGCTATCCTC	ATCATTGCCG	GTGGTACCGG	TGAGTTCGAG	GCTGGTATCT	200
	CGAAGGACGG	TCAGACCCGT	GAGCACGCTC	TGCTCGCTTT	CACCCTGGGT	250
	GTGCGTCAGC	TCATTGTGGC	CGTCAACAAG	ATGGACACCA	CCAAGTACTC	300
	GGAGGACCGC	TTCAACGAGA	TTGTCCGCGA	AGTGTCGAAC	TTCATCAAGA	350
25	AGGTCGGTTT	CAACCCCAAG	ACTGTTGCCT	TCGTCCCAT	CTCGGGCTGG	400
	CACGGTGACA	ACATGATCGA	GGCCACCACC	AACATGCCTT	GGTACAAGGG	450
	CTGGGAGAAG	GAGACCAAGT	CGGGCAAGGT	CACTGGTAAG	ACTCTGCTGG	500
	ACGCCATCGA	CGCCATCGAG	CCCCGACCC	GCCCCACTGA	CAAGCCCCTG	550
	CGTCTCCCTC	TGCAGGATGT	GTACAAGATC	GGTGGTATCG	GTACTGTCCC	600
30	TGTCGGTTCGT	GTTGAGACCG	GTGTGATCAA	GCCCAGTATG	GTTGTGACCT	650
	TCGCTCCCTC	GAACGTCACC	ACTGAAGTTA	AGTCGGTTGA	GATGCACCAC	700
	GAGTCGCTCC	CTGAGGGTCT	CCCCGGTGAC	AACGTTGGTT	TCAACGTGAA	750
	GAACGTCTCG	GTTAAGGACA	TTCGCCGTGG	TAACGTTGCC	TCGGACTCGA	800
	AGAACGACCC	CGCTCAGGAG	GCTGCTTCGT	TCAACGCGCA	GGTCATTGTC	850
35	ATGAACCACC	CTGGTCAGAT	CAGCAACGGT	TACTCGCCCG	TGCTTGACTG	900
	CCCACTGCG	CACATTGCCT	GCCGCTTCAA	CAACATCCTC	CAGAAGATCG	950
	ACCGTCGCTC	GGGTAAGGTG	CTTGAGGAGA	ACCCCAAGTT	CATCAAGTCG	1000
	GGTGACGCTG	CCATGGTGGG	GATGATCCCC	ACCAAGCCCA	TGTGTGTGGA	1050
40	GTCGTTCAAC	GAGTACCCCC	CTCTGGGTGC	TTTCGCTGTG	C	1091

## 2) INFORMATION FOR SEQ ID NO: 441

## (i) SEQUENCE CHARACTERISTICS:

- 45 (A) LENGTH: 749 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

## 50 (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Malassezia pachydermatis*  
 (B) STRAIN: ATCC 42756

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 441

	ACCACCAAGT	ACTCGGAGGA	CCGCTTCAAC	GAGATTATTC	GCGAGACTTC	50
60	GAACCTTCATC	AAGAAGGTGC	GTTACAACCC	GAAGACTGTT	GCCTTCGTCC	100

	CGATCTCGGG	CTGGCACGGT	GACAACATGA	TTGAGGCGAC	CACCAACATG	150
	CCGTGGTACA	AGGGCTGGGA	GAAGGAGACC	AAGTCGGGCA	AGGCCACTGG	200
	TAAGACCCTT	CTGGACGCTA	TTGACGCCAT	TGAGCCGCCG	ACGCGCCCCG	250
	CCGACAAGCC	TCTCCGTCTT	CCTCTCCAGG	ATGTGTACAA	GATCGGTGGT	300
5	ATCGGTACYG	TCCCGGTCTG	CCGTGTTGAG	ACCGGTGTTA	TCAAGCCCCG	350
	TATGGTTGTG	ACCTTCGCTC	CGTCGAACGT	CACSACTGAA	GTTAAGTCGG	400
	TCGAGATGCA	CCACGAGCAG	ATCCCTGAGG	GTCTTCCGGG	TGACAACGTT	450
	GGTTTCAACG	TGAAGAACGT	GTCGGTCAAG	GACATTCCGC	GTGGTAACGT	500
	CGCCTCGGAC	TCGAAGAACG	ACCCGGCTCA	GGAGGCTGCC	TCGTTCAATG	550
10	CTCAGGTCAT	TGTGATGAAC	CACCCTGGTC	AGATCAGCAA	CGGTTACTCG	600
	CCRGTGCTCG	ACTGCCACAC	TGCTCACATT	GCCTGCCGCT	TCAACAACAT	650
	CCTCCAGAAG	ATCGACCGTC	GTTCCGGTAA	GGTTCTYGAA	GAGAACCCCA	700
	AGTTCATCAA	GTCGGGTGAC	GCTGCCATGG	TTGAGATGAT	CCCGACCAA	749

15

## 2) INFORMATION FOR SEQ ID NO: 442

## (i) SEQUENCE CHARACTERISTICS:

20 (A) LENGTH: 1150 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

25 (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Malbranchea filamentosa*  
 (B) STRAIN: ATCC 48174

30

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 442

	ACTGAAGGCC	GAGCGTGAGC	GTGGTATCAC	CATCGATATC	GCCCTCTGGA	50
	AGTTCGAGAC	CCCCAAGTAC	CATGTCACCG	TCATTGGTAC	GTTCGACATG	100
35	TTCGACCTTT	TGCCTAGTGT	CCCCTTCTAA	CCACAGTTTA	TAGACGCCCC	150
	TGGCCATCGT	GATTTTCGTCA	AGAACATGAT	CACTGGTACT	TCCCAGGCTG	200
	ATTGCGCTAT	CCTCATCATT	GCTTCCGGCA	CTGGTGAATT	CGAGGCTGGT	250
	ATCTCCAAGG	ATGGCCAGAC	CCGTGAGCAC	GCTCTGCTTT	CCTTCACCCT	300
	CGGTGTTAGG	CAGCTCATTG	TCGCCCTCAA	CAAGATGGAC	ACTGTCAACT	350
40	TCGCTGAGGC	CCGTTACAAC	GAGATTGTCA	AGGAAGTCTC	CAACTTCATC	400
	AAGAAGGTCG	GCTACAACCC	CAAGGCCGTT	CCTTTCGTCC	CCATCTCCGG	450
	TTTCGAGGGT	GACAACATGA	TCGAGGCCTC	CACCCGCATT	CCTTGGTACA	500
	AGGGCTGGAA	CAAGGAGACC	GCCAGTGGCA	AGAGCACCGG	CAAGACCCTY	550
	CTCGAGGCCA	TTGATGCCAT	CGAACCCCGG	GTCCGTCCCA	CCGACAAGCC	600
45	CCTYCGTCTC	CCTCTTCAGG	ATGTGTACAA	GATCTCCGGT	ATTGGCACTG	650
	TTCTTGTCGG	TCGTGTTGAG	ACTGGTGTCA	TCAAGCCTGG	TATGGTCGTT	700
	ACTTTCGCCC	CCGCCAACGT	CACCACTGAA	GTCAGTCCG	TCGAGATGCA	750
	CCACCAGCAG	CTCCAGGCCG	GTAACCCCGG	TGACAACGTC	GGCTTCAACG	800
	TCAAGAACGT	TTCCGTCAAG	GAAGTCCGCC	GTGGCAACGT	TGCCTCCGAC	850
50	TCCAAGAACG	ACCCCGCCAA	GGGCTGCGAC	TCCTTCAACG	CCCAGGTCAT	900
	CGTCCTTAAC	CACCCCGGTC	AGGTCGGTGC	TGGATACGCT	CCCGTCCTCG	950
	ATTGCCACAC	TGCCACACATT	GCTTGCAAGT	TCTCTGAGCT	TCTTGAGAAG	1000
	ATCGATCGCC	GTACCGGTAA	ATCCGTTGAG	GACCACCCCA	AGTTCATCAA	1050
	GTCTGGTGAT	GCCGCTATCG	TCAAGATGGT	TCCCTCCAAG	CCTATGTGCG	1100
55	TTGAGGCTTT	CACTGACTAC	CCTCCCCTTG	GTCGTTTCGC	CGTCCGTGAC	1150

## 2) INFORMATION FOR SEQ ID NO: 443

60

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1099 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Metschnikowia pulcherrima*  
 (B) STRAIN: DSM 70336

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 443

```

15  GGACAAGTTG AAGGCTGAGA GAGAGAGAGG TATCACCATC GACATTGCCT      50
    TGTGGAAGTT CGAGACTCCT AAGTACCACG TCACCGTYAT TGACGCCCCA      100
    GGTCACAGAG ATTTTCATCAA GAACATGATC ACTGGTACTT CCCAGGCTGA      150
    CTGTGCTATC TTGATTATCG CYGGTGGTGT TGGTGAGTTC GAGGCTGGTA      200
    TCTCCAAGGA TGGCCAGACC AGAGAGCACG CTTTGTGGC  YTACACCTTG      250
20  GGTGTTAGAC ARTTGATTGT TGCCGTCAAC AAGATGGACT CTGTCAAGTG      300
    GGACAAGAAC AGATTGAGG AGATCATCAA GGAGACCTCT AACTTCGTCA      350
    AGAAGGTTGG TTACAACCCCT AAGACYGTGC CATTCGTGCC AATYTCGGT      400
    TGGAACGGTG ACAACATGAT TGAGGCTGCC ACTAACTGCC CATGGTACAA      450
    GGGTTGGGAG AAGGAGACCA AGGCCGGTAA GTCTWCCGGT AAGACCTTGT      500
25  TGGAGGCCAT TGACGCCATT GAGCCACCAA CCAGACCTAC CGACAAGGCC      550
    TTGAGATTGC CTTTGCAGGA TGTCTACAAG ATCGGTGGTA TCGGAACGGT      600
    GCCAGTCGGC CGTGTGAGG CCGGTGTCAT TAAGGCCGGT ATGGTTGTYA      650
    CCTTYGCCCC AGCTGGTGTC ACCACTGAGG TCAAGTCCGT CGAGATGCAC      700
    CACGAGCAGT TGGTCGAGGG TCTTCCAGGT GACAAYGTTG GTTTCACCGT      750
30  CAAGAACGTC TCCGTTAAGG AGATCAGAAG AGGTAACGTC TGTGGTGACT      800
    CCAAGCAGGA CCCACCAAAG GGTGCCGCTT CTTTCACCGC YCAGGTTATT      850
    GTGTTGAACC ACCCTGGTCA GATCTCCTCT GGTACTCTC CAGTGTGGA      900
    CTGYCACACC GCCCACATTG CCTGTAARTT CGACACCTTG TTGGAGAAGA      950
    TTGACAGAAG AACTGGTAAG TCCTTGGAGT CYGAGCCTAA GTTCGTCAAG     1000
35  TCGGGTGACG CCGCCATTGT CAAGATGGTG CCAACCAAGC CAATGTGTGT     1050
    TGAGGCTTTC ACCGACTACC CACCTTTGGG TAGATTCGCC GTCAGAGAC     1099
  
```

## 2) INFORMATION FOR SEQ ID NO: 444

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1153 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Paecilomyces lilacinus*  
 (B) STRAIN: ATCC 42570

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 444

```

55  CAAGCTCAAG GCCGAGCGTG AGCGTGGTAT CACCATCGAC ATTGCCCTCT      50
    GGAAGTTCGA GACTCCCAAG TACTATGTCA CCGTCATTGG TACGTCGACT      100
    CGCGCGAGAC TGGTCGCAAT TTCCACGTCG CTAACGTGCT TGAACAGACG      150
    CTCCCGGCCA CCGTGACTTC ATCAAGAACA TGATCACTGG TACCTCCCAG      200
60  GCTGACTGCG CTATCCTCAT TATCGCTGCC GGCCTGGTG AGTTCGAGGC      250
  
```

	TGGTATCTCC	AAGGATGGCC	AGACCCGTGA	GCACGCTCTG	CTCGCCTACA	300
	CCCTCGGTGT	TAAGCAGCTC	ATCGTCGCTA	TCAACAAGAT	GGACACCACC	350
	AAGTGGTCTG	AGGCCCCTTT	CCAGGAGATC	ATCAAGGAGA	CCTCCAACCTT	400
	CATCAAGAAG	GTCGGCTACA	ACCCCAAGAC	CGTCGCTTTC	GTCCCCATCT	450
5	CTGGTTTCCA	CGGCGACAAC	ATGCTTTCCC	CCTCCACCAA	CTGCCCCCTGG	500
	TACAAGGGCT	GGGAGAAGGA	GACCAAGGCT	GGCAAGTCCA	CCGGCAAGAC	550
	CCTCCTTGAG	GCCATCGACT	CCATCGAGCC	CCCCAAGCGC	CCCAGCGACA	600
	AGCCCCCTCCG	CCTTCCCCTT	CAGGATGTGT	ACAAGATCGG	CGGTATCGGC	650
	ACAGTCCCTG	TCGGCCGTAT	CGAGACTGGT	GTCATCAAGC	CCGGCATGGT	700
10	CGTGACCCTT	GCTCCTTCCA	ACGTCAACAC	CGAAGTCAAG	TCCGTTGAGA	750
	TGCACCACGA	GCAGCTCTCC	GAGGGTGTCC	CCGGTGACAA	CGTCGGCTTC	800
	AACGTCAAGA	ACGTCTCCGT	CAAGGAGATC	CGTCGTGGCA	ACGTGCGCCG	850
	TGACTCCAAG	AACGACCCCC	CTCTGGGTGC	CGCTTCTTTC	GATGCCCAGG	900
	TCATCGTCTT	CAACCACCCC	GGCCAGGTCG	GTGCTGGCTA	CGCCCCCGTC	950
15	CTCGACTGCC	ACACCGCCCC	CATTGCCTGC	AAGTTCGCCG	AGATCAAGGA	1000
	GAAGATCGAC	CGCCGTACCG	GCAAGTCTGT	CGAGTCCGCC	CCCAAGTTCA	1050
	TCAAGTCTGG	CGACTCTGCC	ATCGTCAAGA	TGATTCCCTC	CAAGCCCATG	1100
	TGCGTTGAGG	CTTTCACCGA	CTACCCTCCT	CTGGGCCGCT	TCGCCGTCCG	1150
20	TGA					1153

## 2) INFORMATION FOR SEQ ID NO: 445

- 25 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 763 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

- 30 (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- 35 (A) ORGANISM: *Paracoccidioides brasiliensis*  
 (B) STRAIN: ATCC 32071

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 445

	TACCACTAAG	TGGTCCGAGA	CCCGATTCAA	TGAAATTATC	AAGGAAGTCA	50
40	CCAATTTTCAT	TAAGAAGGTC	GGATATAAACC	CCAAGACTGT	TCCTTTCGTT	100
	CCCATTTCTG	GTTTCGAGGG	TGACAACATG	ATCGAGCCCT	CTGCCAACTG	150
	CCCATGGTAC	AAGGGCTGGT	CCAAGGAGAC	TGCTCAGGGC	AAGTACTCTG	200
	GCAAGACCCT	TCTTGAGGCC	ATCGACGCCA	TTGAGCCCCC	CACCCGTCCT	250
	ACCGATAAAC	CTCTCCGTCT	TCCCCTCCAG	GATGTCTACA	AGATCTCCGG	300
45	TATTGGCACT	GTTCTGTGCG	GACGTGTTGA	GACTGGAGTC	ATCAAGCCCCG	350
	GTATGGTCGT	GACCTTCGCT	CCCGCCAACG	TCACCACTGA	AGTCAAGTCC	400
	GTCGAAATGC	ACCACCAGCA	GCTTACCGCC	GGTAACCCCG	GTGACAACGT	450
	CGGCTTCAAC	GTCAAGAATG	TTTCCGTCAA	AGAAGTCCGC	CGTGGTAACG	500
	TTGCCGGTGA	CTCTAAGAAT	GATCCCCCAA	AGGGCTGCGA	TTCCTTCAAT	550
50	GCCCAGGTCA	TCGTCCTCAA	CCACCCTGGT	CAGGTTGGCG	CTGGTTATGC	600
	CCCAGTCCTC	GACTGCCATA	CTGCCACAT	TGCCTGCAA	TTCGCTGAGC	650
	TCCTTGAGAA	GATTGATCGA	CGAACC GGAA	AGTCTGTTGA	GAACAACCCC	700
	AAGTTCATCA	AGTCCGGTGA	TGCTGCTATC	GTCAAGATGA	TTCCTTCCAA	750
55	GCCCATGTGC	GTC				763

## 2) INFORMATION FOR SEQ ID NO: 446

- 60 (i) SEQUENCE CHARACTERISTICS:

270

(A) LENGTH: 1346 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

5

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Penicillium marneffe*  
 (B) STRAIN: ATCC 64101

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 446

	AAGCTCAAGG	CTGAGCGTGA	GCGTGGTATC	ACCATCGATA	TTGCTCTCTG	50
15	GAAGTTCCAG	ACTGCCAAGT	ACGAGGTTAC	CGTCATTGAC	GCCCCCGGTC	100
	ACCGTGATTT	CATCAAGAAC	ATGATCACTG	GTACCTCCCA	GGCCGATTGC	150
	GCTATTCTCA	TCATTGCCTC	TGGTACTGGT	GAATTCGAGG	CTGGTATCTC	200
	CAAGGATGGC	CAGACTCGTG	AGCACGCTCT	TTTGGCTTTC	ACCCTCGGTG	250
	TCCGTCAGCT	CATTGTTGCC	CTCAACAAGA	TGGACACTTG	CAAGTGGTCT	300
20	CAGGGTGAGT	ACTCGTACCT	GCGTTTGGCC	TTGAATATCT	TACTAATGCA	350
	CCATAGATCG	TTACAACGAA	ATTGTCAAGG	AGACTTCCAA	CTTCATCAAG	400
	AAGGTCGGAT	ACAACCCCAA	GAACGTTCTT	TTCGTTCCCTA	TCTCCGGTTT	450
	CAACGGTGAC	AACATGCTTG	AGCCCTCCCC	CAACTGCCCC	TGGTACAAGG	500
	GTTGGGAGAA	GGAGACCAAG	GCCGGTAAGG	TCACTGGTAA	GACCCTCCTC	550
25	GAGGCCATCG	ACGCCATTGA	GCCCCCTACC	CGTCCCGCCA	ACAAGGTTAG	600
	TCCCTCCTCG	ACTACTCAA	CCCTCCTCAT	AAGTTCAGAT	TACTGACTCG	650
	TTCACAGCCC	CTCCGTCTTC	CCCTCCAGRA	TGTCTACAAG	ATCGGTGGTA	700
	TTGGAACGGT	TCCCGTCGGT	CGTGTGAGA	CTGGTACCAT	CGTTCCTGGT	750
	ATGGTTGTCA	CCTTGTAAGT	CACCTCTCTC	GCTTATCCTA	CCTGAAATCA	800
30	TCATGTGCTA	ACTTGACACT	CAGCGCTCCC	GCCAACGTCA	CCACTGAAGT	850
	CAAGAGTGT	GAAATGCACC	ACCAGCAGCT	CACTGCCGGT	CAGCCCGGTG	900
	ACAACGTTGG	TTTCAACGTG	AAGAACGTCT	CCGTCAAGGA	AATCCGTCGT	950
	GGTAACGTTG	CTGGTGACAG	CAAGAACGAC	CCCCCTGCCG	GTGCTGCCTC	1000
	CTTCAACGCC	CAGGTCATCG	TCCTCAACCA	CCCCGGTCAG	GTCGGTGCTG	1050
35	GTTACGCCCC	AGTCCTCGAT	TGCCACACTG	CCCACATTGC	TTGCAAGTTC	1100
	GCTGAGCTCC	TCGAGAAGAT	TGACCGTCGT	ACCGGAAAGT	CTGTTGAGGA	1150
	CCACCCCAAG	TTCATCAAGT	CCGGTGACGC	TGCCATCGTC	AAGATGATTC	1200
	CTTCCAAGCC	CATGTGTGTT	GAGGCTTTCA	CCGAGTACCC	TCCTCTCGGT	1250
	CGTTTCGCCG	TTCGCGAGTA	AGTTTTATCT	CCGTTGTCTA	TTTTCCATCC	1300
40	TTCCCTTCTC	CTCCGTCTTC	CATATATACT	TTTTCAGTTA	TATGTG	1346

2) INFORMATION FOR SEQ ID NO: 447

45

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1094 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

50

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Pichia anomala*  
 (B) STRAIN: ATCC 18205

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 447

60 AAGTTAAAAG CTGAACGTGA AAGAGGTATC ACTATTGATA TTGCTTTATG 50



	GAAATTTCGAA	ACTCCAAAAT	ACCATGTTAC	CGTTATTGAT	GCTCCAGGTC	100
	ACAGAGATTT	CATCAAAAAT	ATGATTACTG	GTACTTCCCA	AGCTGATTGT	150
	GCTATYTTAA	TTATTGCCGG	TGGTATTGGT	GAATTCGAAG	CTGGTATCTC	200
	AAAAGATGGT	CAAACCAGAG	AACACGCTTT	NTTAGCTTAC	ACCTTAGGTG	250
5	TTAAACAATT	GATTGTTGCT	ATCAACAAGA	TGGATTCCGT	TAAATGGGAT	300
	GAATCTCGTT	TCGAAGAAAT	TGTCAAGGAA	ACYTCAAAC	TTATCAAGAA	350
	AGTTGGTTAC	AACCCAAAAA	CTGTTCCATT	CGTTCCAATC	TCAGGTGGA	400
	ATGGTGATAA	CATGATTGAA	CCATCAWCTA	ACTGTCCATG	GTACAAAGGT	450
	TGGAAAAAAG	AAACCAAAGC	TGGTGAAGCT	AAAGGTAAAA	CTTTATTAGA	500
10	AGCCATTGAT	GCTATTGACC	CACCATCAAG	ACCAACTGAT	AAACCATTAC	550
	GTTTACCATT	ACAAGATGTT	TACAARATTG	GTGGTATTGG	TACTGTGCCA	600
	GTCGGTAGAG	TTGAAACCGG	TGTTATCAAA	CCAGGTATGG	TTGTTACCTT	650
	TGCCCCAGCT	GGTGTTACCA	CTGAAGTCAA	ATCTGTTGAA	ATGCATCATG	700
	AACAATTGAC	TGAAGGTTTA	CCAGGTGACA	ATGTTGGTTT	CAACGTTAAG	750
15	AATGTTTCTG	TTAAAGAAAT	CCGTCGTGGT	AACGTCTGTG	GTGACTCTAA	800
	AAACGATCCA	CCAAAAGCTG	CTGAATCATT	CAATGCTCAA	GTTATTGTCT	850
	TAAACCATCC	AGGTCAAATC	TCTGCTGGTT	ACTCTCCAGT	TTTAGATTGT	900
	CACACTGCTC	ACATTGCTTG	TAAATTTGAC	ACTTTAATTG	AAAAAATTGA	950
	CAGACGTACT	GGTAAGAAAT	TAGAAGAAGC	TCCAAAATTC	ATCAAATCAG	1000
20	GTGATGCTGC	TATTGTTAAA	TTTGTTCAT	CAAAACCATT	ATCAGTTGAA	1050
	GCTTTCCTG	ACTACCCACC	ATTAGGTCGT	TTCGCTGTCA	GAGA	1094

## 25 2) INFORMATION FOR SEQ ID NO: 448

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1100 bases  
 (B) TYPE: Nucleic acid  
 30 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

## 35 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Pichia anomala*  
 (B) STRAIN: ATCC 2149

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 448

40	CTTAGATAAG	TTAAAAGCTG	AACGTGAAAG	AGGTATCACT	ATTGATATTG	50
	CTTTATGGAA	ATTCGAAACT	CAAAAATACC	ATGTTACCGT	TATTGATGCT	100
	CCAGGTCACA	GAGATTCAT	CAAAAATATG	ATTACTGGTA	CTTCCCAAGC	150
	TGATTGTGCT	ATMTTAATTA	TTGCCGGTGG	TATTGGTGAA	TTCGAAGCTG	200
45	GTATCTCAA	AGATGGTCAA	ACCAGAGAAC	ACGCTTTRTT	AGCTTACACC	250
	TTAGGTGTTA	AACAATTGAT	TGTTGCTATC	AACAAGATGG	ATTCCGTTAA	300
	ATGGGATGAA	TCTCGTTTCG	AAGAAATTGT	CAAGGAAACY	TCAAACTTTA	350
	TCAAGAAAGT	TGGTACAACC	CAAAAACCTGT	TCCATTTCGT	CCAATCTCAG	400
	GTTGGAATGG	TGATAACATG	ATTGAACCAT	CAACTAACTG	TCCATGGTAC	450
50	AAAGGTTGGA	AAAAGAAAC	CAAAGCTGGT	GAAGCTAAAG	GTAAAACTTT	500
	ATTAGAAGCC	ATTGATGCTA	TTGATCCACC	ATCAAGACCA	ACTGATAAAC	550
	CATTACGTTT	ACCATTACAA	GATGTTTACA	ARATTGGTGG	TATTGGTACT	600
	GTGCCAGTCG	GTAGAGTTGA	AACCGGTGTT	ATCAAACCAG	GTATGGTTGT	650
	TACCTTTGCC	CCAGCTGGTG	TTACCACTGA	AGTCAAATCT	GTTGAAATGC	700
55	ATCATGAACA	ATTGACTGAA	GGTTTACCAG	GTGACAATGT	TGGTTTCAAC	750
	GTTAAGAATG	TTTCTGTAA	AGAAATCCGT	CGTGGTAACG	TCTGTGGTGA	800
	CTCTAAAAAC	GATCCACCAA	AAGCTGCTGA	ATCATTCAAT	GCTCAAGTTA	850
	TTGTCTTAAA	CCATCCAGGT	CAAATCTCTG	CTGGTTACTC	TCCAGTTTAA	900
	GATTGTCACA	CTGCTCACAT	TGCTTGTAAG	TTTGACACTT	TAATTGAAAA	950
60	AATTGACAGA	CGTACTGGTA	AGAAATTAGA	AGAAGCTCCA	AAATTCATCA	1000

AATCAGGTGA	TGCTGCTATT	GTAAATTG	TTCCATCAAA	ACCATTATCA	1050
GTTGAAGCTT	TCCTGACTA	CCCACCATTA	GGTCGTTTCG	CTGTCAGAGA	1100

5

## 2) INFORMATION FOR SEQ ID NO: 449

## (i) SEQUENCE CHARACTERISTICS:

10

- (A) LENGTH: 1201 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

15

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Pseudallescheria boydii*
- (B) STRAIN: ATCC 44331

20

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 449

CAAGCTCAAG	GCCGAGCGTG	AGCGTGGTAT	CACCATCGAT	ATCGCCCTCT	50
GGAAGTTCGA	GACCCCAAG	TACCAGGTCA	CCGTCATTGG	TATGTCTTTG	100
TGCTTTTGT	GCTTTTGTG	CCTGTGCCTC	GCACAATTCC	AGCCCTCGAT	150
25 AATTATGAAC	CTCGTACTAA	TATGTCGTTT	TCCCACTACC	CACAGACGCC	200
CCCGGCCATC	GTGATTTTCA	CAAGAACATG	ATTACTGGTA	CCTCCCAGGC	250
TGATTGCGCC	ATTCTCATCA	TTGCCTCCGG	TACTGGTGAG	TTCGAGGCTG	300
GCATCTCCAA	GGATGGCCAG	ACCCGTGAGC	ACGCTCTTCT	CGCCTTCACC	350
CTCGGTGTCA	AGAACCTCAT	TGTTGCCATC	AACAAGATGG	ACACCAACAA	400
30 CTGGTCCGAG	GACCGATACA	AGGAGATCAT	CAAGGAGACC	TCCAACCTCA	450
TCAAGAAGGT	CGGCTACAAC	CCCAAGGCCG	TTCTTTTCGT	CCCCATCTCC	500
GGTTTCCACG	GAGACAACAT	GCTTACCCCC	TCCACCAACT	GCCCCTGGTA	550
CAAGGGTTGG	GTCCGTGAGG	TCAAGGGTAA	CACCCTTACC	GGCAAGACCC	600
TTCTCGAGGC	CATCGACTYC	ATCGAGCCCC	CCAAGCGTCC	CACCGAGAAG	650
35 CCCCTCCGTC	TTCCCCTTCA	GGACGTCTAC	AAGATCGGTG	GTATTGGCAC	700
TGTGCCCCGTC	GGCCGTATCG	AGACCGGTAT	CCTCAAGCCC	GGTATGGTCG	750
TCACCTTCGC	TCCCTCCAAC	GTCACCACTG	AAGTCAAGTC	CGTCGAGATG	800
CACCACGAGC	AGCTTACCGA	GGGTGTCCCC	GGTGACAACG	TTGGTTTCAA	850
CGTGAAGAAC	GTCTCCGTCA	AGGATATCCG	CCGTGGCAAC	GTCTGCGGTG	900
40 ACTCCAAGAA	CGACCCCCCC	GCTGCTGCCG	CCTCTTTCCA	GGCCCAGGTC	950
ATTGTCTCTA	ACCACCCCGG	CCAGATCGGT	GCTGGTTACG	CTCCCGTTCT	1000
TGACTGCCAC	ACTGCCCACA	TTGCTTGCAA	GTTCGCCGAG	CTCCTTGAGA	1050
AGATCGACCG	CCGTACCGGT	AAGTCGGTCG	AGAACAACCC	CAAGTTCGTC	1100
AAGTCTGGTG	ATGCCGCCAT	CGTCAAGATG	GTTCCCTCCA	AGCCCATGTG	1150
45 TGTTGAGTCC	TTCACCGAGT	ACCCCCCTCT	CGGTCGTTTC	GCCGTCCGTG	1200
A					1201

## 50 2) INFORMATION FOR SEQ ID NO: 450

## (i) SEQUENCE CHARACTERISTICS:

55

- (A) LENGTH: 1095 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

60

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Rhizopus oryzae*  
 (B) STRAIN: ATCC 56015

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 450

```

5  CAAGCTTAAG GCTGAACGTG AACGTGGTAT CACCATCGAT ATTGCTCTCT 50
   GGAAGTTCGA AACCCCCAAG TACCAAATTA CCGTTATTGA TGCTCCCGGT 100
   CACCGTGATT TCATCAAGAA CATGATTACC GGTACTTCTC AAGCCGATTG 150
   TGCTATTCTT ATCATTGCTG GTGGTACTGG TGAATTCGAA GCTGGTATCT 200
10 CCAAGGATGG TCAAACCCGT GAACACGCCC TTTTGGCTTT CACTCTCGGT 250
   GTCCGTCAAT TGATTGTTGC TGTCAACAAG ATGGATACCA CCAAGTGGTC 300
   CGAAGCTCGT TTCAACGAAA TYGTCAAGGA AGTTTCTTCC TTCATCAAGA 350
   AGATTGGTTA CAACCCCAAG TCTGTTCCCT TCGTCCCAT CTCTGGTTGG 400
   CACGGTGACA ACATGTTGGA AGAATCTACC AACATGCCCT GTTACAAGGG 450
15 ATGGAACAAG GAAACCAAGG CTGGTGCCAA GTCTGGTAAG ACCCTCTTGG 500
   ATGCCATTGA CAACATTGAC CCTCCTACCC GTCCTGTTGA CAAGCCTCTC 550
   CGTCTTCCTC TTCAAGATGT TTACAAGATT GGTGGTATCG GTACTGTCCC 600
   CGTCGGTCGT GTCGAAACTG GTGTCATCAA GGCTGGTATG GTTGTACCT 650
   TCGCTCCTGC TGCTGTCACC ACTGAAGTTA AGTCCGTCGA AATGCACCAC 700
20 GAAACCCTCA CTGAAGGTCT CCCCGGTGAC AACGTCGGTT TCAACGTCAA 750
   GAACGTCTCC GTCAAGGATA TCCGTCGTGG TAACGTCTGT TCTGACTCCA 800
   AGAACGACCC CGCCAAGGAA GCCGGTTCCT TCACCGCTCA AGTCATTATC 850
   TTGAACCACC CTGGTCAAAAT TGGTGCTGGT TACGCTCCYG TTTTGGATTG 900
   TCACACTGCT CACATTGCCT GTAAGTTCGC TGAATTGATC GAAAAGATTG 950
25 ACAGACGTTT CGGTAAGTCC TTGGAAGCTA CTCCCAAGTT CGTCAAGTCT 1000
   GGTGACTCTG CCATCGTCAA GATGATCCCC TCCAAGCCCA TGTGTGTTGA 1050
   AGCTTACACT GACTACCCTC CTCTCGGTGC TTTCGCTGTT CGTGA 1095

```

30 2) INFORMATION FOR SEQ ID NO: 451

## (i) SEQUENCE CHARACTERISTICS:

```

35 (A) LENGTH: 1092 bases
   (B) TYPE: Nucleic acid
   (C) STRANDEDNESS: Double
   (D) TOPOLOGY: Linear

```

## (ii) MOLECULE TYPE: Genomic DNA

40

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Rhodotorula minuta*  
 (B) STRAIN: ATCC 10658

## 45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 451

```

   GCTGAAGGCC GAGCGAGAGC GTGGTATCAC CATCGATATC GCTCTATGGA 50
   AGTTCGAGAC CCCCAAGTAC AACGTCACCG TCATTGACGC TCCAGGACAT 100
   CGTGATTTC AAGAGTGA GTTAACCATA ACATCAAACA GTGTTGCAAA 150
50 CATCAGCTAA TGCATGTTAT GCGTCCAGAC ATGATTACTG GTACTTCCCA 200
   GGCCGATTGC GCTATTCTCA TCATCGCCAC CGGTGTTGGT GAGTTCGAGG 250
   CTGGTATCTC CAAGGATGGC CAGACCCGAG AGCACGCCCT TCTCGCCTTC 300
   ACCCTCGGTG TCAGACAGCT CATCGTTGCC TTGAACAAGA TGGACTCGGT 350
   CAAGGTAGGC TAACTTCACA ACGTCGGCTT CCCATCATTC ATTCACTTAC 400
55 CTGTCTTGTC TTCCACCCTC CAGTTCTCCG AGTCCCGATA CGATGAAATC 450
   GTCAAGGAGA CATCCGGTTT CATCAAGAAG GTCGGATTCT ACCCCAAGGG 500
   TGTTCCCTTC GTCCCATCT CAGGATGGCA CGGAGACAAC ATGATCGAGG 550
   AGTCCACCAA CATGCCTTGG TACAAGGGAT GGAAGAAGAC CACCAAGACC 600
   GGCGAGTACA AGGGAAAGAC CCTGCTCGAG GCCATCGACT CCATCGAGCC 650
60 CCCACCCGT CCTACCGACA AGCCTCTCCG ACTTCCCCTC CAGGATGTCT 700

```

	ACAAGATTGG	TGGTATCGGA	ACAGTGCCAG	TCGGACGAGT	CGAGACTGGT	750
	ACCATCAAGG	CTGGTATGGT	CGTCACCTTC	GCTCCTTCAG	CTGTCAACCAC	800
	CGAAGTCAAG	TCTGTTGAGA	TGCACCACGA	GCAGCTCGAG	GCTGGTCTTC	850
	CAGGTGACAA	CGTCGGATTTC	AACATCAAGA	ACGTTTCAGT	CAAGGATATC	900
5	CGAAGAGGAA	ACGTCTGCGG	TGACTCCAAG	AACGATCCCC	CCAAGGAGGC	950
	TGCTTCCTTC	ACCGCCCAGG	TCATTGTCTT	CAACCACCCC	GGTCAAATCG	1000
	GTAACGGATA	CTCTCCAGTT	CTCGATTGCC	ACACTGGTGA	GTCATTCTTC	1050
	CATATTAGTT	TGAACTCTTT	TGAACAATAC	TAACGTGAAT	CATTATACTT	1100
	TTCAGCCCAC	ATTGCATGCA	AGTTCGACAC	CCTCCTAGAG	AAGATTGACC	1150
10	GACGATCCGG	AAAGTCCATC	GAAGATACCC	CCAAGTTCGT	CAAGTCTGGT	1200
	GACGCCGCCA	TCGTCAAGAT	GGTCCCCACC	AAGCCAATGT	GCGTTGAGGC	1250
	TTTCACCGAC	TACCCACCTC	TTGGACGATT	CGCCGTCCGT	GA	1292

15

## 2) INFORMATION FOR SEQ ID NO: 452

## (i) SEQUENCE CHARACTERISTICS:

	(A)	LENGTH: 1289 bases
20	(B)	TYPE: Nucleic acid
	(C)	STRANDEDNESS: Double
	(D)	TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

25

## (vi) ORIGINAL SOURCE:

	(A)	ORGANISM: <i>Sporobolomyces salmonicolor</i>
	(B)	STRAIN: ATCC 32311

30

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 452

	AAGCTCAAGG	CCGAGCGTGA	GCGTGGTATC	ACCATCGATA	TCGCTCTCTG	50
	GAAGTTCGAG	ACCCCCAAGG	TGCGTTCTCA	CCCCGGCTGA	GGAGCACGCA	100
	CGCGAGGGCT	CACGCTGCGC	CTCTTACAGT	ACATGATCAC	CGTCATCGAC	150
35	GCCCCGGGTC	ACCGTGACTT	CATCAAGAAC	ATGATCACCG	GTACCTCGCA	200
	GGCCGACTGC	GCCATCCTCA	TCATCGCCGC	CGGTACCGGT	GAGTTCGAGG	250
	CTGGTATCTC	GAAGGACGGC	CAGACCCGCG	AGCACGCCCT	CCTCGCCTTC	300
	ACCCTCGGTG	TCCGTCAGCT	CATCGTCGCC	ATCAACAAGA	TGGACACGAC	350
	CAAGTACTCG	GAGGCCCGTT	TCGAGGAGAT	CATCAAGGAG	ACCTCCAACT	400
40	TCATCAAGAA	GGTCGGCTTC	AACCCCCAAGA	ACGTCCCCTT	CGTCCCCATC	450
	TCGGGATGGC	ACGGTGACAA	CATGATTGAG	GAGACCGCCA	ACATGCCCTG	500
	GTACAAGGGA	TGGAAGAAGG	AGACCAAGGC	CGGTGAGGTC	AAGGGCAAGA	550
	CCCTCCTCGA	CGCCATCGAC	GCGATCGAGC	CCCCTTCGCG	CCCTACCGAC	600
	AAGCCCCCTC	GTCTTCCCCT	CCAGGTTTCGT	TTCCCTGCTC	GCGGTTTACG	650
45	CTGCTACTTC	GAGCTGACCC	GCGAGCTCTG	CCCGAACAGG	ATGTCTACAA	700
	GATCGGTGGT	ATCGGCACAG	TCCCCGTGCG	CCGTGTCGAG	ACCGGCACGA	750
	TCAAGGCCGG	TATGGTCGTC	GTCTTTCGCC	CGGCCAACGT	CACCACTGAG	800
	GTCAAGTCGG	TCGAGATGCA	CCACGAGCAG	CTCGAGGCTG	GTCTCCCGGG	850
	AGACAACGTC	GGCTTCAAGT	GCGTCTCATC	ATGTTTTTGC	TTCGCTCGGC	900
50	CATTTTTTCA	GTCCTGACCC	CGTTTTTGCC	CTCGACAGCG	TCAAGAACGT	950
	TTCCGTAAAG	GACATCCGTC	GCGGTAACGT	CTGCGGTGAC	TCGAAGAACG	1000
	ACCCCCCCAA	GGAGGCCGCT	TCCTTCAAGG	CCCAGGTCAT	CGTCATGAAC	1050
	CACCCCGGTC	AGATCGGCAA	CGGTTACGCT	CCCGTTCTCG	ACTGCCACAC	1100
	CGCCACATT	GCCTGCAAGT	TCGACACCCT	CCTCGAGAAG	ATCGACCGTC	1150
55	GCTCGGGCAA	GTCGATTGAG	GACCTCCCCA	AGTTCGTCAA	GTCGGGTGAC	1200
	GCCGCCATCG	TCAAGATGGT	TCCCTCCAAG	CCGATGTGTG	TCGAGTCGTT	1250
	CGCCGAGTAC	CCCCCTCTCG	GACGTTTCGC	CGTCCGTGA		1289

60

## 2) INFORMATION FOR SEQ ID NO: 453

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1070 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Sporothrix schenckii*  
 (B) STRAIN: WSA-148

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 453

```

GTGAGCGCGG TATCACCATC GATATTGCTC TGTGGAAGTT CGAGACCCCC      50
AAGTACTACG TCACCGTCAT TGACGCCCCC GGTCATCGCG ATTTTCATCAA      100
GAACATGATC ACTGGTACCT CGCAGGCCGA CTGCGCCATT CTCATCATTG      150
CCGCTGGTAC TGGTGAGTTC GAGGCTGGTA TCTCCAAGGA TGGCCAGACT      200
CGTGAGCACG CTCTGCTCGC CTACACCCTG GGTGTGCGGC AGCTGATCGT      250
CGCCATCAAC AAGATGGACA CGGCCAAGTG GGCTGAGGCT CGTTACCAGG      300
AGATCATCAA GGAGACCTCC AACTTCATCA AGAAGGTCGG CTACAACCCC      350
AAGACTGTTG CCTTCGTCCC CATCTCGGGC TTCCACGGCG ACAACATGCT      400
TACTCCCTCG ACCAACTGCC CCTGGTACAA GGGCTGGGAG AAGGAGGGCA      450
AGAGCGGCAA GGTTACCGGT AAGACTCTGC TGGACGCCAT TGACGCCGTC      500
GAGCCCCCCA AGCGCCCCAC GGACAAGCCC CTGCGTCTGC CCCTCCAGGA      550
TGTCTACAAG ATCGGCGGTA TCGGCACTGT CCCTGTCTGC CGTATCGAGA      600
CTGGTGTCTT GAAGCCCGGC ATGGTCGTCA CCTTTGCCCC GTCCAACGTC      650
ACCACTGAAG TCAAGTCCGT CGAGATGCAC CACGAGCAGC TTGTTGAGGG      700
TGTTCCCGGC GACAACGTCG GCTTCAACGT CAAGAACGTC TCCGTCAAGG      750
AGATCCGTCG TGGCAACGTT GCCGGTGACT CCAAGAACGA CCCCCCTCG      800
GGCGCCGCCA CCTTCAACGC CCAGGTCATT GTCCTGAACC ACCCCGGCCA      850
GGTCGGCAAC GGCTACGCCC CGGTTCTGGA CTGCCACACC GCCCACATTG      900
CCTGCAAGTT CACCGAGATC CTTGAGAAGA TCGACCGCCG TACCGGCAAG      950
TCGGTTGAGA ACAACCCCAA GTTCATCAAG TCGGGTGACG CCGCCATTGT      1000
CAAGCTGACG CCCTCGAAGC CCATGTGCGT TGAGGCCTTC ACTGACTACC      1050
CCCCTCTGGG CCGTTTCGCC

```

## 2) INFORMATION FOR SEQ ID NO: 454

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1092 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Stephanoascus ciferrii*  
 (B) STRAIN: ATCC 52550

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 454

```

CTTAAGTCTG AGCGTGAGAG AGGTATCACC ATCGATATTG CTCTCTGGAA      50
ATTTCGAGACT CCTAAGTACA ACGTTACCGT CATTGATGCT CCAGGTCACA      100
GAGATTTTCAT CAAGAACATG ATTACTGGTA CCTCCCAGGC CGATCTTGCC      150

```

	ATCCTTATCA	TTGCTGGTGG	TGTCGGTGAG	TTCGAGGCTG	GTATCTCCAA	200
	GGACGGTCAG	ACCAGAGAGC	ACGCTCTTCT	TTCTTTCACC	CTTGGTGTCA	250
	GAAACATGAT	TGTTGCTGTC	AACAAGATGG	ACTCCGTCAA	GTGGTCTGAG	300
	GATCGTTTCA	ACGAAATTGT	CAAGGAGACC	TCCAACCTCG	TCAAGAAGGT	350
5	TGGTTACAAC	CCTAAGAATA	TTGCTTTCGT	TCCTATCTCC	GGTTGGAACG	400
	GTGACAATAT	GATTGAGCCA	TCCACCAACT	GCCCATGGTA	CAAGGGTTGG	450
	GAGCGTGAGA	CCAAGAACGG	TACTGCCAAG	GGTAAGACCA	TCTTGAGAGC	500
	CATTGACTCT	ATGGAGCCAC	CTTCCAGACC	AGTTGACAAG	CCTCTCCGTC	550
	TTCCTCTTCA	GGACGTTTAC	AAGATTGGTG	GTATTGGTAC	GGTGCCAGTT	600
10	GGTCGTGTTG	AGACTGGTGT	TATCAAGCCA	GGTATGGTTG	TTACCTTTGC	650
	CCCAGCTGGT	GTCACCACTG	AAGTCAAGTC	TGTCGAGATG	CACCACGAAC	700
	AGATCCCAGA	AGGTACCCCA	GGTGACAACG	TTGGTTTCAA	CGTCAAGAAC	750
	GTCTCCGTCA	AGGAAATCAG	ACGTGGTAAC	GTTACTGGTG	ACTCCAAGAA	800
	CGACCCACCA	AAGGGCTGCG	ACTCTTTCAA	CGCTCAGGTC	ATCATCTTCA	850
15	ACCACCTTGG	TCAGATCTCT	GCTGGTTACG	CTCCAGTTTT	GGACTGCCAC	900
	ACTGCTCACA	TTGCTTGCAA	GTTTGAGGAG	CTCATTGAGA	AGATTGACAG	950
	ACGTTCCGGT	AAGAAGGTCG	AAGACTCTCC	TAAGTTCGTC	AAGGCCGGTG	1000
	ATGCCGCCAT	TGTCAAGATG	GTTCCATCCA	AGCCAATGTG	TGTTGAAACC	1050
20	TTCACTGAGT	ACCCACCTCT	TGGTCGTTTC	GCCGTCCGTG	AC	1092

## 2) INFORMATION FOR SEQ ID NO: 455

## 25 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1149 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

## 30 (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Trichophyton mentagrophytes*  
 35 (B) STRAIN: WSA-225

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 455

	GCCGAGCGTG	AGCGTGGTAT	CACCATCGAT	ATCGCCCTCT	GGAAGTTCGA	50
40	GACCCCCAAG	TACAATGTCA	CCGTCATTGG	TATGTTTTCT	CTTTACCTTT	100
	CCCCTCCATC	GTCTTGCTGT	GCCATAACTA	ACGAGAGTAG	ACGCCCCCGG	150
	TCACCGTGAC	TTCATCAAGA	ACATGATCAC	TGGTACCTCC	CAGGCCGACT	200
	GTGCTATTCT	CATCATTGCT	GCCGGTACTG	GTGAGTTCGA	GGCTGGTATC	250
	TCCAAGGATG	GCCAGACCCG	TGAGCACGCT	CTGCTCGCCT	TCACCCTTGG	300
45	TGTCAAGCAG	CTCATCGTTG	CCATCAACAA	GATGGACACC	ACCAACTGGT	350
	CCGAGGACCG	TTTCAAGGAA	ATCATCAAGG	AAGTCACCAA	CTTCATCAAG	400
	AAGGTTGGCT	ACGACCCCAA	GGGTGTTCCA	TTCGTTCCAA	TCTCTGGTTT	450
	CAACGGTGAC	AACATGATTG	AGGCCTCCAC	CAACTGCCCA	TGGTACAAGG	500
	GATGGAACAA	GGAGACTAAG	GCCGGTGGTG	CCAAGACTGG	CAAGACCCTC	550
50	CTCGAGGCCA	TCGATGCCAT	CGACATGCCA	ACCCGTCCTA	CCGACAAGCC	600
	CCTCCGTCTC	CCACTCCAGG	ATGTCTACAA	GATCTCTGGT	ATCGGAACTG	650
	TACCAGTCGG	TCGTGTTGAG	ACCGGTATCA	TCAAGCCCGG	TATGGTCGTC	700
	ACCTTCGCCC	CTGCCAACGT	CACCACTGAA	GTCAAGTCCG	TCGAAATGCA	750
	CCACCAGCAG	CTTCAGCAGG	GTGTCCCCGG	TGACAACGTC	GGCTTCAACG	800
55	TCAAGAACGT	TTCCGTCAAG	GAAGTCCGCC	GTGGTAACGT	TGCCGGTGAC	850
	TCCAAGAACG	ACCCACCATC	CGGCTGTGCC	TCCTTCAACG	CCCAGGTCAT	900
	CGTCCTCAAC	CACCCCGGCC	AGATCGGTGC	TGGTTACGCC	CCAGTCCTCG	950
	ACTGCCACAC	TGCTCACATT	GCTTGCAAGT	TCGCTGAGCT	CCTCGAGAAG	1000
	ATTGACCGCC	GTACCGGTAA	ATCCGTCGAA	GCCAACCCCA	AGTTCGTCAA	1050
60	GTCTGGTGAT	GCCGCTATCG	CCAAGATGGT	TCCCTCCAAG	CCTATGTGCG	1100

TTGAGGCTTT CACTGACTAC CCCCCACTTG GTCGTTTCGC C~~G~~T~~C~~C~~G~~T~~G~~A' f149

5 2) INFORMATION FOR SEQ ID NO: 456

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1101 bases  
 (B) TYPE: Nucleic acid  
 10 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

15 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Trichosporon cutaneum*  
 (B) STRAIN: ATCC 62965

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 456

20 TCTTGACAAG CTTAAAGCTG AACGTGAACG TGGTATCACC ATTGATATCG 50  
 CTCTCTGGAA GTTCGAAACT CCTAAGTACT ACGTTACTGT TATTGATGCT 100  
 CCAGGTCACC GTGATTTTCAT CAAGAACATG ATTACTGGTA CTTCCCAAGC 150  
 CGACTGCGCC ATTCTTATCA TTGCTGCCGG TGTCGGTGAA TTCGAAGCTG 200  
 25 GTATCTCCAA GGAAGGTCAA ACCAGAGAAC ACGCTCTTCT CGCTTTCACC 250  
 CTTGGTGTCA GACAACTTAT CATTGCCATC AACAAGATGG ACTCTGTCAA 300  
 GTGGGACCAA AAGAGATACG AAGAAATCGT CAAGGAGGCT TCCAAC TTCG 350  
 TCAAGAAGGT TGGTTACAAC CCAAGTCTG TTCCATTTCG TCCTATCTCT 400  
 GGTGGAACG GTGACAACAT GTTGGAACTT ACCACCAACG CCCCATGGTA 450  
 30 CAAGGGATGG ACCAAGGAAA CCAAGGCTGG TGCCACTAAG GGTATGACTC 500  
 TTATTGAAGC CATTGACGCC ATTGAACCAC CAGTAAGACC ATCCGACAAG 550  
 CCACTCCGTC TCCCACTCCA AGATGTTTAC AAGATTGGTG GTATCGGAAC 600  
 TGTGCCAGTC GGCCGTGTCG AAACCGGTAT CATCAAGGCC GGTATGGTCG 650  
 TCACCTTTGC TCCACCAATG GTCACAACG AAGTTAAGTC CGTTGAAATG 700  
 35 CACCACGAAC AACTTGCTCA AGGTAACCCA GGTGACAACG TTGGTTTCAA 750  
 CGTCAAGAAC GTTTCCGTTA AGGAAATCAG ACGTGGTAAC GTCTGTGGTG 800  
 ACTCCAAGAA CGATCCACCA AAGGGCTGCG AATCTTTCAA CGCTCAAGTT 850  
 ATCGTCTTGA ACCACCCTGG TCAAATCTCT GCTGGTTACT CTCCAGTTCT 900  
 CGATTGCCAC ACTGCCACA TTGCCTGCAG ATTCGACGAA CTCCTTGAAA 950  
 40 AGATCGACCG TCGTTCGGGT AAGAAGATTG AAGACTCTCC AAAGTTTGTC 1000  
 AAGTCTGGTG ATGCCGTAT CGTCAAGATG ATCCCAACCA AGCCAATGTG 1050  
 CGTTGAAACC TCACTGAAT ACCCACCCT TGGTCGTTTC GCCGTCCGTG 1100  
 A 1101

45

2) INFORMATION FOR SEQ ID NO: 457

(i) SEQUENCE CHARACTERISTICS:

- 50 (A) LENGTH: 1085 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

55 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Wangiella dermatitidis*  
 (B) STRAIN: WSA-229

60

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 457

	GTTGAAGGCC	GAGCGTGAGC	GTGGTATCAC	CATCGATATC	GCCCTCTGGA	50
	AGTTCGAGAC	CCCCAAGTAC	TATGTCACCG	TCATCGACGC	CCCGGGTCAT	100
5	CGTGACTTTA	TCAAGAACAT	GATCACTGGT	ACCTCGCAGG	CCGACTGCGC	150
	CATCTTGATC	ATTGCCGCCG	GTACCGGTGA	ATTCGAAGCC	GGTATCTCCA	200
	AGGATGGTCA	GACCCGTGAG	CACGCTCTGC	TCGCCTACAC	CTTGGGTGTC	250
	AAGCAGCTCA	TCGTGCGCCAT	CAACAAGATG	GACACCACCA	AGTGGTCCGA	300
	GGAGCGTTTC	AACGAAATCA	TCAAGGAGAC	TTCCAAC TTC	ATCAAGAAGG	350
10	TCGGCTACAA	CCCCAAGGCC	GTTCC TTTTCG	TCCCCATCTC	CGGCTTCAAC	400
	GGTGACAACA	TGATTGAGGT	CTCCACCAAC	TGCCCCGTGGT	ACAAGGGATG	450
	GGAGAAGGAG	TCCAAGGCTG	GCAAGGCCAC	CGGCAAGACC	CTCCTCGAGG	500
	CCATTGACGC	CATCGACCCA	CCCACCCGTC	CCACCGACAA	GCCTCTCCGT	550
	CTCCCTCTCC	AGGATGTCTA	CAAGATCTCT	GGTATCGGAA	CGGTTCTCTGT	600
15	CGGTCGTGTC	GAGACCGGTA	CCATCAAGGC	CGGTATGGTC	GTCACCTTCG	650
	CTCCGGCCAA	CGTCACCACT	GAAGTCAAGT	CCGTCGAAAT	GCACCACGAG	700
	CAGCTCGCCG	AGGGTCTGCC	AGGTGACAAC	GTTGGCTTCA	ACGTCAAGAA	750
	CGTCTCCGTC	AAGGAGGTTT	GTCGTGGTAA	CGTTGCCGGT	GACTCCAAGA	800
	ACGACCCGCC	CAAGGGTGCC	GAGTCCTTCA	ACGCCCAGGT	CATTGTCCTC	850
20	AACCACCTTG	GTCAGATCGG	TGCCGGCTAC	GCTCCAGTCT	TGGATTGCCA	900
	CACTGCCCAC	ATTGCTTGCA	AGTTCGCCGA	GTTGCTCGAG	AAGATCGACC	950
	GTCGTACCGG	AAAGTCCATC	GAGAACAACC	CCAAGTTCAT	CAAGTCTGGT	1000
	GATGCTGCCA	TCGTCAAGAT	GATTC C CAGC	AAGCCCATGT	GTGTGAGGC	1050
25	TTTCACCGAC	TATCCTCCTC	TGGGTCGTTT	CGCTG		1085

## 2) INFORMATION FOR SEQ ID NO: 458

30 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 492 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

35 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Aspergillus fumigatus*

40 (B) STRAIN: DAL-95

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 458

	TGCTTTCATC	CGGAATTGAT	TGTGAGTCGT	TCCACATGCT	CACCTAGTTT	50
45	TCGCTCGATC	TTTTCACTAA	CGCAAACCAT	GTAAGAACAAC	ATTGCCAAGG	100
	CCCACGGTGG	TTACTCCGTC	TTCACTGGTG	TTGGTGAGCG	TACTCGTGAG	150
	GGTAACGATC	TGTACCACGA	AATGCAGGAG	ACTGGTGTCA	TTCAGCTCGA	200
	GGGTGAATCC	AAGGTCGCAC	TGGTGTTCCG	ACAGATGAAC	GAGCCCCCGG	250
	GTGCCCCGTC	CCGTGTCGCC	CTTACCGGTC	TGACCATTGC	CGAGTACTTC	300
50	CGTGACGAGG	AGGGTCAGGA	CGTGCTGCTC	TTCATTGACA	ACATTTTCCG	350
	TTTCACCCAG	GCCGGTTCTG	AGGTGCTCTG	CCTTCTCGGT	CGTATCCCCT	400
	CTGCCGTCGG	TTACCAGCCC	ACCCTGGCCG	TCGACATGGG	TGGTATGCAG	450
	GAGCGTATCA	CCACCACCAA	GAAGGGTTCT	ATTACCTCCG	TC	492

55

## 2) INFORMATION FOR SEQ ID NO: 459

60 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1154 bases



(B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

5 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Blastoschizomyces capitatus*  
 (B) STRAIN: ATCC 10663

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 459

	GTCCGTTGGTC	AAGAAGTTAT	TGACACTGGT	GCCCCAATTA	CCATTCCTGT	50
	TGGTCGTTGGT	ACTCTTGGTA	GAATTATCAA	CGTCATTGGT	GAACCAATTG	100
15	ACGAACGTGG	TCCTATCAAG	GCTTCTAAGT	ATGCTCCTAT	CCATACTGAA	150
	CCACCAACCT	TTGCTGAACA	ATCTACTTCT	GCTGAAGTTC	TTGAAACTGG	200
	TATCAAGGTT	GTCGATCTTC	TTGCTCCTTA	CGCCCGTGGT	GGTAAGATTG	250
	GTCTTTTCGG	TGGTGCTGGT	GTCGGTAAGA	CTGTCTTCAT	TCAAGAACTT	300
	ATTAACAACA	TTGCCAAGGC	TCACGGTGGT	TTCTCTGTCT	TCACTGGTGT	350
20	CGGTGAAAGA	ACCCGTGAAG	GTAACGATCT	TTACCGTGAA	ATGAAGGAAA	400
	CTGGTGTCAT	CAACCTCGAA	GGTGACTCCA	AGGTCGCTCT	CGTTTTTCGGT	450
	CAAATGAACG	AACCTCCAGG	TGCCCCGTGCC	CGTGTCGCTT	TGACTGGTCT	500
	TACCATTGCC	GAATACTTCC	GTGATGAAGA	AGGACAAGAT	GTCTTGCTTT	550
	TCGTTGACAA	CATTTTCAGA	TTCACCCAAG	CCGGTTCTGA	AGTCTCTGCT	600
25	CTTTTGGGTC	GTATTCCATC	TGCCGTCGGT	TACCAACCTA	CCCTTGCTAC	650
	CGATATGGGT	GCCCTCCAAG	AACGTATTAC	CACCACCCAA	AAGGGTTCCG	700
	TCACATCTGT	CCAAGCCGTC	TATGTCCCAG	CAGACGATTT	GACTGATCCT	750
	GCCCCAGCCA	CCACTTTCGC	TCACTTGGAC	GCCACCACTG	TCTTGTCTCG	800
	TTCCATTTC	GAATTGGGTA	TCTACCCAGC	TGTCGATCCT	CTCGATTCCA	850
30	AGTCTCGTCT	TTTGGATCCT	GAAGTTATTG	GACACGAACA	CTACGAAGTT	900
	GCCACTCAAG	TTCAACAAAC	CCTCCAAGCT	TACAAGTCTC	TCCAAGATAT	950
	CATTGCCATT	TTGGGTATGG	ATGAATTGTC	TGAAGCTGAT	AAGCTTACTG	1000
	TCGAACGTGC	CCGTAAGATC	CAAAGATTCC	TTTCCCAACC	ATTCGCTGTT	1050
	GCCGAAGTTT	TCACTGGTAT	CGAAGGTCGT	CTCGTTCCAT	TGAAGGAAAC	1100
35	CGTCAGATCT	TTCAAGGAAA	TCCTTGAAGG	TAAGTACGAT	CACCTTCCAG	1150
	AAGC					1154

40 2) INFORMATION FOR SEQ ID NO: 460

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1295 bases  
 (B) TYPE: Nucleic acid  
 45 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

50 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Candida albicans*  
 (B) STRAIN: ATCC 18804

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 460

55	CCAATTTCGAC	GAAGGAAACT	TGCCAGCTAT	TTTGAATGCT	TTGACTTTGA	50
	AGAACGGTGA	CCAAGACTTG	GTCTTGGAAG	TTGCTCAACA	TTTGGGTGAA	100
	AACACCGTCA	GAGCTATTGC	TATGGATGGT	ACTGAAGGTT	TAGTCAGAGG	150
	TACCGAAGTC	AACGATACCG	GTGCCCCAAT	CTCCGTCCCA	GTCGGTAGAG	200
60	GTACTTTAGG	TAGAATCATC	AATGTTGTTG	GTGAACCAAT	TGATGACAGA	250

	GGTCCAATTG	AATGTAAGGA	AAAGAAACCA	ATTCACGCTG	AACCACCATC	300
	ATTCGTTGAA	CAATCCACTG	CTGCCGARAT	TTTGGAACC	GGTATCAAGG	350
	TTGTCGACTT	GTTGGCCCCA	TACGCCAGAG	GTGGTAARAT	TGGTTTATTC	400
	GGTGGTGCTG	GTGTCGGTAA	GACCGTCTTT	ATCCAAGAAT	TGATTAACAA	450
5	CATTGCCAAA	GCCCATGGTG	GTTTCTCTGT	CTTTACCGGT	GTGCGTGAAA	500
	GAACCAGAGA	AGGTAACGAT	TTGTACCGTG	AAATGAAAGA	AACCGGTGTC	550
	ATCAACTTGG	AAGGTGACTC	CAAGGTCGCT	TTGGTCTTCG	GTCAAATGAA	600
	CGAACCACCA	GGTGCTAGAG	CTAGAGTTGC	TTTGACTGGT	TTGACCATTG	650
	CTGAATACTT	CAGAGATGAA	GAAGGTCAAG	ATGTCTTGTT	GTTCAATTGAT	700
10	AACATTTTCA	GATTCACCCA	AGCTGGTTCC	GAAGTGTCTG	CTTTGTTAGG	750
	TCGTATTCCA	TCTGCTGTCG	GTTATCAACC	AACCTTAGCC	ACTGATATGG	800
	GTCTTTTGCA	AGAACGTATT	ACCACCACCA	AGAAAGGTTT	CGTCACCTCT	850
	GTCCAAGCTG	TCTATGTCCC	AGCTGATGAT	TTGACCGATC	CTGCTCCAGC	900
	CACTACATTG	GCCCATTTGG	ATGCCACTAC	TGTCTTGTC	AGAGGTATTT	950
15	CTGAATTGGG	TATCTACCCA	GCTGTCGATC	CATTGGATTC	CAAATCCAGA	1000
	TTATTGGACG	CTTCTGTTGT	TGGTCAAGAA	CATTACGATG	TCGCTACTGG	1050
	TGTTCAACAA	ACTTTACAAG	CTTACAAATC	CTTACAAGAT	ATCATTGCTA	1100
	TTTTGGGTAT	GGATGAATTG	TCTGAAGCTG	ATAAATTGAC	TGTCGAAAGA	1150
	GCCCGTAAGA	TCCAAAGATT	CTTGTCTCAA	CCATTCGCTG	TTGCTGAAGT	1200
20	TTTCACTGGT	ATCCAGGTA	GATTAGTCAG	ATTGCAAGAC	ACTGTCAAAT	1250
	CATTCAAGGA	TGTTTTGGAA	GGTAAATACG	ATAACTTGCC	AGAAA	1295

## 25 2) INFORMATION FOR SEQ ID NO: 461

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1277 bases  
 (B) TYPE: Nucleic acid  
 30 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

## 35 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Candida dubliniensis*  
 (B) STRAIN: NCPF 3949

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 461

40	TAACTTGCCA	GCTATTTTGA	ATGCTTTGAC	TTTGAAGAAC	GGTGACCAAG	50
	ATTTAGTTTT	GGAAGTTGCT	CAACATTGCG	GTGAAAACAC	CGTCAGAGCT	100
	ATTGCTATGG	ATGGTACTGA	AGGTTTAGTC	AGAGGTACTG	AAGTCAACGA	150
	TACCGGTGCC	CCAATCTCCG	TTCCAGTCGG	TAGAGGTACC	TTAGGTAGAA	200
45	TCATCAATGT	TGTTGGTGAA	CCAATTGATG	ACAGAGGTCC	AATTGAATGT	250
	AAGGAAAAGA	AACCAATTCA	TGCAGAACCA	CCATCCTTCG	TTGAGCAATC	300
	CACTGCTGCC	GAAATTTTGG	AAACCGGTAT	CAAGGTTGTC	GACTTATTGG	350
	CCCCATACGC	CAGAGGTGGT	AAGATTGGTT	TGTTCCGGTG	TGCTGGTGTC	400
	GGTAAGACCG	TCTTTATCCA	AGAATTGATT	AACAACATTG	CTAAAGCCCA	450
50	TGGTGGTTTC	TCCGTCTTTA	CCGGTGTCCG	TGAAAGAACC	AGAGAAGGTA	500
	ACGATTTGTA	CCGTGAAATG	AAAGAAACCG	GTGTCATCAA	CTTAGAAGGT	550
	GACTCCAAGG	TCGCTTTGGT	CTTTGGACAA	ATGAACGAAC	CACCAGGTGC	600
	TAGAGCTAGA	GTTGCTTTGA	CTGGTTTGAC	TATTGCTGAA	TACTTCAGAG	650
	ATGAAGAAGG	TCAAGATGTC	TTGTTGTTCA	TCGATAACAT	TTTCAGATTC	700
55	ACCCAAGCTG	GTTCCGAAGT	GTCTGCTTTG	TTAGGTCGTA	TTCCATCTGC	750
	CGTCGGTTAT	CAACCAACCT	TAGCTACTGA	TATGGGTCTT	TTGCAAGAAC	800
	GTATTACCAC	CACCAAGAAA	GGTTCCTGTC	CCTCTGTCCA	AGCTGTCTAT	850
	GTCCCAGCTG	ATGATTTGAC	CGATCCTGCT	CCAGCCACCA	CATTGCCCCA	900
	TTTGGATGCC	ACTACTGTCT	TGTCTAGAGG	TATTTCTGAA	TTGGGTATTT	950
60	ACCCAGCTGT	CGATCCATTG	GATTCCAAAT	CCAGATTATT	GGACGCTGCC	1000

	GTTGTTGGTC	AAGAACATTA	TGATGTCGCT	ACTGGTGTTT	AAACAACTTT	1050
	GCAAGCTTAC	AAATCCTTAC	AAGATATCAT	TGCTATTTTG	GGTATGGATG	1100
	AATTGTCTGA	AGCTGATAAA	TTGACTGTCTG	AAAGAGCCCG	TAAGATTCAA	1150
	AGATTCTTGT	CTCAACCATT	CGCCGTTGCT	GAAGTTTTCA	CTGGTATGCC	1200
5	AGGTAGATTA	GTCAGATTGC	AAGACACTGT	CAAATCATTC	AAGGATGTTT	1250
	TGGAAGGTAA	ATACGATCAC	TTGCCAG			1277

## 10 2) INFORMATION FOR SEQ ID NO: 462

## (i) SEQUENCE CHARACTERISTICS:

	(A)	LENGTH: 1278 bases
	(B)	TYPE: Nucleic acid
15	(C)	STRANDEDNESS: Double
	(D)	TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

## 20 (vi) ORIGINAL SOURCE:

(A)	ORGANISM: <i>Candida famata</i>
(B)	STRAIN: ATCC 62894

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 462

25	GTA	ACTTGCC	AGCTATTTTG	AACGCTTTGA	CCTTGAAGAA	CGGTGAAAAC	50
	GACTTAGTTT	TAGAAGTTGC	CCAACATTTG	GGTGAAAACA	CCGTCAGAGC		100
	TATTGCTATG	GATGGTACTG	AAGGTTTAGT	TAGAGGTACT	CCAGTTACCG		150
	ATTCTGGTGC	TCCAATTTCT	GTCCCAGTCG	GTAGAGGTAC	TTTAGGTAGA		200
30	ATCTTGAACG	TTATTGGTGA	ACCAATTGAT	GAACAAGGTC	CAGTTGATGC		250
	CAAGGAAACC	AGACCAATTC	ACCAAGACCC	ACCAGCATTC	GTTGATCAAT		300
	CCACCAAGGC	TGAAGTTTTG	GAAACTGGTA	TCAAGGTTGT	CGATTTATTA		350
	GCCCCCTTACG	CTAGAGGTGG	TAAGATTGGT	TTATTCGGTG	GTGCCGGTGT		400
	CGGTAAGACC	GTCTTTATCC	AAGAATTGAT	TAACAACATT	GCCAAGGCCC		450
35	ATGGTGTTTT	CTCTGTTTTT	ACTGGTGTCG	GTGAAAGAAC	CAGAGAAGGT		500
	AACGATTTAT	ATAGAGAAAT	GAAGGAAACT	GGTGTCATTA	ACTTGGAAGG		550
	TGACTCCAAG	GTCGCCTTGG	TTTTTCGGTCA	AATGAACGAA	CCACCAGGTG		600
	CTAGAGCTAG	AGTTGCTTTA	ACCGGTTTAA	CCATTGCCGA	ATACTTCAGA		650
	GACGAAGAAG	GTCAAGATGT	GTTATTGTTC	GTCGATAACA	TTTTTTAGATT		700
40	CACCCAAGCC	GGTTCCGAAG	TGTCTGCTTT	GTTAGGTCGT	ATTCCATCGG		750
	CTGTCCGTTA	TCAACCAACC	TTAGCCACTG	ATATGGGTCT	TTTACAAGAA		800
	AGAATTACCA	CCACCACCAA	GGGTTCCGTT	ACTTCTGTCC	AAGCTGTCTA		850
	CGTCCCAGCC	GATGATTTAA	CCGATCCTGC	TCCAGCTACC	ACTTTTCGCCC		900
	ACTTGGATGC	TACCACTGTG	TTGTCTCGTG	GTATCTCTGA	ATTGGGTATT		950
45	TACCCAGCTG	TCGATCCATT	GGATTCCAAA	TCCAGATTGT	TAGATGCTGA		1000
	TATCGTTGGT	AAAGAACACT	ACGAAGTTGC	CACTGGTGTC	CAACAAACCT		1050
	TACAAGCTTA	CAAATCTTTA	CAAGATATCA	TTGCTATTTT	AGGTATGGAT		1100
	GAATTGTCTG	AAGCCGATAA	ATTGACTGTC	GAAAGAGCCA	GAAAGATCCA		1150
	AAGATTCTTG	TCTCAACCAT	TCGCCGTTGC	CGAAGTTTTT	ACCGGTATCC		1200
50	CAGGTAGATT	AGTTAGATTG	CAAGACACTG	TTAAATCTTT	CAAGGAAGTC		1250
	TTAGAAGGTA	AATATGATCA	CTTACCAG				1278

## 55 2) INFORMATION FOR SEQ ID NO: 463

## (i) SEQUENCE CHARACTERISTICS:

	(A)	LENGTH: 1154 bases
	(B)	TYPE: Nucleic acid
60	(C)	STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

5 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Candida glabrata*

(B) STRAIN: ATCC 66032

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 463

10  
 TCTGGTCAGA GGCGAGAAGG TCGTCGACAC AGGTGCCCCA ATCTCCGTCC 50  
 CTGTGCGCAG AGAGACCCTG GGCAGAATCA TCAACGTTAT CGGTGAACCT 100  
 ATCGACGAGC GTGGCCCAAT CAACTCAAAG TTGAGAAAGC CTATCCACGC 150  
 CGACCCTCCT TCCTTCGCAG AACAGTCCAC CGCCGCCGAA GTCCTGGAAA 200  
 15 CAGGTATCAA GGTCGTCGAC TTGCTGGCCC CTTACGCCAG AGGTGGTAAG 250  
 ATCGGTCTGT TCGGTGGTGC CGGTGTCGGT AAGACCGTGT TCATCCAAGA 300  
 ACTGATCAAC AACATCGCAA AGGCTCACGG TGGTTTCTCC GTGTTCCACAG 350  
 GTGTCGGTGA AAGAACCAGA GAAGGTAACG ATTTGTACAG AGAAATGAAG 400  
 GAAACCGGTG TCATCAACTT GGAAGGTGAC TCTAAGGTCG CCTTGGTCTT 450  
 20 CGGCCAAATG AACGAACCAC CAGGAGCCAG AGCCAGAGTC GCCTTGACCG 500  
 GTTTGACCAT CGCAGAATAC TTCAGAGATG AAGAAGGTCA AGATGTCCTG 550  
 CTGTTGCTCG ACAACATTTT CAGATTACCC CAAGCCGGTT CAGAAGTCTC 600  
 CGCTTTGCTA GGTCGTATCC CATCCGCCGT CGGTTATCAA CCAACCTTGG 650  
 CCACCGATAT GGGTCTGTTG CAAGAAAGAA TTACCACCAC AAAGAAGGGT 700  
 25 TCCGTCACCT CCGTCCAAGC CGTCTACGTG CCTGCAGATG ATTTAACAGA 750  
 TCCTGCCCTT GCCACTACTT TCGCGCACTT GGACGCCACC ACCGTCTTGT 800  
 CCAGAAGTAT CTCAGAATTG GGTATCTACC CAGCTGTCTGA CCCATTGGAC 850  
 TCCAAGTCTA GATTGCTAGA CGCTGCCGTT GTCGGTGAAG AGCATTACAA 900  
 CGTCGCCACA AAGGTCCAAG AAACTTTACA AACTTACAAG TCTCTGCAAG 950  
 30 ATATCATCGC CATTTTGGGT ATGGATGAAT TGTCCGAACA AGATAAGCTA 1000  
 ACTGTGCAAA GAGCAAGAAA GATCCAAAGA TTCTTGTTCCC AACCATTTCG 1050  
 TGTCGCTGAA GTTTTCACCG GTATCGAAGG TAAGCTGGTC AGATTGAAGG 1100  
 ACACCATCTC CTCTTCAAG GCTGTCTTGG AAGGTAAGTA CGATGATCTT 1150  
 CCAG 1154

## 2) INFORMATION FOR SEQ ID NO: 464

40 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1293 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

45 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Candida guilliermondii*

50 (B) STRAIN: ATCC 6260

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 464

CCACTACGAG GACGGTAACC TTCCTGCTAT TTTCAACGCC TTGACTCTTA 50  
 55 AGAACGGTGA CCAAACTTG GTTTTGGAAG TTGCCAGCA TTTGGGTGAA 100  
 AACACCGTCA GAACCATTC TATGGATGGT ACTGAAGGTT TGGTTAGAGG 150  
 TGCCAGCGTC ACTGACACTG GTGCTCCTAT CTCTGTGCCT GTTGGTCGTG 200  
 GTACTTTGGG TCGTATCATC AACGTTATTG GTGAGCCAAT TGACGAGCGT 250  
 GGACCAATCG AGTCCAAGCA AAAGAAGCCC ATTCACGCTG AACCACCATC 300  
 60 GTTCGTGCAA CAATCCACTT CTGCCGAGGT TTTGGAAACC GGTATCAAGG 350

	TTGTCGACTT	GTTGGCTCCA	TACGCCAGAG	GTGGTAAGAT	TGGATTGTTT	400
	GGTGGTGCCG	GTGTCGGTAA	GACTGTGTTT	ATCCAAGAGT	TGATTAACAA	450
	CATTGCCAAG	GCTCACGGTG	GTTTCTCCGT	GTTCACCGGT	GTCGGTGAAA	500
	GAACCAGAGA	AGGTAACGAT	TTGTACCGTG	AAATGAAGGA	AACTGGTGTC	550
5	ATCAACTTGG	AAGGTGAATC	CAAGGTGGCC	TTGGTGTTTCG	GTCAAATGAA	600
	CGAACCTCCA	GGAGCTAGAG	CCAGAGTTGC	CCTTACCGGT	TTGACCATCG	650
	CTGAATACTT	CAGAGATGAG	GAGGGTCAAG	ATGTGTTGTT	GTTTCGTCGAC	700
	AACATTTTCA	GATTCACTCA	AGCTGGTTCT	GAAGTGTCGG	CTTTGTTGGG	750
	TCGTATTCCCT	TCGGCTGTCTG	GTTACCAACC	TACTTTGGCC	ACCGATATGG	800
10	GTTTGTGTC	AGAGCGTATT	ACCACCACCA	AGAAGGGTTC	CGTCACCTCT	850
	GTCCAAGCTG	TCTATGTGCC	AGCCGATGAT	TTGACCGATC	CTGCTCCTGC	900
	TACTACTTTT	GCTCACTTGG	ATGCTACCAC	TGTGTTGTCT	AGAGGTATCT	950
	CCGAGTTGGG	TATTTACCCA	GCTGTGATC	CTTTGGATTTC	CAAGTCGAGA	1000
	TTGTTGGATG	CCTCTGTTGT	CGGTGAGGAG	CACTACTCGG	TTGCTTCTAA	1050
15	CGTTCAACAA	ACCTTGCAAG	CTTACAAGTC	TTTGCAAGAT	ATCATTGCCA	1100
	TTTTGGGTAT	GGACGAATTG	TCGGAAGCTG	ACAAGTTGAC	CGTCGAGAGA	1150
	GCCCCGTAAGA	TCGAGAGATT	CTTGTCTCAA	CCATTGCTG	TTGCCGAAGT	1200
	TTTCACTGGT	ATCAGTGGTA	AGTTGGTCAG	ATTGGAGGAC	ACTATCAGAT	1250
	CTTTCAAGGA	AGTCTTGGAA	GGTAAGTACG	ATCACTTGCC	AGA	1293
20						

## 2) INFORMATION FOR SEQ ID NO: 465

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1293 bases
  - (B) TYPE: Nucleic acid
  - (C) STRANDEDNESS: Double
  - (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Candida haemulonii*
- (B) STRAIN: ATCC 22991

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 465

	CACTTTGACG	ATGGTAACTT	GCCAGCCATT	TTCAACGCCT	TGAAGTTGAA	50
40	GAACGGTGAC	CAGGACTTGG	TCTTGAGAGT	CGCCCAGCAC	TTGGGTGAGA	100
	ACACCGTCAG	AACCATTGCC	ATGGACGGTA	CCGATGGTTT	GGTCAGAGGC	150
	GAGGCTGTCA	CTGACACTGG	TGCTCCAATC	TCCGTGCCTG	TTGGTTCGTGA	200
	GACTTTGGGT	CGTATCATCA	ACGTTATTGG	TGAGCCAATT	GACGAGAGAG	250
	GACCAATCAA	GTCCAAGAAG	AGAAACCCAA	TCCACACTGA	CCCACCAACC	300
45	TTCGTTGAGC	AGTCTACTTC	TGCTGAGGTT	TTGGAGACTG	GTATTAAGGT	350
	TGTCGACTTG	TTGGCCCCCTT	ACGCCAGAGG	TGGTAAGATT	GGTTTGTTCG	400
	GTGGTGCCGG	TGTCGGTAAG	ACCGTCTTTA	TCCAAGAGTT	GATTAACAAC	450
	ATTGCCAAGG	CCCACGGTGG	TTTCTCTGTC	TTTACCGGTG	TCGGTGAGAG	500
	AACCAGAGAA	GGTAACGATT	TGTACCGTGA	AATGCAGGAG	ACCGGTGTCA	550
50	TCAACTTCGA	GGGTGACTCC	AAGGTCGCCT	TGGTCTTCGG	TCAGATGAAC	600
	GAGCCACCAG	GAGCTAGAGC	TAGAGTTGCT	TTGACCGGTT	TGACCATTGC	650
	CGAATACTTC	AGAGATGAAG	AAGGTCAGGA	TGTGTTGTTG	TTCGTTGACA	700
	ACATTTTCAG	ATTCACTCAG	GCTGGTTCCG	AGGTGTCCGC	CTTGTTGGGT	750
	CGTATTCCAT	CTGCTGTCTG	TTACCAGCCA	ACCTTGGCCA	CCGATATGGG	800
55	TACCTTGCAA	GAAAGAATTA	CCACCACCAA	GAAGGGTTCC	GTCACCTCTG	850
	TCCAGGCCGT	TTACGTGCCA	GCTGATGATT	TGACCGATCC	TGCCCCAGCT	900
	ACCACTTTCG	CTCACTTGGA	TGCTACCACT	GTGTTGTCTA	GAGGTATTTC	950
	CGAGTTGGGT	ATCTACCCAG	CTGTGACACC	ATTGGACTCC	AAGTCTAGAT	1000
	TGTTGGATGC	CTCTGTTGTC	GGTAAGGAGC	ACTACGATGT	TGCTACCAAC	1050
60	GTCCAGCAGA	CCTTGCAGGC	CTACAAGTCC	TTGCAGGATA	TCATTGCCAT	1100

TTTGGGTATG	GATGAATTGT	CCGAAGCCGA	CAAGTTGACT	GTCGAGAGAG	1150
CTAGAAAGAT	TCAGAGATTC	TTGTCCCAGC	CATTCGCCGT	CGCCGAGGTT	1200
TTCAGTGGTA	TCGAGGGTAA	GTTGGTCAGA	TTGGAGGAGA	CCGTCAAGTC	1250
TTTCAAGGAG	GTCTTGGATG	GTAAGTACGA	CCACTTGCCA	GAG	1293

5

## 2) INFORMATION FOR SEQ ID NO: 466

10 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 1111 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

15

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

20 (A) ORGANISM: *Candida inconspicua*  
 (B) STRAIN: ATCC 16783

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 466

AACGGTGGAT	CTAAGTTAGT	CTTAGAAGTT	GCTCAACATT	TGGGTGAAAA	50
CACTGTCAGA	ACCATTGCTA	TGGATGGTAC	TGAAGGTTTA	GTTAGAGGTC	100
AACCAGTTAA	TGATACTGGT	GCTCCAATCT	CTGTCCCAGT	CGGTAGAGGT	150
ACTTTAGGTA	GAATCTTAAA	CGTTATTGGT	GATCCAGTCG	ATGAAAGAGG	200
TCCAATTGAT	TGTAAGGAAA	GAAAACCAAT	TCATCAAGAT	CCTCCTGCTT	250
TCGTTGAACA	ATCTACTGAA	GCTGAAGTTT	TAGAAACCGG	TATTAAGGTT	300
30 GTTGATTTAT	TAGCTCCTTA	CGCTAGAGGT	GGTAAGATTG	GTTTATTCGG	350
TGGTGCTGGT	GTCGGTAAAA	CCGTTTTTCAT	TCAAGAATTA	ATTAACAATG	400
TTGCAAAGGC	TCATGGTGGT	TTCTCAGTTT	TCACTGGTGT	CGGTGAAAGA	450
ACCAGAGAAG	GTAATGATTT	ATACAGAGAA	ATGAAGGAAA	CTGGTGTTAT	500
TAACCTTAGAA	GGTGAATCTA	AGGTCGCCTT	AGTTTTTCGGT	CAAATGAATG	550
35 AACCACCAGG	AGCAAGAGCA	AGAGTTGCTT	TAACCGGTTT	AACTATTGCT	600
GAATACTTCA	GAGATGAAGA	AGGTCAAGAT	GTCTTGTTAT	TCATTGATAA	650
CATTTTCAGA	TTTACTCAAG	CAGGTTCTGA	AGTTTCTGCA	TTGTTAGGTA	700
GAATTCCATC	CGCTGTCGGT	TATCAACCAA	CTTTAGCAAC	TGATATGGGT	750
CTTTTACAAG	AAAGAATTAC	AACTACTAAG	AAAGGTTCCG	TTACTTCTGT	800
40 CCAAGCAGTT	TATGTCCCAG	CAGATGATTT	AACTGATCCT	GCTCCAGCAA	850
CTACTTTCGC	CCACTTAGAT	GCAACTACTG	TCTTATCTAG	AGGTATTTCC	900
GAATTAGGTA	TTTACCCAGC	TGTCGATCCA	TTAGATTCTA	AATCTAGATT	950
ATTAGATGTT	GCTGTTGTTG	GTCAAGAACA	TTATGATGTT	GCAACTCAAG	1000
TTCAAGAAAC	TTTACAAGCA	TACAAATCTT	TACAAGATAT	TATTGCTATT	1050
45 TTAGGTATGG	ATGAATTATC	TGAACAAGAT	AAATTAACCG	TTGAAAGAGC	1100
AAGAAAGATT	C				1111

## 50 2) INFORMATION FOR SEQ ID NO: 467

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 1283 bases  
 (B) TYPE: Nucleic acid  
 55 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

60 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Candida kefyr*  
 (B) STRAIN: ATCC 28838

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 467

```

5   TCGAACCAAGG TCAATTGCCA GAAATTTTGA ACGCTTTGGA GATTGAWACT      50
    CCTCAAGGTA AGTTGGTTTT GGAAGTTGCC CAACATTGCG GTGAAAACAC      100
    CGTCAGAACC ATTGCTATGG ACGGTACCGA AGGTTTGGTC CGTGGTGAGA      150
    AGGTTTTTGA CACTGGTGCT CCAATTTCCG TCCCAGTCGG TAGAGAAACT      200
10  TTGGGTAGAA TCATCAACGT TATTGGTGAG CCAATTGACG AAAGAGGCCC      250
    AATCAAGTCC AAGATGAGAA AGCCAATTCA CGCTGACCCT CCATCCTTTG      300
    TTGAACAATC CACTGCTGCT GAAGTTTTTG AAACCGGTAT CAAGGTTGTC      350
    GACTTGTTGG CCCCATACGC CAGAGGTGGT AAGATTGGTT TGTTCCGTGG      400
    TGCCGGTGTC GGTAAGACCG TTTTCATCCA AGAGTTGATT AACACATTG      450
15  CCAAGGCCCA TGGTGGTTTC TCCGTCTTCA CCGGTGTCGG TGAAAGAACC      500
    AGAGAAGGTA ACGATTGTGA CCGTGAAATG AAGGAAACCG GTGTCATCAA      550
    CTTGGAAGGT GACTCCAAGG TCGCCTTGGT CTTCGGTCAA ATGAACGAAC      600
    CACCTGGAGC TAGAGCCAGA GTTGCCCTGA CCGGTTTGAC TATCGCTGAA      650
    TACTTCAGAG ATGAAGAAGG TCAAGATGTG TTGTTGTTTA TCGACAACAT      700
20  TTTCAGATTC ACACAAGCCG GTTCCGAAGT GTCCGCTTTG TTGGGTCGTA      750
    TTCCATCCGC TGTCGGTTAC CAACCTACTT TGGCCACCGA TATGGGTTTG      800
    TTGCAAGAAA GAATTACCAC TACCAAGAAG GGTTCCGTTA CCTCCGTCCA      850
    AGCTGTCTAC GTCCCTGCTG ATGATTTGAC TGATCCTGCT CCAGCTACYA      900
    CTTTCGCCCA TTTGGACGCC ACCACCGTGT TGTCCAGAGG TATCTCCGAA      950
25  TTGGGTATCT ACCCAGCTGT CGATCCATTG GATTCCAAGT CTAGATTGTT     1000
    GGACGCTGCC GTTGTCGGTC AAGAACATTA CGACGTCGCT ACTCAAGTTC     1050
    AACAACTTT GCAAGCTTAC AAGTCTTTGC AAGATATCAT TGCCATTTTG     1100
    GGTATGGATG AATTGTCTGA ACAAGACAAG TTGACTGTCG AAAGAGCCAG     1150
    AAAGATCCAA AGATTCTTGT CTCAACCATT CGCCGTCGCC GAAGTTTTC     1200
30  CTGGTATCCC AGGTAGATTG GTCAGATTAA AGGACACCAT CGCTTCCTTC     1250
    AAGGCTGTTT TGGAAGGTAA GTACGATCAC TTG                          1283
  
```

## 35 2) INFORMATION FOR SEQ ID NO: 468

## (i) SEQUENCE CHARACTERISTICS:

```

    (A) LENGTH: 1287 bases
    (B) TYPE: Nucleic acid
40  (C) STRANDEDNESS: Double
    (D) TOPOLOGY: Linear
  
```

## (ii) MOLECULE TYPE: Genomic DNA

## 45 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Candida krusei*  
 (B) STRAIN: ATCC 34135

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 468

```

50  CTTCGAACAA GGCCAATTAC CACAAATTTT AAACGCTTTA GTTATGGATA      50
    ATGGTGGTAA CAAGTTAGTT TTAGAAGTTG CTCAACATTT AGGTGAAAAC      100
    ACTGTCAGAA CCATTGCTAT GGATGGTACT GAAGGTTTAG TTAGAGGTCA      150
    AACCGTTAAC GATACCGGTG CTCCAATCTC TGTCCCAGTT GGTAGAGGTA      200
55  CCTTAGGTTAG AATCTTGAAC GTCATTGGTG ATCCAGTCGA TGAAAGAGGT      250
    CCAGTTGACT GTAAGGAAAG AAAGCCAATT CACGCTGATC CTCCAGCTTT      300
    CGTTGAACAA TCCACTGAAG CTGAAGTTTT GGAAACTGGT ATTAAGGTTG      350
    TCGATTTATT AGCACCTTAC GCAAGAGGTG GTAAGATTGG TTTATTCGGT      400
    GGTGCTGGTG TTGGTAAGAC CGTTTTTATC CAAGAATTGA TCAACAATGT      450
60  YGCAAGGCT CATGGTGGTT TCTCCGTTTT CACTGGTGTT GGTGAAAGAA      500
  
```

	CCAGAGAAGG	TAACGATTTA	TACAGAGAAA	TGAAGGAAAC	TGGTGTTATT	550
	AACTTGGAAG	GTGAATCCAA	GGTCGCCTTA	GTTTTTCGGTC	AAATGAACGA	600
	ACCACCAGGA	GCTAGAGCAA	GAGTTGCTTT	AACTGGTTTG	ACCATTGCAG	650
	AATATTTTCAG	AGATGAAGAA	GGTCAAGATG	TCTTGTTATT	CATTGATAAC	700
5	ATTTTCAGAT	TCACCCAAGC	AGGTTCTGAA	GTCTCTGCAT	TATTAGGTAG	750
	AATTCCATCT	GCTGTCGGTT	ATCAACCAAC	TTTAGCAACC	GATATGGGTC	800
	TTTTACAAGA	AAGAATTACC	ACCACCAAGA	AGGGTTCCGT	TACTTCTGTC	850
	CAAGCTGTTT	ATGTCCCAGC	CGATGATTTA	ACCGATCCTG	CTCCAGCTAC	900
	TACTTTCGCC	CACTTGGATG	CAACCACTGT	CTTGTCYAGA	GGTATTTCCG	950
10	AATTAGGTAT	CTACCCAGCT	GTCGATCCAT	TAGATTCTAA	GTCTAGATTA	1000
	TTAGATGTTG	CAGTTGTTGG	TCAAGAACAT	TATGAAGTTG	CAACTCAAGT	1050
	CCAAGAAACT	TTACAAGCTT	ACAAGTCTTT	ACAAGATATT	ATTGCTATTT	1100
	TGGGTATGGA	TGAATTATCT	GAACAAGATA	AGTTAACYGT	TGAAAGAGCA	1150
	AGAAAGATCC	AAAGATTCTT	ATCTCAACCA	TTCTCTGTTG	CAGAAGTTTT	1200
15	CACTGGTATT	CCAGGTAAGT	TAGTCAGATT	AGAAGAAACC	ATCAAGTCTT	1250
	TCAGGGATGT	TCTTGCAGGT	AAGTACGATC	ACTTACC		1287

## 20 2) INFORMATION FOR SEQ ID NO: 469

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1283 bases  
 (B) TYPE: Nucleic acid  
 25 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

## 30 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Candida lambica*  
 (B) STRAIN: ATCC 24750

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 469

35	TCGAACAAGG	TCAATTACCA	CCAATTCTTA	ACGCTTTGGT	CATGGAAAAC	50
	GATGGTCAAA	AGTTAGTTTT	GGAAGTTGCT	CAACATTTGG	GTGAAAACAC	100
	CGTCAGAACC	ATTGCTATGG	ACGGTACCGA	AGGTTTAGTT	AGAGGTCAAC	150
	CTGTTAACGA	CACTGGTGCT	CCAATCTCTG	TCCCAGTTGG	TAGAGGTACT	200
40	CTTGGTAGAA	TCTTGAACGT	CACTGGTGAC	CCAGTYGATG	AAAGAGGTCC	250
	TGTCGAMTGT	AAGGAGAGAA	GACCAATTCA	CCAAGACCCA	CCTGCTTTTCG	300
	TTGACCAATC	CACTGAAGCT	GAAGTTTGG	AAACCGGTAT	TAAGGTTGTC	350
	GATTTATTAG	CACCTTACGC	TAGAGGTGGT	AAGATTGGTT	TGTTTCGGTGG	400
	TGCTGGTGTC	GGTAAGACCG	TTTTCATCCA	AGAATTGATT	AACAATGTTG	450
45	CTAAGGCCCA	CGGTGGTTTC	TCCGTTTTC	CTGGTGTCCG	TGAAAGAACC	500
	AGAGAAGGTA	ACGATTTATA	CAGAGAAATG	AAGGAAACCG	GTGTTATTAA	550
	CCTTGAAGGT	GAATCTAAGG	TCGCCCTCGT	TTTCGGTCAA	ATGAACGAAC	600
	CACCAGGAGC	AAGAGCTAGA	GTIGCTCTTA	CTGGTTTGAC	CATTGCTGAA	650
	TACTTCAGAG	ATGAAGAAGG	TCAAGATGTC	TTGCTTTTCA	TTGACAACAT	700
50	TTTCAGATTC	ACCCAAGCAG	GTTCCGAAGT	GTCTGCTTTG	TTAGGTAGAA	750
	TTCCWTCTGC	CGTTGGTTAC	CAACCAACCT	TAGCAACCGA	TATGGGTTTG	800
	TTACAAGAAA	GAATTACCAC	CACCAAGAAG	GGTTCCGTCA	CCTCCGTCCA	850
	AGCTGTTTAC	GTCCCAGCTG	ATGATTTRAC	TGACCCTGCA	CCAGCAACCA	900
	CTTTCGCCCA	CTTGGATGCT	ACCACCGTCT	TGTCTAGAGG	TATTTCCGAA	950
55	TTAGGTATTT	ACCCAGCTGT	CGATCCATTA	GATTCTAAGT	CTAGATTATT	1000
	GGATGTGCT	GTTGTGCGTC	AAGAACATTA	TACCGTTGCA	ACYCAAGTCC	1050
	AAGAACTTT	ACAAGCTTAC	AAGTCCTTAC	AAGATATCAT	TGCTATTTTG	1100
	GGTATGGACG	AATTATCTGA	ACAAGATAAG	CTTACTGTTG	AAAGAGCAAG	1150
	AAAGATCCAA	AGATTCCTTT	CCCAACCTTT	CTCCGTCGCA	GAAGTTTTCA	1200
60	CTGGTATCCC	AGGTAAGCTT	GTCAGATTAG	AAGAAACCAT	TATTTCTTTC	1250



AGAGATGTCC TCGATGGTAA GTACGACCAC TTA

1283

## 2) INFORMATION FOR SEQ ID NO: 470

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1140 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Candida lusitanae*  
 (B) STRAIN: ATCC 66035

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 470

20	AGGTGCCTCT	GTCACTGACA	CTGGTTCTCC	AATCTCTGTC	CCTGTTGGTC	50
	GTGAAACCTT	GGGTAGAATT	ATCAACGTTG	TTGGTGAGCC	AATTGACGAG	100
	AGAGGCCCAA	TCAACTCCAA	GAAGAGAAAC	CCAATTCACA	CTGAGCCACC	150
	ATCGTTTGT	GAACAATCCA	CTTCTGCTGA	AGTTTGGAG	ACTGGTATCA	200
25	AGGTTGTCGA	CTTGTTGGCC	CCTTACGCCA	GAGGTGGTAA	GATTGGTTTG	250
	TTCGGTGGTG	CCGGTGTCGG	TAAGACCGTT	TTCATCCAAG	AGTTGATTAA	300
	CAACATTGCC	AAGGCCACG	GTGGTTTCTC	TGTTTTCACT	GGTGTCGGTG	350
	AAAGAACCAG	AGAAGGTAAC	GATTTGTACC	GTGAAATGCA	AGAGACCGGT	400
	GTCATCAACT	TCGAGGGTGA	CTCCAAGGTC	GCCTTGGTCT	TCGGTCAAAT	450
30	GAACGAACCA	CCAGGAGCCA	GAGCTAGAGT	TGCTTTGACC	GGTTTGACTA	500
	TTGCCGAGTA	CTTCAGAGAC	GAAGAGGGCC	AAGATGTCTT	GTTGTTTCGTT	550
	GACAACATTT	TCAGATTCAC	CCAGGCCGGT	TCTGAAGTGT	CTGCTTTGTT	600
	GGGTCGTATT	CCATCCGCTG	TCGGTTACCA	ACCAACCTTG	GCCACCGATA	650
	TGGGTGCTTT	GCAAGAGAGA	ATTACCACCA	CCAAGAAGGG	TTCCGTCACC	700
35	TCTGTCCAAG	CCGTTTATGT	TCCAGCTGAT	GACTTGACTG	ACCCTGCTCC	750
	AGCCACCACC	TTCGCCCACT	TGGACGCCAC	CACTGTGTTG	TCCAGAGGTA	800
	TCTCTGAATT	GGGTATCTAC	CCAGCTGTCG	ACCCATTGGA	CTCCAAGTCT	850
	AGATTGTTGG	ACGCTTCTAT	TGTTGGTAAG	GAGCACTACG	AAGTTGCTTC	900
	TAACGTTCAA	CAAACCTTGC	AAGCTTACAA	GTCTTTGCAA	GATATCATTG	950
40	CCATTTTGGG	TATGGATGAA	TTGTCTGAGG	CTGACAAGTT	GACCGTTGAG	1000
	AGAGCCAGAA	AGATCCAAAG	ATTCTTGTCT	CAACCATTCG	CTGTTGCCGA	1050
	GGTTTTCACT	GGTATCCAG	GTAGATTGGT	CAGATTGGAG	GACACTGTCA	1100
	GATCCTTCAA	GGAAGTTTGT	GACGGTAAGT	ACGACCACTT		1140

## 2) INFORMATION FOR SEQ ID NO: 471

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1296 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Candida norvegensis*  
 (B) STRAIN: ATCC 22977

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 471

	TCAATTCGAA	CAAGGTCAAT	TACCACCAAT	TTTAAACGCT	TTAGTCATGG	50
	ACAACGGTGG	AACTAAGTTA	GTTTTAGAAG	TTGCTCAACA	TTAGGTGAA	100
5	AACACCGTCA	GAACCATTCG	TATGGATGGT	ACTGAAGGTT	TAGTTAGAGG	150
	TCAACCAGTT	AATGATACTG	GTGCTCCAAT	CTCTGTCCCA	GTCGGTAGAG	200
	GTACTTTAGG	TAGAATCTTA	AACGTTATTG	GTGATCCAGT	CGATGAAAGA	250
	GGTCCAATCG	ATTGTAAGGA	AAGAAAACCA	ATTCATCAAG	ATCCTCCTGC	300
	TTTCGTTGAA	CAATCAACTG	AAGCTGAAGT	TTTAGAAACT	GGTATTAAAG	350
10	TTGTCGATTT	ATTAGCTCCT	TACGCTAGAG	GTGGTAAGAT	TGGTTTATTC	400
	GGTGGTGCCG	GTGTTGGTAA	AACCGTTTTT	ATTCAGAAT	TAATTAACAA	450
	TGTTGCAAAA	GCTCATGGTG	GTTTCTCCGT	TTTCACTGGT	GTCGGTGAAA	500
	GAAGTAGAGA	AGGTAACGAT	TTATACAGAG	AAATGAAGGA	AACTGGTGTT	550
	ATTAATTTAG	AAGGTGATTC	TAAGGTCGCA	TTAGTTTTTCG	GTCAAATGAA	600
15	CGAACCACCT	GGAGCAAGAG	CAAGAGTTGC	TTAACTGGT	TTAACTATTG	650
	CTGAATATTT	CAGAGATGAA	GAAGGTCAAG	ATGTCTTGTT	ATTCATTGAT	700
	AACATTTTCA	GATTTACTCA	AGCAGGTTCT	GAAGTTTCCG	CTTTGTTAGG	750
	TAGAATTCCA	TCCGCTGTCG	GTTATCAACC	AACTTTAGCA	ACTGATATGG	800
	GTCTTTTACA	AGAAAGAATT	ACTACTACTA	AGAAAGGTTT	TGTTACTTCC	850
20	GTTCAAGCAG	TTTATGTCCC	AGCAGATGAT	TTAACTGATC	CTGCTCCAGC	900
	AACTACTTTC	GCCCACTTAG	ATGCAACTAC	TGTCTTATCT	AGAGGTATTT	950
	CCGAATTAGG	TATTTACCCA	GCTGTGCGATC	CATTAGATTC	TAAATCTAGA	1000
	TTATTAGATG	TTGCAGTTGT	TGGTCAAGAA	CATTATGATG	TTGCAACTCA	1050
	AGTTCAAGAA	ACTTTACAAG	CTTACAAATC	TTTACAAGAT	ATTATTGCTA	1100
25	TTTTAGGTAT	GGATGAATTA	TCTGAACAAG	ATAAATTAAC	CGTTGAAAGA	1150
	GCTAGAAAAA	TTCAAAGATT	CTTATCTCAA	CCTTTCTCTG	TCGCAGAAGT	1200
	TTTCACTGGT	ATCCCAGGTA	AGCTTGTTAG	ATTAGAAGAA	ACTATTTCTT	1250
	CATTCAGAGA	TGTCTTAGCA	GGTAAGTACG	ATCACTTACC	AGAAAA	1296

30

## 2) INFORMATION FOR SEQ ID NO: 472

## (i) SEQUENCE CHARACTERISTICS:

- |    |     |                      |
|----|-----|----------------------|
| 35 | (A) | LENGTH: 1297 bases   |
|    | (B) | TYPE: Nucleic acid   |
|    | (C) | STRANDEDNESS: Double |
|    | (D) | TOPOLOGY: Linear     |

## 40 (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- |  |     |                                       |
|--|-----|---------------------------------------|
|  | (A) | ORGANISM: <i>Candida parapsilosis</i> |
|  | (B) | STRAIN: ATCC 90018                    |

45

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 472

	AACTTTCGAA	GAAGGAAACT	TGCCAGCTAT	TTTGAACGCT	TTGACCTTGA	50
	AAAACGGTAA	ACAAGACTTG	GTCTTGGAAG	TTGCCCAACA	TTTGGGTGAA	100
50	AACACCGTCA	GAGCAATTGC	TATGGATGGT	ACTGAAGGTT	TAGTTAGAGG	150
	TACTTCTGTC	ACTGACACTG	GTGCCCCAAT	TTCTGTCCCA	GTTGGTAGAG	200
	GTACTTTGGG	TAGAATCATC	AATGTTACTG	GTGACCCAAT	TGATGAAAGA	250
	GGTCCAATTG	AATGTAAGAA	GAGAAACCCA	ATCCACGCTG	AACCACCTTC	300
	ATTCATTGAA	CAATCCACTG	CTGCTGAAGT	TTTGGAAACC	GGTATTAAAGG	350
55	TTGTCGACTT	GTTGGCTCCA	TACGCTAGAG	GTGGTAAGAT	TGGTTTGTTT	400
	GGTGGTGCCG	GTGTCGGTAA	AACCGTGTTT	ATCCAAGAAT	TGATCAACAA	450
	CATTGCCAAG	GCACATGGTG	GTTTCTCGGT	TTTCACTGGT	GTTGGTGAAA	500
	GAACCAGAGA	AGGTAACGAT	TTGTACCGTG	AAATGAAGGA	AACTGGTGTT	550
	ATCAACTTGG	AAGGTGACTC	CAAGGTCGCT	TTGGTTTTTCG	GTCAAATGAA	600
60	CGAACCACCT	GGAGCTAGAG	CTAGAGTTGC	TTTGACTGGT	TTGACCATTG	650

	CTGAATACTT	TAGAGATGAA	GAAGGTCAAG	ATGTCTTGTT	GTTTATTGAC	700
	AACATTTTCA	GATTCACCCA	AGCTGGTTCA	GAAGTGTCTG	CTTTGTTGGG	750
	TCGTATTCCA	TCCGCTGTCTG	GTTATCAACC	AACCTTGGCC	ACCGATATGG	800
	GTCTTTTGCA	AGAACGTATT	ACCACTACCA	AAAAGGGTTC	AGTTACTTCA	850
5	GTCCAAGCCG	TTTACGTGCC	AGCTGATGAT	TTAACCGATC	CTGCTCCAGC	900
	TACCACTTTC	GCTCACTTGG	ATGCCACCAC	TGTGTTGTCT	AGAGGTATTT	950
	CGGAGTTGGG	TATTTACCCA	GCTGTGCGATC	CATTGGATTG	CAAATCCAGA	1000
	TTGTTGGATG	CTGCCGTTGT	TGGTCAAGAA	CATTACGACG	TTGCCACTGG	1050
	TGTTCAACAA	ACTTTACAAG	CTTACAAGTC	CTTGCAAGAT	ATCATTGCTA	1100
10	TCTTGGGTAT	GGATGAATTG	TCCGAACAAG	ATAAATTGAC	TGTCGAAAGA	1150
	GCTCGTAAGA	TTCAAAGATT	CTTGTCTCAA	CCATTGCTG	TCGCTGAAGT	1200
	TTTCACTGGT	ATTCCAGGTA	AATTGGTTAG	ATTGTCTGAA	ACTGTCAAGT	1250
	CATTCAAGGA	AGTCTTGGA	GGTAAGTACG	ATAACTTGCC	AGAAAAT	1297

15

## 2) INFORMATION FOR SEQ ID NO: 473

## (i) SEQUENCE CHARACTERISTICS:

- 20 (A) LENGTH: 1285 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

## 25 (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Candida rugosa*  
 (B) STRAIN: ATCC 96275

30

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 473

	CCAGTTTGGC	AACGACCTCC	CTGCCATTTT	GAACGCCCTC	ACTCTTCAGC	50
	GTGAAGACGG	TAACAAGCTT	GTTCTTGAGG	TTGCCCAGCA	TCTCGGTGAG	100
35	AACACCGTCC	GTACCATTTG	TATGGACGGT	ACCGAGGGTT	TGGTGCGTGG	150
	CACTGGTGTC	CACGACACCG	GACACCCCAT	CATGACTCCC	GTCGGTGACG	200
	GTACCCTGGG	ACGTATTCTT	AACGTCACCG	GTGACCCTGT	AGACGAGCGT	250
	GGTCCCCTCA	AGACTGACAA	GTTCCGCCCC	ATCCACGCCG	AGGCCCTGTC	300
	CTTCGATGAG	CAGGCTACCA	GTGCCGAGGT	TCTTGAGACC	GGTATCAAGG	350
40	TTGTCGACTT	GCTCGCTCCT	TACGCCAAGG	GTGGTAAGAT	TGGTTTGTTT	400
	GGTGGTGCCG	GTGTCGGCAA	GACCGTCTTC	ATCCAGGAGC	TGATTAACAA	450
	CATCGCCAAG	GCCCACGGTG	GTTACTCCGT	GTTCACTGGT	GTCGGTGAGC	500
	GTAATCGTGA	GGGTAACGAT	TTGTACAAGG	AAATGATCGA	GTCCGGTGTC	550
	ATCAACCTCG	ATGGTGAGTC	CAAGGTCGCC	TTGGTGTTTC	GTCAGATGAA	600
45	CGAGCCCCCT	GGAGCCCCTG	CCCGTGTGCG	CCTTACCGGT	CTTACCATCG	650
	CTGAGTATTT	CCGTGATGAG	GAGGGTAAGG	ATGTCTTGTT	GTTCTGTTGAC	700
	AACATTTTCC	GCTTCACTCA	GGCCGGTTCT	GAGGTGTCCG	CCTTGCTTGG	750
	TCGTATTCTT	TCCGCTGTCTG	GTTACCAGCC	TACCTTGGCC	ACCGATATGG	800
	GTGCCCTTCA	GGAGCGTATC	ACCACCACCA	AGAAGGGTTC	CGTTACATCC	850
50	GTCCAGGCCG	TCTACGTCCC	TGCCGATGAT	TTGACTGATC	CCGCCCCCTGC	900
	CACCACCTTC	GCCCATTTTG	ATGCCACCAC	TGTCTTGTCT	CGTGCCATCT	950
	CTGAGTTGGG	TATCTACCCC	GCTGTGCGAC	CTCTCGACTC	CAAGTCCCCT	1000
	CTTCTTGACG	CCGCTGTCTG	TGGTCAGGAG	CACTACGATA	CTGCCACCTC	1050
	CGTTCAGCAG	ACTTTGCAGG	CTTACAAGTC	TTTGCAAGAT	ATCATTGCCA	1100
55	TTCTTGGTAT	GGATGAGTTG	TCCGAGTCTG	ACAAGCTCAC	CGTCGAGCGT	1150
	GCTCGTAAGA	TCCAGCGTTT	CCTCTCCAG	CCTTTGCTG	TTGCTGAGGT	1200
	CTTCACTGGT	ATTCAAGGCC	GTCTTGTTCC	TCTCAAGGAC	ACTGTCCGCT	1250
	CCTTCAAGGA	GATTCTCGAA	GGTAAGTACG	ATGCT		1285

60

## 2) INFORMATION FOR SEQ ID NO: 474

## (i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 1283 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

## 10 (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Candida sphaerica*  
 (B) STRAIN: ATCC 2504

15

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 474

TTGAACAAGG TCAATTGCCA GCTATTTTGA ACGCTTTGGA AATCGACACT 50  
 CCAGAAGGAA AGTTGGTTTT GGAAGTCGCT CAACATTTGG GTGAAAACAC 100  
 20 TGTGAGAACC ATTGCTATGG ATGGTACTGA AGGTTTAGTC CGTGGTGAAA 150  
 ACGTTTCTGA CACTGGTGCT CCAATTTCCTG TCCCAGTTGG TAGAGAAACC 200  
 TTGGGTAGAA TTATCAACGT TATTGGTGAG CCAATTGACG AAAGAGGTCC 250  
 AATCAACTCC AAGATGAGAA AGCCAATTCA TGCTGATCCT CCATTATTCG 300  
 TTGAACAATC CACTGCTGCT GAAGTTTGG AAAGTGGTAT CAAGGTTGTC 350  
 25 GACTTGTTGG CCCCATACGC CAGAGGTGGT AAGATTGGTT TGTTGCGGTGG 400  
 TGCCGGTGTC GGTAAGACCG TTTTCATCCA AGAATTGATT AACAACATTG 450  
 CCAAGGCTCA TGGTGGTTTC TCTGCTTCA CTGGTGTCTG TGAAAGAACC 500  
 AGAGAAGGTA ACGATTTGTA CCGTGAAATG AAGGAAACTG GTGTTATCAA 550  
 CTTGGAAGGT GATTCTAAGG TCGCGTTGGT TTTCGGTCAA ATGAACGAAC 600  
 30 CTCCTGGAGC TAGAGCTAGA TCGCGCTTGA CTGGTTTGAC CATCGCTGAA 650  
 TACTTCAGAG ATGAAGAAGG TCAAGATGTC TTGTTGTTTA TCGACAACAT 700  
 TTTCAGATTC ACACAAGCCG GTTCCGAAGT GTCCGCTTTG TTGGGTCGTA 750  
 TTCCATCCGC TGTCGGTTAT CAACCAACTT TGGCCACCGA TATGGGTTTG 800  
 TTGCAAGAAA GAATTACTAC CACCAAGAAG GGTTCGGTCA CTTCTGTCCA 850  
 35 AGCCGTTTAC GTGCCAGCTG ATGATTTGAC TGATCCTGCT CCAGCTACCA 900  
 CTTTCGCGCA TTTGGATGCC ACCACTGTGT TGTCCAGAGG TATCTCTGAA 950  
 TTGGGTATCT ACCCAGCTGT CGATCCTTTG GATTCCAAAT CTAGATTGTT 1000  
 GGATGCTGCC GTCGTTGGTC AAGAACATTA CGATGTCGCT ACTCAAGTTC 1050  
 AACAACTTT GCAAGCTTAC AAGTCTTTGC AAGATATCAT TGCCATTTTG 1100  
 40 GGTATGGATG AATTGTCCGA ACAAGATAAG TTGACCGTCG AAAGAGCTAG 1150  
 AAAGATTCAA AGATTCTTGT CTCAACCTTT CGCTGTCGCT GAAGTCTTCA 1200  
 CTGGTATCCC AGGTAGATTG GTCAGATTAA AGGACACCAT CTCTTCTTTC 1250  
 AAGGCTGTCT TGGACGGTAA GTACGATCAC TTG 1283

45

## 2) INFORMATION FOR SEQ ID NO: 475

## (i) SEQUENCE CHARACTERISTICS:

- 50 (A) LENGTH: 1290 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

## 55 (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Candida tropicalis*  
 (B) STRAIN: ATCC 13803

60

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 475

	CGACGAAGGT	AACTTGCCAG	CTATTTTGAA	TGCTTTGACT	TTGAAGAACG	50
	GTGACCAAGA	CTTGGTTTTG	GAAGTTGCTC	AACATTTGGG	TGAAAACACC	100
5	GTCAGGGCTA	TTGCTATGGA	TGGTACCGAA	GGTTTAGTCA	GAGGTACTGC	150
	TGTCACTGAT	ACCGGTGCTC	CAATTTCTGT	CCCAGTTGGT	AGAGGTACCT	200
	TGGGTAGAA	TATCAACGTT	GTTGGTGAAC	CAATTGATGA	CAGAGGTCCA	250
	ATTGAATGTA	AGGAAAGAAA	GCCAATTCAC	GCTGAACCAC	CTTCATTTCG	300
	TGAACAATCT	ACTGCTGCCG	AAATTTTGGA	AACCGGTATT	AAGGTTGTCG	350
10	ATTTGTTGGC	TCCTTACGCT	AGAGGTGGTA	AGATTGGTTT	GTTTCGGTGGT	400
	GCTGGTGTCT	GTAAAACCGT	CTTCATCCAA	GAATTGATTA	ACAACATTGC	450
	CAAAGCTCAT	GGTGGTTTCT	CTGTCTTTAC	CGGTGTCGGT	GAAAGAACCA	500
	GAGAAGGTAA	CGATTTGTAC	CGTGAAATGA	AAGAACTGG	TGTCATCAAC	550
	TTGGAAGGTG	ACTCCAAGGT	CGCCTTGGTC	TTCGGTCAAA	TGAACGAACC	600
15	ACCTGGTGCT	AGAGCTAGAG	TTGCTTTGAC	TGGTTTGACC	ATTGCTGAAT	650
	ACTTCAGAGA	TGAAGAAGGT	CAAGATGTCT	TGTTGTTCAT	TGACAACATT	700
	TTCAGATTCA	CCCAAGCTGG	TTCCGAAGTG	TCTGCTTTGT	TGGGTCGTAT	750
	TCCATCTGCT	GTCGGTTATC	AACCAACCTT	GGCCACTGAT	ATGGGTCTTT	800
	TGCAAGAACG	TATTACCACC	ACCAAGAAAG	GTTCTGTTC	TTCTGTCCAA	850
20	GCTGTTTATG	TCCCAGCCGA	TGATTTAACC	GATCCAGCTC	CAGCTACCAC	900
	CTTCGCTCAC	TTGGATGCCA	CTACTGTCTT	GTCTAGAGGT	ATTTCTGAAT	950
	TGGGTATTTA	CCCAGCTGTC	GATCCATTGG	ATTCTAAATC	CAGATTATTG	1000
	GATGCTACTG	TTGTTGGTCA	AGAACATTAT	GATGTTGCCA	CTGGTGTTCA	1050
	ACAAACTTTA	CAAGCTTACA	AGTCCTTGCA	AGATATCATT	GCTATTTTGG	1100
25	GTATGGATGA	ATTGTCCGAA	GCCGATAAAT	TGACTGTCGA	AAGAGCTCGT	1150
	AAGATTCAAA	GATTCTTGTC	CCAACCATT	GCTGTTGCCG	AAGTTTTTCA	1200
	TGGTATCCCA	GGTAGATTGG	TTAGATTACA	AGATACTGTT	AAATCTTTCA	1250
	AAGATGTCTT	GGAAGGTAAA	TACGATCACT	TGCCAGAAAA		1290

30

## 2) INFORMATION FOR SEQ ID NO: 476

## (i) SEQUENCE CHARACTERISTICS:

35	(A)	LENGTH: 1267 bases
	(B)	TYPE: Nucleic acid
	(C)	STRANDEDNESS: Double
	(D)	TOPOLOGY: Linear

40 (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

	(A)	ORGANISM: <i>Candida utilis</i>
45	(B)	STRAIN: Csp 388

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 476

	TTTGAACGCC	CTTGAGATCA	AGAACCACGA	GTCTGGAAGA	TTGGTCCTCG	50
	AGGTTGCCCA	GCACTTGGGT	GAGAACACTG	TCAGAACTAT	TGCCATGGAT	100
50	GGTACCGAAG	GTCTCGTCCG	TGGTGAGTCT	GTTGTTGACA	CCGGTTCTCC	150
	AATTACTGTC	CCAGTTGGTC	GTGAGACCTT	GGGTCGTATC	ATCAACGTTA	200
	TTGGTGAGCC	AATTGATGAG	CGTGGTCCAA	TCAACACCAA	GCACAGAAAC	250
	CCAATTCACG	CTGAGCCACC	ATCCTTCGCT	GAGCAGTCTA	CTGCTGCTGA	300
	GGTTTTGGAG	ACTGGTATCA	AGGTTGTCGA	CCTTCTCGCC	CCATACGCCA	350
55	GAGGTGGTAA	GATTGGTCTC	TTTGGTGGTG	CCGGTGTCGG	TAAGACCGTT	400
	TTCATCCAGG	AGTTGATTAA	CAACATTGCC	AAGGCCACG	GTGGTTTCTC	450
	TGTTTTTACC	GGTGTCGGTG	AGAGAACCAG	AGAGGGTAAC	GATTTGTACC	500
	GTGAGATGAA	GGAGACTGGT	GTCATCAATC	TCGAGGGTGA	GTCCAAGGTT	550
	GCTCTCGTCT	TCGGTCAGAT	GAACGAGCCA	CCAGGTGCCC	GTGCCCGTGT	600
60	CGCTTTGACC	GGTTTGACCA	TTGCTGAGTA	CTTCAGAGAT	GAGGAGGGTC	650

	AGGATGTCTT	GTTGTTTATT	GACAACATTT	TCAGATTCAC	CCAGGCCGGT	700
	TCCGAGGTGT	CTGCCTTGCT	TGGTCGTATT	CCATCCGCTG	TCGGTTACCA	750
	GCCAACTTTG	GCCACCGATA	TGGGTTTGT	GCAGGAGAGA	ATTACCACCA	800
	CCCAGAAGGG	TTCCGTCAC	TCTGTCCAGG	CCGTTTACGT	CCCAGCTGAT	850
5	GATTTGACTG	ATCCTGCTCC	AGCCACCACT	TTCGCCCACT	TGGACGCCAC	900
	CACTGTGTTG	TCCCGTGGTA	TCTCTGAGTT	GGGTATTTAC	CCAGCTGTCG	950
	ACCCATTGGA	CTCCAAGTCC	AGATTGTTGG	ACGCTGCCGT	TGTTGGTGAC	1000
	GAGCACTACA	ACACCGCCAC	CGATGTCCAG	CAGACCCTTC	AGGCTTACAA	1050
	GTCTCTCCAG	GATATCATTG	CTATTTTGGG	TATGGATGAG	TTGTCTGAGG	1100
10	CTGACAAGTT	GACTGTGCGAG	AGAGCCAGAA	AGATTCAGCG	TTTCCTTTCC	1150
	CAGCCATTTCG	CTGTGCGCTGA	GGTTTTTCACC	GGTATCCCAG	GTAGATTGGT	1200
	TAGACTTCAG	GACACCATCA	AGTCCTTCAG	AGAGGTTTTG	GACGGTAAGT	1250
	ACGACCACTT	GCCAGAG				1267

15

## 2) INFORMATION FOR SEQ ID NO: 477

## (i) SEQUENCE CHARACTERISTICS:

- 20 (A) LENGTH: 1296 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

## 25 (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Candida viswanathii*  
 (B) STRAIN: ATCC 28269

30

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 477

	CCAATTCGAC	GAAGGTAGCT	TGCCAGCTAT	CTTGAACGCC	TTGACCTTGA	50
	AGAACGGTGA	CCAAGACTTG	GTCTTGGAAG	TTGCCCAACA	CTTGGGTGAA	100
35	AACACTGTCA	GAGCTATTGC	TATGGATGGT	ACCGAAGGTT	TGGTCAGAGG	150
	TACTGCTGTC	ACTGACACCG	GTGCTCCAAT	CTCCGTCCCA	GTCGGTAGAG	200
	GTACCTTGGG	TAGAATCATC	AACGTTGTTG	GTGAACCAAT	TGACGACAGA	250
	GGTCCAATTG	AATGTAAGGA	AAGAAAGCCA	ATTCACGCTG	AACCACCTTC	300
	TTTCGTTGAA	CAATCCACTG	CTGCCGAAAT	TTTGGAACC	GGTATCAAGG	350
40	TTGTCGACTT	GTTGGCCCCA	TACGCCAGAG	GTGGTAAGAT	TGGTTTGTTT	400
	GGTGGTGCCG	GTGTCGGTAA	GACTGTCTTT	ATCCAAGAGT	TGATTAACAA	450
	CATTGCCAAG	GCCCATGGTG	GTTTCTCTGT	CTTCACTGGT	GTCGGTGAAA	500
	GAACCAGAGA	AGGTAACGAT	TTGTACCGTG	AAATGAAGGA	AACCGGTGTC	550
	ATCAACTTGG	AAGGTGACTC	CAAGGTCGCC	TTGGTTTTTCG	GTCAAATGAA	600
45	CGAACCACCT	GGTGCTAGAG	CTAGAGTTGC	TTTGACTGGT	TTGACCATTG	650
	CCGAATACTT	CAGAGACGAA	GAAGGTCAAG	ATGCTTGTT	GTTTATTGAC	700
	AACATTTTCA	GATTCACCCA	AGCCGGTTCC	GAAGTGTCTG	CTTTGTTGGG	750
	TCGTATTCCA	TCTGCCGTCG	GTTATCAACC	AACCTTGGCC	ACCGATATGG	800
	GTCTTTTGCA	AGAACGTATT	ACCACCACCA	AGAAGGGTTC	CGTCACCTCT	850
50	GTCCAAGCTG	TCTATGTCCC	AGCCGATGAT	TTGACCGATC	CTGCTCCAGC	900
	CACCACCTTC	GCTCACTTGG	ATGCCACTAC	TGTCTTGTTT	AGAGGTATTT	950
	CCGAATTGGG	TATCTACCCA	GCTGTGCGATC	CATTGGACTC	CAAGTCCAGA	1000
	TTGTTGGATG	CTGCTGTTGT	TGGTCAAGAA	CATTACGATG	TTGCCACTGG	1050
	TGTCCAACAA	ACCTTGCAAG	CTTACAAGTC	TTTGCAAGAT	ATCATTGCCA	1100
55	TTTTGGGTAT	GGATGAATTG	TCTGAATCCG	ATAAGTTGAC	TGTCGAAAGA	1150
	GCTCGTAAGA	TCCAAAGATT	CTTGTCGCAA	CCATTTGCTG	TTGCCGAAGT	1200
	TTTCACTGGT	ATCCCAGGTA	GATTAGTTAG	ATTGCTGGAA	ACCGTCCAAT	1250
	CTTTCAAAGA	CGTCTTGCT	GGTAAATACG	ATCACTTGCC	AGAAAA	1296

60

## 2) INFORMATION FOR SEQ ID NO: 478

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1295 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Candida zeylanoides*  
 (B) STRAIN: ATCC 7351

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 478

	TCAATTCGAG	CAAGGCAACC	TCCCTGCCAT	CTTGAACGCT	CTCACCTTGA	50
	AGAATGGTGA	CAACGACTTG	GTTTTGGAAG	TTGCCCAGCA	CTTGGGTGAG	100
20	AACACCGTCA	GAGCCATTGC	CATGGATGGT	ACCGAGGGTT	TGGTTAGAGG	150
	TGCGTCCGTC	AAGGACACTG	GCGCCCCTAT	CTCGGTCCCC	GTTGGCCGCG	200
	GGACTTTGGG	TCGTATCATC	AACGTCACCG	GTGACCCCAT	TGACGAGAGA	250
	GGTCCCATCG	AGCTGACCCA	GAGAAACCCT	ATCCACGCCG	ACCCCCCTC	300
	GTTTCGTTGAG	CAGTCCACCA	ACGCTGAGGT	TTTGGGAGACT	GGTATCAAGG	350
25	TTGTCGATTT	GTTGGCTCCC	TACGCCAGAG	GTGGTAAGAT	TGGTTTGTTT	400
	GGTGGTGCCG	GTGTCGGTAA	GACCGTCTTC	ATTCAGGAGT	TGATCAACAA	450
	CATCGCCAAG	GCCCACGGTG	GGTTCTCGGT	CTTCACTGGT	GTCGGTGAGA	500
	GAAC TAGAGA	GGGTAACGAC	TTGTACCGTG	AGATGAAGGA	GACCGGTGTC	550
	ATCAACTTGG	AGGGTGACTC	CAAGGTGGCC	TTGGTGTTTCG	GTCAGATGAA	600
30	CGAGCCCCCT	GGAGCCAGAG	CCAGAGTCGC	CTTGACCGGG	TTGACCATTG	650
	CCGAATACTT	TAGAGACGAG	GAGGGTCAGG	ATGTGTTGTT	GTTTCGTCGAC	700
	AACATCTTCA	GATTCACCCA	AGCTGGTTCG	GAGGTGTCGG	CCTTGTTGGG	750
	TCGTATTCCC	TCTGCCGTCG	GTTACCAGCC	CACCTTGGCA	ACTGATATGG	800
	GATTGTTGCA	GGAGCGTATC	ACCACGACCA	AGAAGGGTTC	CGTCACCTCA	850
35	GTGCAGGCCG	TCTACGTCCC	CGCTGATGAC	TTGACTGACC	CTGCTCCCGC	900
	CACCACCTTT	GCCCACTTGG	ACGCCACCAC	CGTGTGTGTC	AGAGGTATCT	950
	CTGAGTTGGG	TATCTACCCC	GCCGTCGACC	CCTTGGA CT	CAAATCGAGA	1000
	TTGTTGGACG	CTGCCGTGGT	CGGT CAGGAG	CACTACGATG	TTGCCTCGAA	1050
	CGTCCAGCAG	ACCTTG CAGG	CCTACAAGTC	CTTGCAGGAT	ATCATTGCCA	1100
40	TTTTGGGTAT	GGATGAGTTG	TCCGAGGCTG	ACAAGTTGAC	CGTTGAGAGA	1150
	GCCAGAAAGA	TCCAGAGATT	CTTGTCGCAG	CCCTTCGCTG	TTGCCGAGGT	1200
	TTTCACTGGT	ATCAAGGGTA	GATTGGTCAG	ATTGGAGGAC	ACCGTCAGAT	1250
	CTTTCAAGGA	GGTTTTGGAG	GGTAAGTACG	ACCACTTGCC	CGAGA	1295

## 2) INFORMATION FOR SEQ ID NO: 479

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 534 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Coccidioides immitis*  
 (B) STRAIN: Silveira

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 479

5 TTCAGGAATT GATTGTAAGT TCTGTTATCA ACTAAAGCCG ACAGCGGTTG 50  
 CTGATATGCT CTAGAACAAC ATTGCTAAGG CTCACGGTGG TTACTCCGTG 100  
 TTCACTGGTG TCGGTGAGCG TACCCGTGAG GGTAACGATT TGTACCATGA 150  
 AATGCAAGAG ACCCGTGTCA TTCAACTCGA CGGAGAGTCC AAGGTCGCTC 200  
 TTGTCTTCGG TCAAATGAAC GAGCCCCCTG GTGCCCCGTGC CCGTGTTGCC 250  
 CTTACCGGTT TGACCATTCG TGAATACTTC CGTGACGAGG AAGGCCAAGA 300  
 CGGTAGGCTT CATGCTTCTA TCGCTAGGGG CGTGTGATAC AGGAGGCTAA 350  
 10 TCGCTTTTCT AGTGCTTCTC TTTATTGACA ACATTTTCCG TTCTACTCAA 400  
 TCTGGTTCTG AAGTGTCTGC CTTGCTCGGT CGTATTCCCT CCGCTGTCGG 450  
 TTACCAACCT ACTCTCGCCG TCGACATGGG TGTATGCAG GAACGTATCA 500  
 CCACCACCAC CAAGGGATCC ATTACTTCAG TGCA 534

15

## 2) INFORMATION FOR SEQ ID NO: 480

20 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 494 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

25 (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Cryptococcus albidus*  
 (B) STRAIN: ATCC 66030

30

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 480

35 CGTCTTGATT CAAGAATTGA TCAACAACAT CGCCAAGGCC CACGGTGGTT 50  
 ACTCGGTCTT CACCGGTGTC GGTGAGCGAA CTCGAGAGGG TAACGATCTG 100  
 TACCACGAAG TGAGTTGCGC CGTCCGAGTG TTTCCCGGGG AATCGCAAGA 150  
 CTGATGTTGT CCCTTCTTCT CAGATGAGGG AAACCGGTGT CATCAACCTC 200  
 GAGGGTGACT CCAAGGTCGC CTTGGTCTTC GGTCAGATGA ACGAGCCCCC 250  
 TGGAGCCCGA GCCCGAGTCG CCTTGACCGG TTTGACCATT GCCGAATACT 300  
 TCCGAGACGA GGAGGGTCAG GATGTCTTGT TGTTCAATTGA CAACATTTTC 350  
 40 CGATTCACCC AAGCCGGTTC CGAAGTGTC GCCTTGTTGG GTCGTATCCC 400  
 CTCCGCCGTC GGTACCAGC CCACTCTGTC CACCGACATG GGTACCATGC 450  
 AGGAGCGAAT TACCACCACC AAGAAGGGTT CCATCACTTC CGTC 494

45

## 2) INFORMATION FOR SEQ ID NO: 481

50 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 415 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

55 (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Fusarium oxysporum*  
 (B) STRAIN: WSA-212

60 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 481



	TTCAGGAGCT	TATCAACAAC	ATCGCCAAGG	CCCACGGTGG	TTACTCCGTC	50
	TTCACTGGTG	TCGGTGAGCG	AACTCGTGAG	GGTAACGATC	TGTACCACGA	100
	AATGCAGGAG	ACTTCCGTCA	TTCAGCTTGA	TGGCGAGTCC	AAGGTCGCCC	150
5	TGGTCTTTCG	TCAGATGAAC	GAGCCCCCTG	GAGCTCGTGC	CCGTGTCGCC	200
	CTTACCGGTC	TTACTGTAGC	TGAATACTTC	AGAGATGAGG	AGGGTCAGGA	250
	CGTGCTGCTC	TTCATTGACA	ACATTTTCCG	ATTCACTCAG	GCCGGTTCCG	300
	AGGTGTCTGC	CCTTCTCGGT	CGTATCCCCT	CTGCCGTCGG	TTACCAGCCC	350
	ACCTCTGCCG	TCGACATGGG	TGGTATGCAA	GAGCGTATTA	CCACCACCAC	400
10	CAAGGGTTCC	ATTAC				415

## 2) INFORMATION FOR SEQ ID NO: 482

15

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1281 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

20

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Geotrichum* spp.  
 (B) STRAIN: Lev-4

25

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 482

30	AGGACAACCT	CCCCGCTATT	CTTAACGCTC	TTGAGCTTAA	GAGAGATAAC	50
	GGTGAGAAGC	TCGTTCTCGA	GGTTGCCAG	CATCTGGGTG	AGAACACTGT	100
	CCGTACTATT	GCTATGGACG	GTACTGAGGG	TCTCGTCCGT	GGTCAGCCCCG	150
	TTGTTGACAC	CGGTGCCCCC	ATTACCATTTC	CCGTTGGTTCG	TGGTACTCTT	200
	GGTAGAATTA	TCAACGTCAT	TGGTGAGCCC	ATCGATGAGC	GTGGACCCAT	250
35	TGAGGCTACC	AAGTACCTCC	CCATCCACAC	CGAGCCCCCC	ACCTTCGCTG	300
	AGCAGTCTAC	CTCCGCTGAG	GTTCTTGAGA	CTGGTATCAA	GGTTGTCGAT	350
	CTCCTTGCCC	CCTACGCCCC	TGGTGGAAG	ATTGGTCTCT	TCGGTGGTGC	400
	CGGTGTCGGT	AAGACCGTTT	TCATTACAGGA	GCTGATTAAC	AACATTGCCA	450
	AGGCCCATGG	TGGTTTCTCC	GTTTTACCCG	GTGTCGGTGA	GAGAACCCGT	500
40	GAGGGTAACG	ATTTGTACCG	TGAGATGAAG	GAGACCGGTG	TCATCAACCT	550
	CGAGGGTGAG	TCTAAGGTCG	CTCTCGTTTT	CGGTCAGATG	AACGAGCCCC	600
	CTGGAGCCCC	TGCCCGTGTT	GCTCTTACTG	GTCTTACCAT	TGCTGAGTAC	650
	TTCCGTGATG	AGGAGGGTCA	GGATGTGTTG	CTCTTCGTTG	ACAACATTTT	700
	CCGTTTCACT	CAGGCCGGTT	CCGAGGTGTC	TGCCCTTTTG	GGTCGTATTC	750
45	CCTCCGCTGT	CGGTTACCAG	CCCACCCTTG	CCACTGATAT	GGGTGCCCTG	800
	CAAGAGCGTA	TTACCACCAC	CCAGAAGGGT	TCCGTCACTT	CCGTCCAGGC	850
	CGTCTACGTC	CCTGCCGATG	ATTTGACCGA	TCCTGCCCCCT	GCTACCACCT	900
	TCGCCCATT	GGATGCCACC	ACCGTCTTGT	CGCGTTCCAT	TTCTGAGTTG	950
	GGTATCTACC	CCGCTGTCGA	TCCCCTTGAT	TCCAAGTCTC	GTCTTTTGGG	1000
50	TATCACCGTC	GTTGGCCAGG	AGCACTACGA	TGTTGCTACC	CAGGTCCAGC	1050
	AGACCCTCCA	GTCCTACAAG	TCTCTTCAGG	ATATCATTGC	CATTTTGGGT	1100
	ATGGATGAGT	TGTCTGAGGC	TGATAAGCTT	ACTGTCGAGC	GTGCCCCGTA	1150
	GATCCAGAGA	TTCCTTTCCC	AGCCCTTCAC	TGTCGCTGAG	GTTTTCACTG	1200
	GTATCGAGGG	CCGTCTCGTT	CCTTTGAAGG	ACACTGTTTCG	CTCTTTCAAG	1250
55	GAGATCCTTG	AGGGCAAGTA	CGACCACCTC	C		1281

## 2) INFORMATION FOR SEQ ID NO: 483

60

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 586 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Histoplasma capsulatum*  
 (B) STRAIN: G185A5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 483

```

15  ATTCAAGAAT TGATCGTACG TTCCTCCGCC CCACACACGA TCAATGGAGA      50
    AAGAAACAAA TTTTGTGGGA GTGGTCATTT TTTCTAATAA TTCGAATAGA      100
    ACAACATTGC CAAAGCCCAC GGTGGTTACT CCGTGTTTAC TGGTGTCTGGC      150
    GAGCGGACCC GTGAAGGAAA TGACTTGTAC CACGAAATGC AGGAAACCCG      200
    TGTATATCCAG CTCGATGGAG AGTCCAAGGT CGCCCTCGTT TTCGGTCAGA      250
20  TGAACGAGCC TCCCGGAGCC CGTGCCCGTG TTGCCCTCAC TGGTCTGACC      300
    GTTGCCGAGT ACTTCCGTGA CGAGGAAGGC CAAGACGGTA TGTATAAGTA      350
    TACACCGTAG CAAATCAACA CAGAGCTTCA CTCACGCTCG GATTTAGTGC      400
    TTCTCTTCAT CGACAACATT TTCCGCTTCA CTCAGGCCGG TTCCGAAGTG      450
    TCTGCCCTGC TCGGCCGTAT TCCCTCCGCC GTCGGTTACC AACCCACCCT      500
25  CGCCGTGGAC ATGGGTGGTA TGCAGGAACG TATCACCACCT ACCACCAAGG      550
    GCTCCATCAC CTCTGTGTCAR GCCGTCTACG TCCCCG      586
  
```

## 30 2) INFORMATION FOR SEQ ID NO: 484

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1145 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Malassezia furfur*  
 (B) STRAIN: ATCC 42132

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 484

```

45  GCGTGGCCAG AAGGTCATTG ACACTGGTGC TCCCATCACC ATCCCCGTCG      50
    GTGGTGCCAC ACTGGGTCGT ATTCTGAACG TCACGGGTGA CCCTATTGAC      100
    GAGCGTGGCC CCGTTAAGAC TGACGTTTTC CGCCCCATTC ACCGTGACCC      150
    CCCTGCCTTT GTCGAGCAGT CGACTGATGC CGAGATTCTC GAGACTGGTA      200
50  TCAAAGTCGT TGACCTGATT GCCCCTTACG CCCGTGGTGG TAAGATTGGT      250
    CTGTTCGGTG GTGCCGGTGT CGGTAAGACC GTGCTTATCC AGGAGCTCAT      300
    CAACAACATC GCCAAGGCCG ACGGTGGTTT CTCCGTGTTC ACTGGTGTCTG      350
    GTGAGCGTAC TCGTGAGGGT AACGATTGTG ACCACGAGAT GATTGAAACC      400
    GGTGTCATTA ACCTCGAGGG TGACTCGAAG GTGGCTCTGG TGTTCGGTCA      450
55  GATGAACGAG CCCCCGGGTG CCCGTGCGCG TGTCGCTCTT ACTGGTCTGA      500
    CTGTGGCCGA GTAATTCCGT GACGACGAGG GCCAGGATGT GCTGCTGTTC      550
    ATTGACAACA TTTTCCGTTT CACCCAGGCC GGTTCCGAGA CTTCGGCTCT      600
    GCTGGGTCGT ATCCCTTCGT CGGTCCGGTA CCAGCCCCTT TTGTCGACCG      650
    ATATGGGTGC CATGCAGGAG CGTATCACCA CCACCAAGAA GGGTTCGATT      700
60  ACGTCGGTGC AGGCCGTCTA CGTGCCCGCC GATGATGTCA CTGACCCTGC      750
  
```

	CCCTGCCACT	ACCTTCGCCC	ACCTTGACGC	TACCACTGTG	CTTGACCGTT	800
	CGATCGCTGA	GCTGGGTATC	TACCCCGCTG	TTGACCCGTT	GAACCTCGAAC	850
	TCGCGTATGC	TTGACCCCGC	TATTGTGGGT	CAGGAGCACT	ACGACGTGGC	900
	CTCTGGCGTG	CAGAAGCTGC	TCCAGGACTA	CAAGTCGCTT	CAAGATATCA	950
5	TTGCCATTCT	GGGTATGGAT	GAGCTTTCTG	AGGAGGACAA	GCTCACTGTC	1000
	GAGCGTGCCC	GTAAGATGCA	GCGTTTCATG	TCGCAGCCTT	TCGCTGTCGC	1050
	CCAGGTCTTT	ACTGGTATCG	AAGGTCGTCT	TGTTGCCCTG	AAGGACACGA	1100
	TCAAGGCCTG	CAAGGAGATC	CTGTCGGGCA	AGCACGACAA	CCTCC	1145

10

## 2) INFORMATION FOR SEQ ID NO: 485

## (i) SEQUENCE CHARACTERISTICS:

- 15 (A) LENGTH: 1261 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

## 20 (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Malassezia pachydermatis*  
 (B) STRAIN: ATCC 42756

25

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 485

	TCCCGCCATC	TTCAACGCCC	TGGAGGTCCA	GGACATGAAG	AACGGTGGCC	50
	GCCTTGTTCT	GGAGGTTGCC	CAGCACCTTG	GTGAGAACAC	TGTTTCGTTGC	100
30	ATTGCTATGG	ACGGTACCGA	GGGTCTTGTC	CGTGGTCAGA	AGGTCCTTGA	150
	CACTGGTGCC	CCGATCACTA	TCCCTGTCGG	TAACGGTACC	TTGGGCCGYA	200
	TCCTGAACGT	CACTGGTGAG	CCTGTGGATG	AGCGTGGTCC	GGTTAAGACT	250
	GACGTCTACC	GTCCAATCCA	CCGTGAGCCC	CCGGCGTTCG	TTGAGCAGTC	300
	GACTGATGCT	GAGATTCTTG	AGACTGGTAT	CAAGGTGGTC	GACCTGCTCG	350
35	CCCCATACGC	TCGTGGTGGT	AAGATTGGTC	TWTTCCGGTGG	TGCYGGTGTY	400
	GGTAAGACCG	TGCTGATTCA	GGAGCTTATC	AACAACATTG	CCAAGGCCCA	450
	CGGTGGTTTC	TCGGTGTTCA	CTGGTGTCGG	TGAGCGTACT	CGTGAGGGTA	500
	ACGATCTGTA	CCATGAAATG	ATTGAGACTG	GTGTCATCAA	CGTTGACGGT	550
	GACTCGAAGG	TCGCTCTCGT	GTTTCGGTCAG	ATGAACGAGC	CCCCGGGTGC	600
40	CCGTGCCCGT	GTCGCCCTGA	CYGGTCTGAC	CATCGCCGAG	TACTTCCGTG	650
	ACGACGAGGG	TCAGGATGTG	CTGCTCTTCA	TTGACAACAT	TTTCCGTTTC	700
	ACTCAGGCTG	GTTCGGAGAC	TTCGGCTCTG	CTGGGTCGTA	TCCCGTCGGC	750
	TGTCGGTTAC	CAGCCKACCC	TTGCCACGGA	TATGGGTGCC	ATGCAGGARC	800
	GTATYACCAC	CACCAAGAAG	GGTTCGATTA	CCTCGGTGCA	GGCYGTTTAC	850
45	GTTCCGGCCG	ACGATGTGAC	TGACCCTGCC	CCGGCCACGA	CCTTCGCCCA	900
	CTTGGACGCC	ACCACGGTGT	TGGACCGTTC	GATTGCGYAG	CTGGGTATCT	950
	ACCCGGCCGT	CGACCCGCTG	AACCTGAAGT	CGCGTATGCT	TGACCCGTCA	1000
	ATTGTCGGTG	TGGAGCACTA	CAACGTTGCT	TCGGGTGTCC	AGAAGCTTCT	1050
	YCAGGACTAC	AAGTCGCTCC	AAGATATCAT	TGCCATTCTG	GGTATGGATG	1100
50	AGTTGTCGGA	GGAGGACAAG	CTCACTGTCTG	AGCGTGCCCG	TAAGATGCAG	1150
	CGTTTCCTGT	CGCAGCCTTT	CGCTGTGGCC	CAGGTCTTCA	CTGGTATCGA	1200
	GGGTCTGCTT	GTGTCGCTCA	AGGACACCAT	CAACGCCTGC	AAGGAGATTC	1250
	TGTCCGGTAA	G				1261

55

## 2) INFORMATION FOR SEQ ID NO: 486

## (i) SEQUENCE CHARACTERISTICS:

- 60 (A) LENGTH: 1282 bases

(B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

5 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Metschnikowia pulcherrima*  
 (B) STRAIN: DSM 70336

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 486

	AGGAGGGCAA	CTTGCCAGCT	ATCTTCAACG	CTTTGACGTT	GAAGAACGGC	50
	GACCAGAAGT	TGGTCTTGGA	GGTGGCCCAG	CACTTGGGTG	AGAACACCGT	100
15	CAGAACCATT	GCCATGGACG	GTACCGAGGG	TTTGGTCAGA	GGCGCCTCTG	150
	TCACCGACAC	YGGTGCCCTT	ATCTCCGTGC	CTGTGCGCCG	TGAGACCTTG	200
	GGTCGTATTA	TCAATGTTGT	TGGTGAGCCA	ATCGACGAGA	GAGGCCCAAT	250
	CAACACCAAG	AAGAGAAACC	CTATTACAC	CGACCCACCT	TCGTTTGTCC	300
	AGCAATCCAC	TTCCGCCGAG	GTCTTGAGAG	CTGGTATCAA	GGTTGTGCGAC	350
20	TTGTTGGCCC	CTTACGCCAG	AGGTGGTAAG	ATTGGTTTGT	TCGGTGGTGC	400
	CGGTGTCGGT	AAGACCGTGT	TCATCCAGGA	GTTGATTAA	AACATTGCCA	450
	AGGCCACCG	TGGTTTCTCC	GTTTTCACCG	GTGTCGGTGA	GAGAACCAGA	500
	GAGGGTAACG	ATTTGTACCG	TGAAATGCAG	GAGACTGGTG	TCATCAACTT	550
	CGAGGGTGAC	TCCAAGGTGC	CCTTGGTTTT	CGGTCAGATG	AACGAGCCTC	600
25	CAGGAGCTAG	AGCYAGAGTT	GCCTTGACCG	GTTTGACCAT	CGCCGAGTAC	650
	TTCAGAGACG	AGGAGGGTCA	GGATGTGTTG	TTGTTGTCG	ACAACATTTT	700
	CAGATTCACC	CAAGCCGGTT	CTGAGGTGTC	TGCCTTGTTG	GGTCGTATTC	750
	CATCCGCTGT	CGGATACCAG	CCAACCTTGG	CCACCGATAT	GGGTGCCTTG	800
	CAGGAGAGAA	TTACCACCAC	CAAGAAGGGT	TCCGTACCT	CCGTCCAGGC	850
30	CGTCTACGTG	CCAGCCGATG	ACTTGACTGA	CCCTGCGCCA	GCCACCACTT	900
	TCGCCCCTT	GGACGCCACC	ACTGTGTTGT	CCAGAGGTAT	CTCTGAGTTG	950
	GGTATCTACC	CCGCTGTGCA	CCCCTTGGAC	TCCAACCTCA	GATTGTTGGA	1000
	CGCCACCGTT	GTTGGCCAGG	AGCACTACGA	CGTCGCCACC	AACGTCCAGC	1050
	AAACTTTACA	AGCTTACAAG	TCCTTGACAG	ATATCATTGC	CATTTTGGGT	1100
35	ATGGATGAGT	TGTCCGAGAC	CCGACAAGTT	GACCCGTCGA	GAGAGCCAGA	1150
	AAGATCCAGA	AGTTCTTGTC	CCAGCCATTT	GCCGTCGCCG	AGGTTTTTAC	1200
	CGGTATTGAG	GGTAGATTGG	TTAGATTGGA	GGACACCGTT	AGATCCTTTA	1250
	AGGAGGTTTT	GGAAGGTAAG	TACGACCACT	TG		1282

40

2) INFORMATION FOR SEQ ID NO: 487

(i) SEQUENCE CHARACTERISTICS:

45 (A) LENGTH: 482 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

50 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Penicillium marneffe*  
 (B) STRAIN: WSA-214

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 487

	TGTCTTTATC	CAGGAGTTGA	TTGTACGTCT	TTACCTTTCT	GCCTGACTGT	50
	TTACGACAAC	TAACGAAAGC	GTAGAACAAC	ATTGCCAAGG	CTCACGGTGG	100
60	TTACTCTGTC	TTCACTGGTG	TCGGTGAACG	TACTCGTGAG	GGTAACGATT	150

TGTACCACGA	AATGCAGGAA	ACTGGTGTCA	TTCAGCTCGA	GGGTGAATCC	200
AAGGTCGCCC	TCGTGTTCGG	TCAGATGAAC	GAGCCCCCGG	GTGCCCCGTGC	250
CCGTGTGCTC	CTTACTGGTT	TGACCATTCG	CGAGTACTTC	CGTGACGAGG	300
AAGGTCAGGA	CGTGCTTCTC	TTCATTGACA	ACATTTTCCG	TTTCACTCAG	350
5 GCCGGTTCTG	AGGTGTCTGC	CCTTCTGGGT	CGTATCCCCT	CTGCCGTCGG	400
TTACCAGCCC	ACCCTTGCCG	TCGACATGGG	TATCATGCAG	GAGCGTATTA	450
CCACCACCAC	CAAGGGTTCC	ATCACCTCCG	TC		482

10

## 2) INFORMATION FOR SEQ ID NO: 488

## (i) SEQUENCE CHARACTERISTICS:

15

- (A) LENGTH: 1290 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

20

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Pichia anomala*
- (B) STRAIN: ATCC 18205

25

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 488

TCGAACAAGG	TAACCTACCA	GCTATCTTGA	ATGCTTTAGA	AATCAAAACC	50
CCAAGTGGA	CTCCATTAGT	TTTAGAAGTT	GCTCAACATT	TAGGTGAAAA	100
CACTGTCAGA	ACTATTGCTA	TGGATGGTAC	TGAAGGTTTA	GTTTCGTGGT	150
30 AACAAAGTTAC	TGATACTGCT	TCTCCAATCA	CTGTCCCAGT	TGGTCGTGAA	200
ACTTTAGGTC	GTATTATCAA	CGTTGTTGGT	GAACCAATTG	ATGAACGTGG	250
TCCAATTAAC	ACCAAACAAA	GAAACCCAAT	TCACGCTGAA	CCACCTTCAT	300
TCAGTGAACA	ATCAACTGCT	GCTGAAGTTT	TAGAAACTGG	TATCAAAGTT	350
GTYGATTTAT	TAGCTCCATA	CGCTAGAGGT	GGTAAAATTG	GTTTATTCGG	400
35 TGGTGCCGGT	GTCGGTAAAA	CTGTCTTTAT	CCAAGAATTG	ATTAACAACA	450
TTGCTAAAGC	TCATGGTGGT	TTCTCAGTTT	TCACCGGTGT	TGGTGAAAGA	500
ACCAGAGAAG	GTAACGATTT	ATACCGTGAA	ATGAAAGAAA	CTGGTGTTAT	550
TAACCTGGAA	GGTGATTCTA	AGGTCGCTTT	AGTTTTCGGT	CAAATGAATG	600
AACCACCAGG	TGCTAGAGCT	CGTGTTGCTT	TAACCTGGTT	GACCATTGCT	650
40 GAATACTTCA	GAGATGAAGA	AGGTCAAGAT	GTCTTGTTAT	TCGTTGATAA	700
CATTTTCAGA	TTCACCCAAG	CCGGTTCAGA	AGTTTCTGCC	TTATTAGGTC	750
GTATTCCATC	TGCTGTGCGT	TATCAACCAA	CTTTAGCAAC	TGATATGGGT	800
TTGTTACAAG	AACGTATTAC	CACCACACAA	AAAGGTTTCA	TTACTTCTGT	850
CCAAGCTGTT	TATGTCCAG	CTGATGATTT	AACAGATCCT	GCTCCAGCTA	900
45 CCACTTTCGC	CCATTTGGAT	GCTACTACTG	TCTTGTCTCG	TGGTATTTCA	950
GAATTAGGTA	TTTACCCAGC	TGTCGATCCA	TTAGATTCTA	AATCAAGATT	1000
ATTAGATGCT	TCAGTTGTTG	GTCAAGAACA	TTATGATGTT	GCTACCAACG	1050
TTCAACAAAC	TTTACAAGCT	TACAAATCTT	TACAAGATAT	TATTGCTATT	1100
TTAGGTATGG	ATGAATTGTC	TGAACAAGAT	AAATTGACTG	TCGAAAGAGC	1150
50 AAGAAAAATC	CAAAGATTCT	TATCTCAACC	ATTGCTGTT	GCCGAAGTTT	1200
TCACTGGTAT	YCCAGGTAGA	TTGGTTAGAT	TAAAAGACAC	TATCAAATCA	1250
TTCAAAGATG	TTTTGGAAGG	TAAATATGAT	CACTTACCAG		1290

55

## 2) INFORMATION FOR SEQ ID NO: 489

## (i) SEQUENCE CHARACTERISTICS:

60

- (A) LENGTH: 1291 bases
- (B) TYPE: Nucleic acid

300

(C) STRANDEDNESS: Double  
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

5

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Pichia anomala*  
(B) STRAIN: ATCC 2149

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 489

	CCAATTCGAA	CAAGGTAAC	TACCAGCTAT	CTTGAATGCT	TTAGAAATCA	50
	AAACCCCAAG	TGGTACTCCA	TTAGTTTATAG	AAGTTGCTCA	ACATTTAGGT	100
	GAAAACACTG	TCAGAACTAT	TGCTATGGAT	GGTACTGAAG	GTTTAGTCCG	150
15	TGGTGAACAA	GTTACTGATA	CTGGTTCTCC	AATCACTGTC	CCAGTTGGTC	200
	GTGAAACTTT	AGGTCGTATT	ATCAACGTTG	TTGGTGAACC	AATTGATGAA	250
	CGTGGTCCAA	TTAACACCAA	ACAAAGAAAC	CCAATTCACG	CTGAACCACC	300
	TTCATTACAGT	GAACAATCAA	CTGCTGCTGA	AGTTTTAGAA	ACTGGAATCA	350
	AAGTTGTTGA	TTTATTAGCT	CCATACGCTA	GAGGTGGTAA	AATTGGTTTA	400
20	TTCGGTGGTG	CCGGTGTCGG	TAAAACTGTC	TTTATCCAAG	AATTGATTAA	450
	CAACATTGCT	AAAGCTCATG	GTGGTTTCTC	AGTTTTCACC	GGTGTGGTG	500
	AAAGAACCAG	AGAAGGTAAC	GATTTATACC	GTGAAATGAA	AGAAACTGGT	550
	GTTATTAAC	TGGAAGGTGA	TTCTAAGGTC	GCTTTAGTTT	TCGGTCAAAT	600
	GAATGAACCA	CCAGGTGCTA	GAGCTCGTGT	TGCTTTAACT	GGTTTGACCA	650
25	TTGCTGAATA	CTTCAGAGAT	GAAGAAGGTC	AAGATGTCTT	GTTATTCGTT	700
	GATAACATTT	TCAGATTCAC	CCAAGCCGGT	TCAGAAGTTT	CTGCCTTATT	750
	AGGTCGTATT	CCATCTGCTG	TCGGTTATCA	ACCAACTTTA	GCAACTGATA	800
	TGGGTTTGTT	ACAAGAACGT	ATTACCACCA	CACAAAAGG	TTCAGTTACT	850
	TCTGTCCAAG	CTGTTTATGT	CCCAGCTGAT	GATTTAACAG	ATCCTGCTCC	900
30	AGCTACCACT	TTCGCCCAT	TGGATGCTAC	TACTGTCTTG	TCTCGTGGTA	950
	TTTCAGAATT	AGGTATTTAC	CCAGCTGTCG	ATCCATTAGA	TTCTAAATCA	1000
	AGATTATTAG	ATGCTTCAGT	TGTTGGTCAA	GAACATTATG	ATGTTGCTAC	1050
	CAACGTTCAA	CAAACTTTAC	AAGCTTACAA	ATCTTTACAA	GATATTATTG	1100
	CTATTTTAGG	TATGGATGAA	TTGTCTGAAC	AAGATAAATT	GACTGTCGAA	1150
35	AGAGCAAGAA	AAATCCAAAG	ATTCTTATCT	CAACCATTTG	CTGTTGCCGA	1200
	AGTTTTCACT	GGTATCCCAG	GTAGATTGGT	TAGATTAAAA	GACACTATCA	1250
	AATCATTCAA	AGATGTTTTG	GAAGGTAAAT	ATGATCACTT	A	1291

40

2) INFORMATION FOR SEQ ID NO: 490

(i) SEQUENCE CHARACTERISTICS:

45 (A) LENGTH: 508 bases  
(B) TYPE: Nucleic acid  
(C) STRANDEDNESS: Double  
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

50

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Rhodotorula minuta*  
(B) STRAIN: ATCC 10658

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 490

	CGTATTGATT	CGTGAGTGGC	CGTTCCCTTA	CAGCAAGCTT	ATAAAGGAGC	50
	GAAAAAGATC	TGACATTCGG	CTTATGTGCT	ATACAGAGGA	ACTCATCAAC	100
	AACGTCGCCA	AGGCTCATGG	TGGTTACTCT	GTCTTCACCG	GTGTCGGAGA	150
60	GCGAACACGT	GAAGGTAACG	ATCTCTACCA	CGAAATGATT	GAAACCGGTG	200

5

2) INFORMATION FOR SEQ ID NO: 491

## 15

- (ii) MOLECULE TYPE: Genomic DNA

20

(A) ORGANISM: *Rhodotorula mucilaginosa*  
(B) STRAIN: ATCC 66034

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 491

30

TGTCCTCATT	CAGGAGCTCA	TCAACAACAT	CGCCAAGGCC	CACGGTGGGT	50
ACTCGGTCTT	CACCGGTGTC	GGCGAGCGTA	CCCGTGAGGG	TAACGGTGAG	100
TCTCCCCCTT	CAAACCTTTT	GCCGGCTAGT	TGGCGCAGCG	CAAAC TGACG	150
CGCGCGCCCT	GTCCAGACTT	GTACCACGAG	ATGATCGAGA	CTGGTGTCAT	200
CCAGCTCGAG	AACGACAAC	CGAAGTGCGC	TCTCGTGTTT	GGCCAGATGA	250
ACGAGCCCCC	TGGTGCCCGT	GCCCGTGTCG	CTCTCACTGG	GTTCGTCCTT	300
TCTCTCTCTC	GAGCGTCCTG	GCTTGATACG	GAACGCTGAC	ACGTCACGCA	350
GTCTCACTAT	TGCTGAGTAC	TTCCGTGACG	AGGAGGGCCA	GGACGTGCTC	400
CTCTTCATCG	ACAACATCTT	CCGTTTCACC	CAGGGTGAGC	CGCCTCCGCG	450
GGCATTCTCC	CGTTTCTTTT	GCGCTGACGT	CTGTCCCCTA	TAGCCGGTTC	500
GGAGGTGTCT	GCCCTTCTCG	GACGTATCCC	GTCCGCTGTC	GGATACGAG	550
CGACTCTCTC	GACCGACATG	GGTCAGATGC	AGGAGCGTAT	CACGTAAGTT	600
TGGCCGCAGC	TCCGTCCGCG	GCGCCCTTTG	TGTCTGACCG	TGTTCCACCG	650
CTCAGCACCA	CCAAGAAGGG	CTCGATCACC	TGTGTC		686

45

## 2) INFORMATION FOR SEQ ID NO: 492

## 50

- (A) LENGTH: 625 bases  
(B) TYPE: Nucleic acid  
(C) STRANDEDNESS: Double  
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

## 55

- (A) ORGANISM: *Sporobolomyces salmonicolor*  
(B) STRAIN: ATCC 32311

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 492

60

TGTCTTGATT CAGGAGCTCA TCAACAACGT CGCCAAGGCG CACGGTGGTT 50

	ACTCCGTTTT	CACCGGTGTC	GGTGAGCGTA	CCCGTGAGGG	TAACGGTGAG	100
	CACACTTTTCG	CCGACCTGGC	CATTCCGGAA	CGTGCGGACT	GACGAGGACC	150
	ACCTCGAACA	GATCTCTACC	ACGAGATGAT	CGAGACCGGT	GTCATTTCAGC	200
	TCGACAACGA	CAAGTCGAAG	ACTGCTCTCG	TCTTCGGCCA	GATGAACGAG	250
5	CCCCCTGGCG	CCCGTGCCCC	TGTCGCTCTT	ACTGGTCTCA	CCATCGCGGA	300
	GTACTTCCGT	GACGACGAGG	GCCAGGACGT	GCTTCTCTTC	ATCGACAACA	350
	TCTTCCGTTT	CACCCAGGGT	ACGTTCCGATC	CCGCCCCGTCC	AACACGAATG	400
	TCGTGGTGAC	TGACAACCTG	TTGCGCGTGC	AGCCGGTTCG	GAGGTGTCTG	450
	CCCTTCTCGG	TCGTATCCCC	TCCGCTGTGC	GATACCAGCC	CACTCTCTCG	500
10	ACCGACATGG	GTGGCATGCA	GGAGCGTATC	ACGTACGCCC	TCTTCTGCTT	550
	TCTCTCGTTT	CGCTCTGCAT	CGCTCACGCA	TGTTTCGCCC	ACAGCACCAC	600
	CAAGAAGGGT	TCGATCACCT	GTGTC			625

15

## 2) INFORMATION FOR SEQ ID NO: 493

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1211 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

- (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Sporothrix schenckii*
- (B) STRAIN: WSA-148

30

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 493

	TCTCGTCCGT	GGTGCTAAGG	CCACTGACAC	TGGTTCCCCC	ATTACCATCC	50
	CCGTCCGCCC	CGGTACCCTC	GGTCGCATCA	TGAACGTCAC	CGGTGACCCG	100
35	ATCGACGAGC	GCGGTCCCAT	CAAGACCGAC	AAGTTCCGTC	CCATCCACGC	150
	TGAGGCTCCC	GAGTTCGTTG	ACCAGTCGAC	CACCGCTGAG	GTTCTCGTGA	200
	CTGGTATCAA	GGTCGTCGAT	CTGCTTGCTC	CCTACGCCCC	TGGTGGTAAG	250
	ATTGGTCTGT	TTGGCGGTGC	CGGTGTTGGC	AAGACCGTGT	TCATCCAGGA	300
	GCTCATCAAC	AACATCGCCA	AGGCCCACGG	TGGTTACTCC	GTCTTCACCG	350
40	GTGTCGGCGA	GCGTACCCGT	GAGGGTAACG	ATCTGTACCA	CGAAATGCAG	400
	GAGACCTCTG	TCATTCAGCT	TGACGGTGAC	TCCAAGGTCG	CCCTGGTGT	450
	CGGTCAGATG	AACGAGCCCC	CTGGTGCTCG	TGCCCGTGTC	GCCTTGACCG	500
	GTTTGACTGT	CGCTGAGTAC	TTCCGTGACG	AGGAGGGCCA	GGATGGTATG	550
	TTTTGAATTA	TTTCCTTGTC	GTACAGTTCC	AAATCGAAGA	ATTACTAACT	600
45	TGTCAGTGCT	TCTCTTCATC	GACAACATTT	TCCGCTTCAC	CCAGGCCGGT	650
	TCTGAGGTGT	CTGCCCTTCT	GGGTCGTATT	CCCTCCGCTG	TCGGTTACCA	700
	GCCCACGCTC	GCCGTGGACA	TGGGTCTGAT	GCAGGAGCGT	ATTACCACCA	750
	CCCGCAAGGG	CTCAATTACC	TCCGTCCAGG	CCGTCTACGT	GCCCGCTGAC	800
	GATCTGACGG	ATCCCGCCCC	CGCCACCACC	TTCGCCCATC	TGGACGCCAC	850
50	CACTGTGCTG	TCCCGAGGTA	TCTCTGAGCT	GGGTATCTAC	CCCGCTGTCTG	900
	ACCCCTCGA	CTCCAAGTCG	CGTATGCTGG	ACCCCGGTAT	TGTCGGTGAC	950
	GACCACTACG	AGACCGCCAC	TCGCGTCCAG	CAGATCCTCC	AAGAGTACAA	1000
	GTCGCTGCAG	GACATCATCG	CCATTCTGGG	TATGGACGAG	CTGTCTGAGG	1050
	CCGACAAGCT	TACAGTCGAG	CGTGCTCGTA	AGATCCAGCG	TTTCCTGAGC	1100
55	CAGCCGTTCA	CGGTGCGCGA	GGTCTTCACT	GGTATCGAAG	GCCAGCTGGT	1150
	CGATCTGAAG	GACACTATCG	CTTCGTTCAA	GGCTATCCTG	AGCGGTGAGG	1200
	GTGACAGCCT	T				1211

60



## 2) INFORMATION FOR SEQ ID NO: 494

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1133 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Stephanoascus ciferrii*  
 (B) STRAIN: ATCC 52550

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 494

```

TCTTGTTAGA GGCACCCAG TCAAGGACAC TGGTGCTCCA ATTACCATTC      50
CAGTTGGTAA CGGCACTTTG GGCCGTATCG TCAACGTTCT CGGTGAGCCA      100
ATTGATGAGC GTGGACCAGT CAAGGCTGAC AAGTTCAGAC CTATTCACGC      150
TGAGCCACCA ACCTTCGCTG ACCAGTCCAC CTCTGCCGAG GTTCTTGAGA      200
CCGGTATTAA GGTTGTCGAC TTGCTTGCCC CTTATGCCAG AGGTGGTAAG      250
ATTGGTCTTT TCGGTGGTGC CGGTGTCGGT AAGACTGTGT TCATTCAGGA      300
GCTTATTAAC AACATTGCTA AGGCCACCGG TGGTTACTCT GTCTTCACTG      350
GTGTCGGTGA GCGAACTCGT GAAGGTAACG ATTTGTACCA CGAAATGATG      400
GAGACCGGTG TCATCAACCT TGAGGGTGAC TCCAAGGTGT CTCTTGTGTT      450
CGGTCAGATG AACGAGCCTC CAGGAGCCCG TGCCCGTGTT GCCTTGACCG      500
GTTTGACCAT TGCCGAGTAC TTCAGAGATG AGGAGGGCCA GGATGTCCTG      550
TTGTTCATTG ACAACATTTT CCGATTCACC CAGGCCGGTT CTGAGGTCTC      600
TGCCTTGTTG GGTGCTATCC CATCTGCCGT CGGTTACCAA CCAACCTTGG      650
CTACTGATAT GGGTGGTCTT CAAGAACGTA TTACCACCAC TCAAAGGGT      700
TCCGTCACCT CTGTCCAGGC TGTCTACGTC CCAGCTGACG ATTTGACTGA      750
TCCTGCCCCA GCTACCACCT TCGCCCATTT GGACGCCACC ACCGAATTGT      800
CCCGATCTAT CTCTGAGTTG GGTATCTACC CAGCTGTCGA CCCTCTTGGT      850
TCCAAGTCCC GTCTTTTGGA TGCCTCCGTC GTCGGCCAAG AGCACTACGA      900
CGTTGCCGCC AACGTCCAAC AGACCTTGCA GGCCTACAAG TCTCTCCAGG      950
ATATCATTGC CATTTTGGGT ATGGACGAAT TGTCTGAGGC TGATAAGCTC     1000
ACTGTCGAGC GTGCTCGTAA GATGCAGAGA TTCCTTTCTC AGCCATTAC      1050
CGTCGCTGAG GTCTTCACTG GTCTCGAGGG TAGACTCGTT TCTTTGAAGG     1100
ACACCATCCG ATCCTTCAAG GAGATCCTTG ACG                        1133

```

## 2) INFORMATION FOR SEQ ID NO: 495

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 608 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Trichophyton mentagrophytes*  
 (B) STRAIN: WSA-225

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 495

```

GGAGTTGATT GTAAGTCATT TGAAACCCAG CCCAAGAAA CAGAAGCTAG      50
GCGAAAATTG GACAATTGAG CAATTTAGCC ATTGGAGAAA AGAAATTTCG      100

```

	AGTATTAATT	GTTTTTATAG	AACAACATTG	CCAAGGCTCA	CGGTGGTTAC	150
	TCTGTCTTCA	CTGGTGTCGG	AGAGCGTACC	CGTGAAGGAA	ACGATCTCTA	200
	CCATGAAATG	CAGGAGACCC	GTGTCATTCA	GCTTGATGGC	GAGTCCAAGG	250
	TCGCCCTGGT	CTTCGGCCAG	ATGAACGAGC	CCCCAGGTGC	CCGTGCCCGT	300
5	GTTGCTCTTA	CTGGTTTGAC	CATTGCTGAG	TACTTCCGTG	ATGAGGAAGG	350
	TCAAGACGGT	GAGTTTCTTA	TGGATAAAAA	AAAATTTTTT	TTTTTTTTTT	400
	TTTTTTTCAA	GAAATTCATG	TTCTAACAAA	GTGTATTCTA	GTGCTTCTCT	450
	TCATCGACAA	CATTTTCCGT	TTCACTCAGG	CTGGTTCCGA	AGTGTCTGCC	500
	CTGCTTGGTC	GTATCCCATC	TGCCGTCGGT	TACCAACCCA	CTCTTGCCGT	550
10	CGACATGGGT	GGTATGCAGG	AACGTATTAC	CACCACCAAG	AAGGGATCCA	600
	TTACCTCC					608

15 2) INFORMATION FOR SEQ ID NO: 496

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 794 bases  
 (B) TYPE: Nucleic acid  
 20 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

25 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Wangiella dermatitidis*  
 (B) STRAIN: WSA-229

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 496

30	GTTTATTCAA	GAATCATTG	TGGGTGGCAT	TCTCATAATG	TTTCGGCCAC	50
	AATTACTGAT	TGAAAATAGA	ACAACATTGC	AAAGGCTCAT	GGTGGTACT	100
	CCGTGTTCAC	TGGTGTCGGC	GAGCGAACTC	GTGAGGGTAA	CGACTTGTA	150
	CACGAAATGC	AGGAGACCTC	TGTCATTGAG	CTCGATGGCG	AGTCCAAGGT	200
35	CGCGCTGGTG	TTTGGTCAA	TGAACGAACC	TCCTGGTGCT	CGTGCTCGTG	250
	TTGCTCTGAC	TGGGTAAGTT	GTTCCTTCGC	TTCTTGCGCG	TATCCACATC	300
	CCCATCTTGA	GAATACGTCT	GCCACCATGT	CATGTGATGT	TGGGCTGGTT	350
	CTGGTTTTTG	GGAGGCCCTC	AAGTTCAATT	TTTGGATGAC	AGCACCAGCT	400
	TTACAAGATT	ATGCTAACTT	AATGGAGTCT	TACGGTGGCT	GAGTTCTTCA	450
40	GGGATGAGGA	GGGACAGGAT	GGTAAGTTTG	ATAACAATCT	CGTCGGTGTC	500
	AATATCGACG	GCGTACTCTT	CGCATCAAAA	AACCAAAGAG	GTGGTTTGGT	550
	GTGAGAAGTG	CGCCGGAAT	AATGGCAACC	ACGTGACAAT	GACCACGTGT	600
	GGGGCTCCCG	TGCTAACACG	TGACAGTCTT	GCTCTTCATC	GACAACATTT	650
	TCCGATTAC	TCAASCCGGT	TCTGARGTGT	CTGCCTTGCT	TGGTTCGTATT	700
45	CCATCTGCCG	TCGGTTACCA	ACCCACACTC	GCCGTCGACA	TGGGTCTCAT	750
	GCAGGAACGT	ATCACCACCA	CCCGGAAGGG	ATCCATCACA	TCTG	794

50 2) INFORMATION FOR SEQ ID NO: 497

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1148 bases  
 (B) TYPE: Nucleic acid  
 55 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

60 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Yarrowia lipolytica*  
 (B) STRAIN: ATCC 38295

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 497

```

5  TCTTGTCGGA GGCACCGCCG TCGCTGACAC CGGTGCTCCC ATCACTATCC      50
   CCGTCGGCCG AGGTACCCTT GGTCTGAATCA TCAACGTCTG TGGTGAGCCC      100
   ATTGACGAGC GAGGACCCAT CGAGGCTTCC AAGTACCTCC CCATCCACGC      150
   TGACCCCCCT ACCTTCGCTG AGCAGTCTAC CTCCGCTGAG GTTCTCGAGA      200
10 CCGGTATTAA GGTCTGCGAC CTCCTCGCCC CTTACGCCCC AGGTGGTAAG      250
   ATTGGTCTCT TCGGTGGTGC CGGTGTCGGT AAGACTGTCT TCATCCAGGA      300
   GCTGATTAAAC AACATTGCCA AGGCCCATGG TGGTTTCTCC GTTTTCTGCG      350
   GTGTCGGTGA GCGAACCCGA GAGGGTAACG ATCTTTACCG AGAGATGAAG      400
   GAGACTGGTG TCATCAACCT CGAGGGTGAG TCTAAGGTCA CCCTCGTCTT      450
15 CCGTCAGATG AACGAGCCTC CCGGAGCCCG TGCCCGAGTC GCCCTTACTG      500
   GTCTGACCAT TGCCGAGTAC TTCCGAGACG AGGAGGGTCA GGATGTGTTG      550
   CTCTTCGTTG ACAACATTTT CCGATTACAC CAGGCCGGTT CCGAGGTGTC      600
   CGCTCTGCTT GGTCTGAATTC CCTCCGCTGT CGGTTACCAG CCCACTCTGG      650
   CCACCGATAT GGGTGCCCTC CAGGAGCGAA TTACCACCAC CCAGAAGGGT      700
20 TCCGTCACCT CCGTCCAGGC CGTCTACGTG CCTGCCGATG ATTTGACCGA      750
   TCCTGCTCCC GCCACCACCT TCGCCCATCT TGACGCCACC ACCGTCTGT      800
   CCCGAGGTAT TTCCGAGCTG GGTATCTACC CCGCTGTCTG TCCCCTTGAT      850
   TCCAAGTCTC GACTTCTGGA TATCGATGTT GTCGGAAAGG AGCACTACGA      900
   TGTTGCTTCC AACGTCCAGC AGACCCTCCA GGCTTACAAG TCTCTCCAGG      950
25 ATATCATTGC CATTCTTGGT ATGGATGAGC TGTCCGAGCA GGACAAGCTG      1000
   ACCGTCGAGC GAGCTCGAAA GATCCAGCGA TTCCTGTCTC AGCCCTTCAC      1050
   CGTCGCCGAG GTTTTCACCG GTATTGAGGG ACGACTTGTC TCTCTCAAGG      1100
   AACTGTCCG ATCCTTCAAG GAGATCCTTG ACGGTAAGCA CGATGCTC      1148

```

30

## 2) INFORMATION FOR SEQ ID NO: 498

## (i) SEQUENCE CHARACTERISTICS:

```

35 (A) LENGTH: 966 bases
   (B) TYPE: Nucleic acid
   (C) STRANDEDNESS: Double
   (D) TOPOLOGY: Linear

```

40 (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Aspergillus fumigatus*  
 (B) STRAIN: WSA-172

45

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 498

```

   GCGCTATTGT CGTTGTTGCT GCCTCCGACG GTCAGATGTA GGTGGAACAT      50
   CTTGGGAAAT ACGTCGTAAA ACACGTCGCT TACGTTTTTC CGAATAGGCC      100
50 CCAGACTCGT GAGCATTTGC TGCTCGCCCG CCAGGTTGGT GTCCAGAAGA      150
   TCGTTGTCTT CGTCAACAAA ATCGATGCTA TTGATGATCC GGAGATGCTG      200
   GAACTGGTCG AACTCGAGAT GCGTGAGCTG CTGAACAGCT ACGGTTTCTGA      250
   GGGTGAAGAG ACTCCGATCA TTTTCGGTTC CGCTCTCTGT GCTCTCGAAG      300
   GACGCCGTGA CGACATCGGT AAAGACAGAA TTGAGCAGCT TATGAACGCT      350
55 GTCGACACCT GGATCCCCAC TCCTCAGCGT GACCTCGACA AACCTTTCTT      400
   GATGTCTGTC GAGGAAGTGT TCTCTATCGC CGGCCGTGGT ACCGTGGCTT      450
   CTGGTCGTGT CGAGCGTGTT ATCTTGAAGA AGGACTCTGA GGTGAGATT      500
   GTTGGAGGCT CCTTCGAACC CAAGAAGACC AAAGTCACCG ACATTGAAAC      550
   CTTCAAGAAG AGCTGTGATG AATCGGTGTC TGGTGACAAC TCTGGTCTCC      600
60 TCCTGCGTGG TATCCGACGT GAAGACGTCA AGCGTGGTAT GGTCATTGCT      650

```

GTTCCCGGCA	GCACCAAGGC	TCACGACAAG	TTCCTCGTCT	CCATGTACGT	700
CCTGACCGAG	GCGGAGGGTG	GTCGTCTGTAC	TGGCTTCGGT	GCCAACTACC	750
GTCCCAAGT	CTTCATCCGT	ACTGCAGGTA	AGTTCCCGCA	CACCGTGTCC	800
AGATCTTCCG	AGAGATTAGC	GATATATGCT	AATGATTCAT	CAGACGAGGC	850
5 TGCTGACCTC	AGCTTCCCTG	ACGGCGACCA	ATCTCGCAGA	GTTATGCCTG	900
GTGACAACGT	CGAGATGATC	CTGAAGACCC	ACCACCCTGT	TGCTGCTGAG	950
GCTGGTCAAC	GCTTCA				966

10

## 2) INFORMATION FOR SEQ ID NO: 499

## (i) SEQUENCE CHARACTERISTICS:

- 15 (A) LENGTH: 846 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

20

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Blastoschizomyces capitatus*  
 (B) STRAIN: ATCC 10663

25

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 499

TGGTGCTATT	ATTGTTGTTG	CTGCTTCTGA	TGGTCAAATG	CCCCAAACCC	50
GTGAGCACTT	GCTTCTTGCT	CGTCAAGTTG	GTGTTAAGCA	CATTGTTGTT	100
TTCGTTAACA	AGATTGATAC	TATTGATGAT	CCTGAAATGT	TGGAAGTTGT	150
30 CGAAATGGAA	ATGAGAGAAC	TTCTTTCTTC	TTACGGTTTT	GATGGCGATA	200
ACACCCCTGT	CATTATGGGT	TCTGCTCTCT	GTGCTCTTGA	AGGTCGTGAA	250
CCAGAAATTG	GTGAACAAAG	AATCAACCAA	CTCCTTGATG	CTATCGATGA	300
ATACATTCTT	ACCCAGTTC	GTGATATGGA	CCAACCTTTC	TTGATGCCAC	350
TTGAAGGTGT	TTTCTCTATT	CCAGGTCGTG	GTACTGTTGC	CACTGGACGT	400
35 GTCTATCGTG	GTACTTTGAA	GAGAGGTGAA	GAAGTTGAAG	TTGTTGGCTA	450
CAATGATGCT	CCAATCAAGA	CCACCGTTAC	TGGTATTGAA	ATGTTCAAGA	500
AGGAAGTTGA	TCAAGCTCAA	GCTGGTGACA	ACGCTGGTAT	TCTTTTGAGA	550
GGTGTTAAGC	GTGAAGACCT	TAAGCGTGGT	ATGGTTGTTG	CTAAACCAGG	600
TACCGTTAAG	CCACACACCA	AGTTCCTTGC	CTCCATCTAT	GTTTTGACTA	650
40 AGGAAGAAGG	TGGCAGACAC	TCTGGCTTTG	GTCTTAACTA	CAGACCTCAA	700
CTTTTCCTTG	GTTCTGCTGA	TGTTACCACT	GTCTTGACCT	TCCCAGAGGG	750
TGTTGACCAA	AGCACTCAAG	TCATGCCAGG	TGACAACACT	GAAATGGTTT	800
GCGAAGTTGT	TCACCCAGTT	GCTGTCTGAAC	AAGGCCAACG	TTTCAA	846

45

## 2) INFORMATION FOR SEQ ID NO: 500

## (i) SEQUENCE CHARACTERISTICS:

- 50 (A) LENGTH: 846 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

55

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Candida rugosa*  
 (B) STRAIN: ATCC 96275

60

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 500

	GGTGCCATTA	TTGTTGTTGC	TGCCTCTGAT	GGACAGATGC	CCCAGACCCG	50
	TGAGCATCTT	TTGCTTGCCC	GCCAAAGTCGG	TATGCAAAAG	GTCGTTGTGT	100
5	TTGTTAACAA	GATTGATACC	ATTGATGACC	CTGAAATGCT	TGATCTTGTC	150
	GAGATGGAGA	TGCGTGAAC	GTTGAATGAA	TATGACTTCG	ATGGAGATAA	200
	CTCTCCTGTC	ATTATGGGCT	CTGCTCTTGC	TGCTCTTGAG	GACAAGAACC	250
	CCGAGATTGG	TAAGGACCGT	ATCATGCAGC	TCTTGGACGC	TGTTGATGAA	300
	TGGATCCCTA	CCCCCGAGCG	TGACCTTGAC	AAGCCTTTCA	TGATGCCTAT	350
10	TGAGGCCTCT	TTCTCCATTT	CTGGTCGTGG	TACTGTTGCC	ACTGGCCGTG	400
	TCGAGCGTGG	TATTCTCAAG	AAGGGTGAGG	AAGTCGAGAT	CGTTGGTTTC	450
	AACAAGCAGC	CCCTGAAATC	TGTTGTTACT	GGTATTGAAA	TGTTCAAGAA	500
	GGAACCTTGAT	CAGGCCCAGG	GCGGTGATAA	TGCTGGTATC	TTGCTTCGTG	550
	GTATTCGTCG	TGAGGACTTG	CAGCGTGTA	TGGTTTTGGC	CAAGCCTGGA	600
15	ACTGTAAAGG	CTCACACCAA	GTTCCCTTCC	TCCATCTACG	TTCTCTCCAA	650
	GGAAGAGGGC	GGCCGTCAC	CTCCTTTCGG	TATGAACAT	CGTCCCCAGA	700
	TGTTCTGTTTC	TGCAGCTGAT	GTCACCGTTA	CTCTTACTTT	CCCTGAGGGT	750
	GTTGAACAGC	ACACTCAGGT	CTTCCCTGGT	GAGAACACCG	AGATGGTTGG	800
20	CGAGCTCGTT	CACCCTACTG	CTATTGAGGT	TGGTCAACGC	TTCAAC	846

## 2) INFORMATION FOR SEQ ID NO: 501

## 25 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 944 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

## 30 (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Coccidioides immitis*  
 (B) STRAIN: Silveira

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 501

	AGTTGTCGTC	GTTGCTGCTT	CAGACGGTCA	AATGTATGCA	ACCGAGAGCA	50
40	CTCCCCGATC	TTGGTTTAAA	TGGCACTAAT	ATAAGACAGG	CCTCAAACCTC	100
	GAGAGCATT	ACTTCTCGCC	CGTCAGATCG	GTATCCAAAA	AATCGTCGTC	150
	TTCGTGAACA	AGGTTGATGC	CATCGAGGAC	AAAGAGATGT	TGGAGCTTGT	200
	TGAATTGGAG	ATGCGTGAAC	TCCTAACCAG	CTACGGTTTC	GAGGGTGAAG	250
	AAACTCCCAT	CATTTTTTGGC	TCTGCTCTCT	GTGCCCTCGA	AGGAAGACAA	300
45	CCCGAGATCG	GTGTTACCAA	GATTGATGAG	CTCTTGCAGG	CCGTCGACAC	350
	CTGGATTCCC	ACTCCTCAGC	GTGAGACTGA	CAAGCCCTTC	TTGATGTCCA	400
	TTGAGGAAGT	GTTCTCTATT	TCCGGACGAG	GAACCGTTGT	CTCCGGCCGT	450
	GTGGAGCGTG	GTATCCTCAA	GAAGGACTCC	GAAGTTGAAA	TTGTCGGCGG	500
	TTCGCCCGAG	CCAATCAAAA	CCAAGGTTAC	CGATATCGAA	ACCTTTAAGA	550
50	AGTCTTGCGA	CGAGTCTCGC	GCTGGTGATA	ACTCCGGCTT	GCTCCTACGA	600
	GGCGTTAAGC	GTGAAGATAT	TAGCCGTGGC	ATGGTCGTCG	CTGTACCAGG	650
	AAGTGTC AAG	GCCCATACTG	AATTCTTAGT	TTCGCTTTAC	GTCCTCACCG	700
	AAGCTGAGGG	TGGGCGCAAA	TCTGGATTCA	GCAGCAAGTA	CCGCCCACAG	750
	ATGTTTCATC	GCACTGCCGG	TATGTAATAC	TGTGATAATT	TCGTTGACAT	800
55	GGTACTGATT	GAATTCTATA	GACGAAGCGG	CTCAGCTCAG	CTGGCCCCGA	850
	GAAGATCAAG	ACAAGATGGC	TATGCCAGGA	GACAATATCG	AAATGATTTG	900
	CACCACCTTG	CACCCAGTTG	CCGCCGAGGC	TGGCCAGCGA	TTCA	944

## 2) INFORMATION FOR SEQ ID NO: 502

## (i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 849 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Fusarium oxysporum*  
 (B) STRAIN: WSA-212

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 502

10  
 20  
 25  
 30  
 35

GCTATCATCG	TCGTTGCTGC	CTCCGATGGA	CAGATGCCCC	AGACCCGTGA	50
ACACTTGCTC	CTCGCTCGTC	AGGTCGGTGT	CCAGCGAATT	GTCGTCTTCG	100
TCAACAAGGT	CGATGCCATT	GATGACCCCG	AGATGCTTGA	GCTCGTCGAG	150
ATGGAGATGC	GCGAGCTTCT	TAACACCTAC	GGCTTCGAAG	GCGACGACAC	200
TCCCGTCATC	ATGGGCTCTG	CTCTTATGTC	TCTCCAGAAC	CAGCGCCCCG	250
AGATTGGCAC	CGAGAAGATC	GATGAGCTCC	TTGCTGCCGT	CGACGAGTGG	300
ATCCCAACCC	CCGAGCGTGA	CCTTGACAAG	CCCTTCCTTA	TGTCCGTCGA	350
GGATGTCTTC	TCCATTGCCG	GCCGTGGTAC	CGTCGTGTCT	GGCCGTGTGG	400
AGCGTGGTAT	TCTGAAGCGT	GATCAGGAGA	TCGAGCTTGT	CGGAAAGGGG	450
CAGGAGGTTA	TCAAGACCAA	GGTTACCGAC	ATTGAGACCT	TCAAGAAGTC	500
TTGTGAGCAG	TCCCAGGCTG	GTGACAACCT	TGGTCTCCTC	ATCCGAGGTG	550
TTCGCCGTGA	GGATGTCCGC	CGTGGTATGG	TTGTCTGCGC	TCCTGGCACC	600
GTCAAGTCTC	ATACCCAGTT	TCTCGCTTCC	CTCTACGTCC	TCACCAAGGA	650
GGAGGGTGGC	CGACACACCG	GTTTCCAGGA	GCACTACCGA	CCCCAGCTCT	700
ATCTCCGAAC	TGCAGATGAG	TCCATTGACC	TGACTTTCCC	CGAGGGTACT	750
GAGGATGCCT	CCAGTAAGAT	GGTCATGCCT	GGTGACAACA	CCGAGATGGT	800
TGTCACCATG	GGTCACCCCA	ATGCCATCGA	GGTTGGTCAG	CGATTCAAC	849

## 2) INFORMATION FOR SEQ ID NO: 503

## (i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 1064 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Histoplasma capsulatum*  
 (B) STRAIN: G186A5

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 503

55  
 60

TGGTGCTATT	GTCGTTGTTG	CTGCTGCTGA	CGGCCAAATG	TAAGACGCCG	50
CGAGGGACTG	CTGAGGGTTT	TATGCTTTTT	AGGCCCCCTT	GTTTCTGAGA	100
GCATGATGAT	ACTAATATTC	GGAAACGTAT	CTATTAGGCC	TCAAACACGT	150
GAGCATTTCG	TCCTTGCCCG	ACAGGTCGGT	GTCCAAAAGA	TCGTCGTTTT	200
CGTGAACAAA	GTCGACGCCC	TTGAGGACAA	GGAGATGTTG	GAGCTTGTCG	250
AGTTAGAAAT	GAGAGAGCTC	TTAAACACCT	ACGGCTTCGA	GGGTGAAGAG	300
ACACCCATCA	TCTTTGGTTC	TGCCCTTTGC	GCCATGGAAG	GCCGTGAGCC	350
TGAGTTGGGA	GAAAAGAAAA	TTGATGAATT	GCTGGAGGCT	GTTGATACTT	400

	GGATCCCCAC	ACCACAACGT	GATACCGAAA	AACCTTTCTT	GATGTCCGTT <sup>1</sup>	450
	GAGGAAGTAT	TCTCTATCTC	CGGCCGTGGA	ACCGTTGCCT	CCGGTCGTGT	500
	TGAGCGCGGT	GTCCTCAAGA	AGGATTGAGA	AGTCGAGCTA	ATTGGGGGCG	550
	GCTCCACCCC	CATCAGGACG	AAGGTAAGTG	ATATCGAAAC	TTTCAAGAAA	600
5	TCCTGTGACG	AGTCTAGAGC	TGGGGACAAC	TCCGGTCTTT	TATTGCGTGG	650
	TATCAAGCGT	GAAGATATCC	GCCGTGGTAT	GGTAGTTGCC	GTTCTGGCA	700
	GCGTCAAGGC	CCACGACAAG	TTCTTGGTGT	CGATGTATGT	CCTGACCGAA	750
	GCTGAGGGTG	GTCGCCGAAC	CGGATTCCGC	CAGAACTATC	GTCTCAAAT	800
	GTTTCATCCGC	ACAGCTGGTA	TGTCAAAATG	GGACCCCTTT	TCATAATCCT	850
10	TTCTTTTTTT	CCTTTTCCTC	TCTATCTCTC	TTTCTGTTTC	CTTTCAACTC	900
	GCCTGATTCA	CGAAATTAAC	TAACCCGTTT	GATTATAGAC	GAAGCCGCCC	950
	ATCTCAGCTT	CCCTAGTGGA	GCAGATGAAA	GCAAACCTCGT	TATGCCTGGT	1000
	GACAACGTCG	AGATGATCCT	CCAGACACAC	CGCCCCGTGG	CTGCTGAGGC	1050
15	CGGCCAGCGA	TTCA				1064

## 2) INFORMATION FOR SEQ ID NO: 504

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 982 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Paracoccidioides brasiliensis*

(B) STRAIN: ATCC 32071

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 504

	TGGTGCTATC	GTCGTTGTTG	CTGCCTCTGA	CGGCCAAATG	TAGGGATTTT	50
35	GCAAGACTGG	TGAAAAAATC	TAAAGAAAAT	AGAAAAGATT	GTGCTGATGT	100
	TTGGTATCAG	CCCCCAAACA	CGCGAGCATC	TGCTTCTTGC	CAGACAAGTC	150
	GGTGTTTACA	AAATCGTTGT	TTTCGTCAAC	AAGGTCGATG	CTGTAGAGGA	200
	TAAGGAGATG	TTGGAGCTTG	TCGAATTGGA	GATGAGAGAG	CTCTTGACCA	250
	CCTATGGGTT	CGAGGGTGAG	AAGACACCTA	TCATCTTTGG	TTCTGCGCTC	300
40	TGTGCTATGG	AGGGCCGTCA	GCCCGAGTTG	GGAGAGCAGA	AAATTGATGA	350
	ATTACTCGAG	GCTGTGGATA	CTTGGATCCC	TACGCCACAG	CGTGATACTG	400
	ACAAGCCCTT	CCTGATGTCC	ATTGAGGAGG	TGTTCTCTAT	CTCTGGACGA	450
	GGAACCGTTG	CCTCCGGCCG	CGTTGAGCGT	GGTATCCTCA	AGAAGGACTC	500
	CGAAGTTGAA	ATTATTGGCG	GCGGTGTTCC	CACAATCCTG	ACCAAGGTGA	550
45	CTGATATCGA	AACCTTCAAG	AAGTCTTGCG	ACGAGTCCAG	AGCCGGGGAC	600
	AACTCCGGCC	TCTTGTTGCG	CGGTGTCAAG	CGTGAGGATA	TCCGCCGTGG	650
	TATGGTCGTT	GCAGTTCCCG	GAAGCGTCAA	AGCACATGAC	AGATTCTTGG	700
	TGTCGATGTA	CGTTCTGACC	GAGGCTGAGG	GTGGTCGCCG	CACTGGCTTC	750
	GGTCAGAACT	ATCGTCCTCA	AATGTTTCATC	CGCACAGCTG	GTACGTTTCAT	800
50	TCTTTCACTA	TATTCCTATA	TGCATAGCCC	GATCCTCCCA	TTAACTAATT	850
	GACACAGACG	AGGCTGCTGA	ACTCAGCTGG	CCTGATGGAG	ACGACGAAGC	900
	CAAAATGGTC	ATGCCCGGTG	ACAATGTTGA	AATGGTCCTG	AAGTCACACC	950
	GCCCCGGGGCC	GCTGAGGCTG	GACAGCGATT	CA		982

## 2) INFORMATION FOR SEQ ID NO: 505

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 931 bases

(B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

5 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Penicillium marneffe*

(B) STRAIN: ATCC 58950

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 505

	CGCTGTTGTT	GTCGTCGCTG	CTTCTGATGG	TCAAATGTAA	CATATCCACG	50
	AGCTGCCAAT	TATGGACACT	GCTGATAAGA	ATAGGCCCCA	AACCCGTGAG	100
15	CACTTGCTCC	TCGCCCCTCA	GGTCGGTGTT	CAAAAGATCG	TCGTCTTCGT	150
	CAACAAGGTT	GATGCCGTCG	AGGACCCCGA	GATGTTGGAA	CTTGTCGAAT	200
	TGGAAATGCG	TGAACTCTTG	ACCACCTACG	GTTTCGAGGG	TGAAGAGACC	250
	CCTATCATT	TCGGATCCGC	TCTTTGCGCC	TTGGAAGGCC	GCAAGCCCGA	300
	GATTGCGGAA	CAGAAGATTG	ACGAGCTCAT	GAACGCCGTT	GATACCTGGA	350
20	TCCCCACCCC	CCAGCGTGAC	CTTGACAAGC	CCTTCTTGAT	GTCCGTTGAG	400
	GAAGTTTTCT	CCATCTCTGG	TCGTGGTACC	GTTGCATCTG	GTCGTGTTGA	450
	GCGTGGTATT	TTGCGCAAGG	ATTCTGAGGT	TGAGATTATC	GGATACCAGA	500
	AGAACCCTAT	CAAGACCAAG	GTTACCGACA	TTGAGACCTT	CAAGAAGTCT	550
	TGCGATGAAT	CTCGTGCTGG	TGACAACTCT	GGCTTGCTTC	TCCGTGGTAT	600
25	CAAGCGTGAG	GACATTCGTC	GTGGTATGGT	TATCGCTGCT	CCTGGAACCA	650
	CCAAGGCTCA	TGACAACTTC	TTGGTCTCCA	TGTATGTCTT	GACTGAGGCT	700
	GAAGGTGGTC	GTCGTACTGG	ATTGCGCGCC	AACTACCGTC	CTCAAGCTTT	750
	CATCCGTACT	GCCGGTATGT	TCCCTTTCAA	AGTCAATTAA	TGAGCGATTT	800
	GCTAACGAGT	TATAGATGAG	GCTGCTACTC	TCAGCTTCCC	CGGTGACGAT	850
30	CAGTCCAAGC	AGGTCATGCC	CGGTGACAAC	GTTGAGATGA	TCTTGAAGAC	900
	ACACCGTCCC	GTTGCCGCCG	AAGCTGGTCA	G		931

35 2) INFORMATION FOR SEQ ID NO: 506

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 846 bases

(B) TYPE: Nucleic acid

40 (C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

45 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Pichia anomala*

(B) STRAIN: ATCC 18205

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 506

50	TGGTGCTATT	ATTGTTGTTG	CTGCTTCTGA	TGGTCAAATG	CCTCAAACCA	50
	GAGAACATTT	RTTATTGGCT	AGACAAGTTG	GTGTTCAACA	CATTGTTGTC	100
	TTTGTTAACA	AAGTTGATAC	TATTGATGAC	CCAGAAATGT	TGGAATTAGT	150
	TGAAATGGAA	ATGAGAGAAT	TGTTAAGTAC	TTATGGTTTT	GATGGTGATA	200
55	ACGTCCCAGT	TGTTATGGGT	TCTGCTTTAT	GTGCCTTGGA	AGGTCGTGAA	250
	GAAGAAATTG	GTGTCAAAGC	TATTGATAAA	TTATTAGCTG	CTGTTGATGA	300
	ATATATCCCA	ACCCACAAA	GAGATTTAGA	AAAACCATT	TTGATGGGTG	350
	TTGAAGATGT	CTTYTCAATC	TCAGGTAGAG	GTACCGTTGT	TACTGGTCGT	400
	GTTGAACGTG	GTAACCTGAA	GAAAGGTGAT	GAAGTTGAAA	TTGTTGGTTT	450
60	AAACAAAAC	CCATTGAAAA	CTACTGTYAC	NGGTATTGAA	ATGTTCAAAA	500



	AAGAATTGGA	CCAAGCTATG	GCTGGTGATA	ACTGTGGTAT	CTTATTACGT	550
	GGTATCAAAA	GAGATGACAT	YAAAAGAGGT	ATGGTTATTG	CTAAAACCGG	600
	TACCATCTCW	GCTCACACTA	AATTCTTAGC	CTCAATGTAT	ATTTTGACTA	650
	AAGAAGAAGG	TGGTCGTCAC	TCAGGTTTTG	GTGAACATTA	CAGACCTCAA	700
5	TTATTCATCA	GAAGTGGTGA	TGTTACCGTT	GTTTTAACCT	TYCCAGAAGG	750
	TGGTGATTCA	TCTCAACAAA	TCTTACCAGG	TGACAATGTC	GAAATGGTTT	800
	GTGAATTGGT	TCACCCAAC	GCTTTAGAAG	CTGGTCAAAG	ATTCAA	846

10

## 2) INFORMATION FOR SEQ ID NO: 507

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 964 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

20

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Trichophyton mentagrophytes*  
 (B) STRAIN: WSA-225

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 507

	GGAGCTGTTG	TCGTTGTCGC	AGCTTCTGAC	GGTCAAATGT	AATTGAATGC	50
	CCGCCCAGAC	GGATGAAAGG	ATTTGACGTT	TCTAACATCA	GTCTAGGCCT	100
	CAGACCAGAG	AACATTTGCT	CCTTGCCCGC	CAGGTCGGTG	TCCAGAAGCT	150
30	GGTCGTTTTT	GTTAACAAGG	TCGATGCCGT	TGAGGACCCA	GAGATGTTGG	200
	AGCTTGTCGA	ACTTGAAATG	CGTGAAGTCC	TCAGCCACTA	CAGTTTTGAG	250
	GGTGAGGAGA	CCCCCATCAT	TTTTGGCTCT	GCTCTCTGTG	CCCTCGAGTC	300
	CCGTCGACCT	GAGCTTGGTG	TCGAGAAGAT	TGACGAGCTA	TTGAACGCCG	350
	TCGACACCTG	GATCCCCACC	CCCGAGCGCG	CCACTGATAA	GCCTTTCCTC	400
35	ATGTCCATTG	AGGAAGTGTT	CTCTATCTCT	GGTCGTGGTA	CCGTCGTCTC	450
	CGGTCGTGTT	GAGCGTGGTA	TCCTCAAGAA	GGATTCCGAC	GTCGAAATTG	500
	TTGGTGGCTC	TACCACCCCT	ATCAAGACCA	AGGTCACAGA	TATCGAAACC	550
	TTCAAGAAGT	CCTGCGATGA	ATCTCGAGCT	GGTGACAACT	CTGGTCTCCT	600
	TCTCCGAGGT	ATCAAGCGTG	AGGACTTGAA	GCGTGGAATG	GTTGTTGCTG	650
40	CCCCCGGATC	CACCAAGGCT	CACACCGACT	TCATGGTCTC	CCTCTACGTC	700
	CTGACTGAGG	CTGAGGGTGG	TCGTTCCAAC	GGCTTCACCC	ACAAGTACCG	750
	CCCTCAAATG	TTCATCCGTA	CTGCTGGTAT	GTAACCAAAG	TTTCCGCTAT	800
	TTACTAAGTA	GATCATTGCT	AACTTGATTT	CCCTTCCGTA	GACGAAGCCG	850
	CATCTTTTCA	CTGGCCTGGA	GAAGACCAAG	ACAAGAAGGC	TATGCCTGGT	900
45	GACAACGTCG	AGATGATTTG	CAAAACCCTC	CACCCCATTG	CTGCCGAGGC	950
	TGGCCAACGA	TTCA				964

## 50 2) INFORMATION FOR SEQ ID NO: 508

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 844 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

## 60 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Yarrowia lipolytica*

(B) STRAIN: ATCC 38295

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 508

5  
GGTGCTATCA TTGTCGTTGC TGCTGGAGAC GGTTC CAAGC CCCAGACCCG 50  
AGAGCATCTG CTGCTTGCTC GACAGGTCGG TGTCCAGAAC CTGGTTGTGT 100  
TTGTTAACAA GGTTGATCAG ATTGATGATA AGGAGATTCT TGAGCTCGTT 150  
GACATGGAGA TGCAGATCT GCTGACCCAG TACGGTTTTG ATGGTGACAA 200  
10 CACCCCCGTT GTCATGGGCT CTGCTCTGTG CGCTCTTGAG GGCAAGCAGA 250  
AGGATATTGG AGAGGACGCC ATCATGGCCC TTATGGATGC CGTTGATGAG 300  
CACATCCCTA CCCCTAACCG TGACCTTGAG AAGCCCTTCC TGATGCCCGT 350  
TGAGGACGTT TTCTCCATCT CTGGCCGAGG AACTGTTGTT ACTGGCCGAG 400  
TCGAGCGAGG AAACCTGAAG AAGGGTGAGG AAATCGAGAT TGTTGGCTAC 450  
15 AACAACAAGC CCATCAAGGC TGTGTTTACC GGTATTGAGA TGTTCAAGAA 500  
GGAGCTCGAG TCCGCCATGG CCGGTGACAA CGCCGGTATC CTGCTCCGAG 550  
GTATCAAGCG AGACGAGATC AAGCGAGGTA TGGTCATGTG CAAGCCTGGC 600  
ACCGTCAACG CCCACACCAA GTTCCTTGCT TCTCTTTACA TCATCCCCAC 650  
CGAGGAGGGT GGTCAACCA GCTCTTTCGG CGCCAACCTAC CGACCCAGAG 700  
20 TGTTTCATCCG AACTTCTTCC GTCACCGCCA CTCTCACCTT CCCCAGGGGT 750  
ACCGACGAGT CCCAGACCGT CAACCCCGGT GACAACACTG AGATGGTTCT 800  
CGAGCTTGTT CACCCTACCG CCATTGAGGT CAACCAGCGA TTCA 844

25  
2) INFORMATION FOR SEQ ID NO: 509

## (i) SEQUENCE CHARACTERISTICS:

30 (A) LENGTH: 1067 bases  
(B) TYPE: Nucleic acid  
(C) STRANDEDNESS: Double  
(D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

35 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Babesia bigemina*  
(B) STRAIN: Suarez-2

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 509

CTTGGACAAG CTGAAGAGCG AGCGTGAGCG TGGTATCACC ATTGACATTA 50  
CCCTGTGGAA GTTCGAAACT GGCAAGTACT ACTACACCGT CATTGACGCC 100  
CCCGGTCACC GTGACTTCAT TAAGAACATG ATTACGGGTA CCTCCCAGGC 150  
45 CGATGTTGCT ATGCTTGTCG TGCCCGCCGA GGCTGGTGGT TTCGAAGCTG 200  
CCTTCTCTAA GGAAGGTCAG ACCCGTGAGC ACGCTCTTTT GGCCTTCACC 250  
CTTGGTGTC AAGCAGATCAT TTGCGCCATC AACAAGATGG ACAAGTGCGA 300  
CTACAAGGAG GACCGTTACA GCGAAATCCA GAAGGAAGTT CAGGGTTACC 350  
TGAAGAAGGT CGGTTACAAC ATCGAGAAGG TGCCTTTCGT CGCCATCTCC 400  
50 GGTTTCATGG GTGACAACAT GGTTGAGCGC TCCACCAACA TGCCGTGGTA 450  
CAAGGGCAAG ACCTTGGTCG AGGCCCTCGA CATGATGGAG CCCCCGAAGA 500  
GGCCCGTCGA CAAGCCCTTG CGTCTTCCCC TCCAGGGTGT GTACAAGATC 550  
GGTGGTATCG GTACCGTCCC TGTCGGTTCG GTGGAGACTG GTCAGCTCAA 600  
GGCCGGTATG GTCCTCACCT TCGCCCCCAA CCCGATCACT ACTGAGTGCA 650  
55 AATCCGTCGA AATGCACCAC GAAGTTATCG ATGTTGCCAG CCCTGGTGAC 700  
AACGTTGGTT TCAACGTGAA GAACGTGTCC ACCTCTGACA TCCGCACTGG 750  
TCACGTCGCT TCTGACTCCA AGAACGACCC CGCCAAGGCC GCCGTGTCTT 800  
TCACCGCCCA GGTGATCATC TTGAACCACC CTGGTACCAT CAAGGCCGGT 850  
TACTCCCTTG TGGTTGACTG CCACACTGCC CACATCTCGT GCAAATTCGA 900  
60 CGAGATCACC AGCCGTATGG ACAAGCGTAC CGTAAGGCC CTTGAGGAGA 950

ACCCCAAGAC	CATCAAGAAC	GGCGACGCCG	CTATGGTCGT	CCTGAAGCCG	1000
TGCAAGCCCA	TGGTCGTCGA	GGCCTTCACT	GAATACGCTC	CCCTTGGTCTG	1050
TTTCGCCCGT	CGTGACG				1067

5

## 2) INFORMATION FOR SEQ ID NO: 510

## (i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 1049 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

15 (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Babesia bovis*  
 (B) STRAIN: Suarez-3

20

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 510

GTGAACGTGA	ACGTGGTATT	ACTATTGATA	TTACCTTATG	GAAGTTCGAG	50
ACCACCAAGT	ACTACTACAC	CGTCATTGAT	GCCCCTGGTC	ACCGTGACTT	100
25 CATCAAGAAC	ATGATTACGG	GTACTTCTCA	AGCCGATGTT	GCTATGCTTG	150
TTGTACCAGC	TGAGGCTGGT	GGTTTCGAGG	CCGCTTCTC	CAAGGAAGGA	200
CAGACCCGTG	AGCACGCTCT	TTTGCTTTC	ACCCTTGGTG	TCAAACAGAT	250
CATCTGTGCC	ATTAACAAGA	TGGACAAGTG	CGACTACAAG	GAGGACCGTT	300
ACAGTGAAAT	CCAGAAGGAA	GTCCAGGGTT	ACCTCAAGAA	GGTCGGTTAC	350
30 AATATTGAGA	AGGTGCCCTT	CGTTGCCATC	TCCGGTTTCA	TGGGAGACAA	400
CATGGTTGAG	CGTTCCACCA	ACATGCCCTG	GTATAAGGGA	AAGACATTGG	450
TCGAGGCCCT	TGATCAGATG	GAACCCCCAA	AGAGGCCCGT	TGACAAGCCA	500
CTTCGTCTTC	CCCTCCAGGG	TGTCTACAAG	ATCGGTGGTA	TCGGTACCGT	550
CCCCGTCGGT	CGTGTTGAAA	CTGGTATGTT	GAAGGCTGGT	ATGATTCTAA	600
35 CCTTTGCTCC	TAACCCAATC	ACCACTGAAT	GCAAATCCGT	TGAAATGCAC	650
CACGAAACCG	TTGAGGTTGC	TTACCCCGGT	GACAACGTCG	GTTTCAACGT	700
AAAGAACGTT	TCTACTTCTG	ACATTCGCAG	TGGTCACGTT	GCCTCTGATT	750
CTAAGAACGA	CCCTGCCAAG	GCTGCTGTTT	CCTTCACTGC	CCAGGTCATT	800
GTGCTCAACC	ACCCTGGTAC	CATTAAGGCC	GGTTACTGCC	CCGTCGTCGA	850
40 TTGCCACACC	GCTCACATTT	CATGTAAATT	CGAAGAGATC	ACCAGCCGTA	900
TGGACAAGCG	TACCGGTAAA	TCTCTTGAGG	AAAACCCCAA	GACCATCAAG	950
AACGGTGACG	CTGCCATGGT	TGTGCTCAAG	CCAATGAAGC	CCATGGTTGT	1000
CGAATCCTTC	ACTGAGTATG	CTCCTCTGGG	TCGTTTCGCT	GTTTCGTGAC	1049

45

## 2) INFORMATION FOR SEQ ID NO: 511

## (i) SEQUENCE CHARACTERISTICS:

- 50 (A) LENGTH: 1070 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

55 (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Crithidia fasciculata*  
 (B) STRAIN: ATCC 11745

60

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 511

	TGGACAAGCT	GAAGGCGGAG	CGCGAGCGCG	GTATCACGAT	CGATATTGCC	50
	CTGTGGAAGT	TCGAGTCGCC	CAAGTCCGTG	TTCACGATCA	TCGATGCCCC	100
5	CGGCCACCGC	GACTTTCATCA	AGAACATGAT	CACCGGCACC	TCCCAGGCCG	150
	ATGCCGCCAT	TCTGATGATT	GACTCGACCC	AGGGTGGCTT	CGAGGCTGGC	200
	ATCTCCAAGG	ACGGCCAGAC	CCGCGAGCAC	GCCCTGCTTG	CCTTCACGCT	250
	GGGCGTGAAG	CAGATGGTTG	TGTGCTGCAA	CAAGATGGAC	GACAAGACGG	300
	TGCAGTACGC	CCAGGCCCGC	TACGAGGAGA	TCAGCAAGGA	GGTCGGCGCG	350
10	TACCTGAAGC	GCGTGGGCTA	CAACCCGGAG	AAGGTGCGCT	TCATCCCGAT	400
	CTCGGGCTGG	CAGGGCGACA	ACATGATCGA	GAAGTCCGAC	AACATGTCGT	450
	GGTACAAGGG	TCCCACGCTG	CTGGAGGCGC	TCGACCTGCT	GGAGGCCCCC	500
	GTGCGTCCGG	TGGACAAGCC	GCTGCGCCTG	CCCCTGCAGG	ACGTGTACAA	550
	GATCGGCGGT	ATCGGCACTG	TGCCCCGTGGG	CCGTGTGGAG	ACCGGCGTGA	600
15	TGAAGCCGGG	CGACGTTGTG	GTGTTGCGCG	CTGCCAACGT	GACGACCGAG	650
	GTGAAGTCGA	TCGAGATGCA	CCACGAGCAG	CTGGCTGAGG	CCGTGCCCGG	700
	CGACAACGTG	GGCTTCAACG	TGAAGAACGT	GTCCGTGAAG	GATATCCGCC	750
	GTGGTAACGT	GTGCGGCAAC	ACGAAGAGCG	ACCCCCGAA	GGAGGCGGCC	800
	GACTTCACTG	CCCAGGTGAT	CGTGCTGAAC	CACCCCGGCC	AGATCAGCAA	850
20	CGGCTACGCG	CCGGTGCTGG	ACTGCCACAC	GAGCCACATC	GCGTGCAAGT	900
	TCGCGGACAT	CGAGTCCAAG	ATCGACCGCC	GCTCTGGCAA	GGAGCTGGAG	950
	AAGAGCCCGA	AGGCCATCAA	GTCCGGCGAT	GCGGCCATCG	TGAAGATGAT	1000
	CCCGCAGAAG	CCGATGTGCG	TGGAGGTGTT	CAACGACTAC	CCGCCGCTGG	1050
25	GCCGCTTCGC	TGTCCGCGAT				1070

## 2) INFORMATION FOR SEQ ID NO: 512

- 30 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1052 bases
  - (B) TYPE: Nucleic acid
  - (C) STRANDEDNESS: Double
  - (D) TOPOLOGY: Linear
- 35 (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
- (A) ORGANISM: *Entamoeba histolytica*
  - (B) STRAIN: HM1-IMMS
- 40

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 512

	GCTGAAAGAG	AAAGAGGAAT	TACTATTGAT	ATTTTCATTAT	GGAAATTTCGA	50
45	AACATCTAAA	TACTACTTCA	CTATTATTGA	TGCCCCAGGT	CAYAGAGATT	100
	TCATTAAGAA	CATGATTACT	GGAAC TTCAC	AAGCTGATGT	TGCCATCCTT	150
	ATTGTTGCTG	CTGGTACTGG	WGAATTTGAA	GCTGGTATTT	CAAAGAATGG	200
	ACAAACCAGA	GAACAYATTC	TTCTTTTCATA	CACCTTTGGA	GTAAACAAA	250
	TGATTGTTGG	WGTTAACAAG	ATGGATGCTA	TTCAATATAA	ACAAGAAAGA	300
50	TATGAAGAAA	TTAAGAAAGA	AATTAGTGCA	TTCTTAAGA	AGACWGGATA	350
	TAATCCAGAC	AAGATTCCAT	TTGTCCCAAT	TTCAGGATTC	CAAGGAGATA	400
	ATATGATTGA	ACCATCAACC	AACATGCCAT	GGTACAAAGG	ACCAACATTA	450
	ATTGGAGCAC	TTGATTCAAG	CACACCACCA	GAAAGACCAG	TTGATAAACC	500
	ACTTAGACTT	CCACTTCAAG	ATGTTTAYAA	GATTTTCAGGT	ATTGGAAGCTG	550
55	TACCATGTGG	AAGAGTTGAA	ACTGGAGTTC	TTAGACCAGG	AACTATTGTT	600
	CAATTTGCAC	CATCAGGAGT	TTCATCTGAA	TGTAAATCAG	TTGAAATGCA	650
	TCACACAGCA	CTTGCTCAAG	CTATTCCAGG	TGATAATGTT	GGATTCAATG	700
	TTAGAAAYTT	AACAGTTAAA	GATATTAAGA	GAGGAAATGT	AGCATCAGAT	750
	GCTAAGAATC	AACCAGCTGT	TGGATGTGAA	GATTTCACTG	CTCAAGTCAT	800
60	TGTCATGAAC	CATCCAGGAC	AAATTAGAAA	GGGATATACA	CCAGTTCTTG	850

ATTGCCATAC	ATCACACATT	GCATGTAAAT	TCGAAGAATT	ATTAAGCAAG	900
ATTGATAGAA	GAACAGGTAA	ATCCATGGAA	GGAGGAGAAC	CAGAATATAT	950
TAAGAATGGA	GATTCAGCAC	TTGTTAAGAT	TGTTCCAAC	AAACCACTTT	1000
GTGTTGAAGA	ATTTGCTAAA	TTCCACCAT	TGGGAAGATT	TGCTGTTAGA	1050
5 GA					1052

## 2) INFORMATION FOR SEQ ID NO: 513

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1082 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Giardia lamblia*  
 (B) STRAIN: Faubert-1

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 513

25	GACGAGCGCG	AGCGCGGGAT	CACGATCAAC	ATCGCGCTCT	GGAAGTTCGA	50
	GACGAAGAAG	TACATCGTCA	CGATCATCGA	CGCCCCGGGC	CACCGCGACT	100
	TCATCAAGAA	CATGATCACG	GGGACGTCCC	AGGCCGACGT	CGCGATCCTC	150
	GTCGTCGCGG	CGGGCCAGGG	CGAGTTCGAG	GCCGGGATCT	CGAAGGACGG	200
	CCAGACGCGC	GAGCACGCGA	CCCTTGCGAA	CACGCTCGGG	ATCAAGACGA	250
30	TGATCATCTG	CGTCAACAAG	ATGGACGACG	GCCAGGTCAA	GTACTCGAAG	300
	GAGCGCTACG	ACGAGATCAA	GGGCGAGATG	ATGAAGCAGC	TCAAGAACAT	350
	CGGCTGGAAG	AAGGCCGAGG	AGTTCGACTA	CATCCCGACG	TCCGGCTGGA	400
	CCGGGGACAA	CATCATGGAG	AAGTCCGACA	AGATGCCCTG	GTACGAGGGC	450
	CCGTGCCTGA	TCGACGCGAT	CGACGGGCTC	AAGGCCCCGA	AGCGCCCGAC	500
35	CGACAAGCCC	CTCCGCCTCC	CGATCCAGGA	CGTCTACAAG	ATCTCGGGCG	550
	TCGGGACCGT	CCCCGCGGGC	CGCGTCGAGA	CGGGCGAGCT	CGCGCCCGGG	600
	ATGAAGGTCG	TCTTCGCCCC	GACGTCCCAG	GTCTCGGAGG	TCAAGTCCGT	650
	CGAGATGCAC	CACGAGGAGC	TCAAGAAGGC	CGGGCCCGGG	GACAACGTCG	700
	GCTTCAACGT	CCGCGGGCTC	GCCGTCAAGG	ACCTCAAGAA	GGGCTACGTC	750
40	GTCGGGGACG	TGACGAACGA	CCCGCCCGTC	GGCTGCAAGA	GCTTCACCGC	800
	CCAGGTCATC	GTCAATGAAC	ACCCGAAGAA	GATCCAGCCC	GGCTACACGC	850
	CCGTCAATCG	CTGCCACACC	CGCGACATCG	CGTGCCAGTT	CCAGCTCTTC	900
	CTCCAGAAGC	TCGACAAGCG	CACGCTCAAG	CCCGAGATGG	AGAACCCGCC	950
	CGACGCAGGC	CGCGGCGATT	GCATCATCGT	CAAGATGGTC	CCCCAGAAGC	1000
45	CCCTGTGCTG	CGAGACGTTT	AACGACTACG	CGCCCCTCGG	CCGCTTCGCC	1050
	GTCCGCGACA	TGCGCCAAAC	CGTTGCCGTC	GG		1082

## 2) INFORMATION FOR SEQ ID NO: 514

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1098 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Leishmania tropica*

(B) STRAIN: ATCC 30816

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 514

5  
 ACGCGTGGGT GCTCGACAAG CTGAAGGCGG AGCGCGAGCG CGGCATCACG 50  
 ATCGACATTG CGCTGTGGAA GTTCGAGTCG CCCAAGTCCG TGTTACGAT 100  
 CATCGATGCG CCCGGCCACC GCGACTTCAT CAAGAACATG ATCACGGGCA 150  
 CGTCGCAGGC GGACGCCGCC ATCCTGATGA TCGACTCGAC GCATGGTGGC 200  
 10 TTCGAGGCTG GCATCTCGAA GGACGGCCAG ACCCGCGAGC ACGCGCTGCT 250  
 TGCCTTCACT CTTGGCGTGA AGCAGATGGT GGTGTGCTGC AACAAGATGG 300  
 ACGACAAGAC GGTGACGTAC GCGCAGTCGC GCTACGATGA GATCAGCAAG 350  
 GAGGTGGGCG CGTACCTGAA GCGCGTGGGC TACAACCCGG AGAAGGTGCG 400  
 CTTTCATCCCG ATCTCGGGCT GGCAGGGCGA CAACATGATC GAGAAGTCGG 450  
 15 ACAACATGCC GTGGTACAAG GGTCCCACGC TGCTGGACGC GCTCGACATG 500  
 CTGGAGCCGC CGGTGCGCCC GGTGGACAAG CCGCTGCGCC TGCCCCTGCA 550  
 GGACGTGTAC AAGATCGGCG GTATCGGGAC GGTGCCCCGTG GGGCGCGTGG 600  
 AGACCGGCAT CATGAAGCCG GGCGACGTGG TGACGTTTCGC GCCCGCCAAC 650  
 GTGACGACTG AGGTGAAGTC GATCGAGATG CACCACGAGC AGCTGGCGGA 700  
 20 GGCGCAGCCC GGCGACAACG TCGGCTTCAA CGTGAAGAAC GTGTGCGTGA 750  
 AGGACATCCG CCGTGGTAAC GTGTGCGGCA ACTCGAAGAA CGACCCGCCG 800  
 AAGGAGGCGG CCGACTTCAC GGCGCAGGTG ATCGTGCTGA ACCACCCCGG 850  
 CCAGATCAGC AACGGCTACG CGCCGGTGCT GGACTGCCAC ACGAGCCACA 900  
 TTGCGTGCCG CTTGCGCGAA ATCGAGTCCA AGATCGACCG CCGCTCCGGC 950  
 25 AAGGAGCTGG AGAAGAACCC CAAGGCGATC AAGTCTGGCG ATGCCGCGAT 1000  
 CGTGAAGATG GTGCCGAGA AGCCGATGTG CGTGGAGGTG TTCAACGACT 1050  
 ACGCGCCGCT GGGCCGCTTT GCCGTGCGCG ACATGCGCCA AACCGTTG 1098

30  
 2) INFORMATION FOR SEQ ID NO: 515

(i) SEQUENCE CHARACTERISTICS:

35 (A) LENGTH: 1104 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

40 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Leishmania aethiopica*  
 (B) STRAIN: ATCC 50119

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 515

TACGCGTGGG TGCTCGACAA GCTGAAGGCG GAGCGCGAGC GCGGCATCAC 50  
 GATCGACATT GCGCTGTGGA AGTTCGAGTC GCCCAAGTCC GTGTTACGA 100  
 TCATCGATGC GCCCGGCCAC CGCGACTTCA TCAAGAACAT GATCACGGGC 150  
 50 ACGTCGCAGG CGGACGCCGC CATCCTGATG ATCGACTCGA CGCATGGTGG 200  
 CTTGAGGCT GGCATCTCGA AGGACGGCCA GACCCGCGAG CACGCGCTGC 250  
 TTGCCTTCAC TCTTGGCGTG AAGCAGATGG TGGTGTGCTG CAACAAGATG 300  
 GACGACAAGA CGGTGACGTA CGCGCAGTCG CGCTACGAGG AGATCAGCAA 350  
 GGAGGTGGGC GCGTACCTGA AGCGCGTGGG CTACAACCCG GAGAAGGTGC 400  
 55 GCTTCATCCC GATCTCGGGC TGGCAGGGCG ACAACATGAT CGAGAAGTCG 450  
 GACAACATGC CGTGGTACAA GGGTCCCACG CTGCTGGACG CGCTCGACAT 500  
 GTGGAGCCG CCGGTGCGCC CGGTGGACAA GCCGCTGCGC CTGCCCCTGC 550  
 AGGACGTGTA CAAGATCGGC GGTATCGGGA CGGTGCCCGT GGGCCGCGTG 600  
 GAGACCGGCA TCATGAAGCC GGGCGACGTG GTGACGTTTCG CGCCCGCCAA 650  
 60 CGTGACGACT GAGGTGAAGT CGATCGAGAT GCACCACGAG CAGCTGGCGG 700

	AGGCGCAGCC	CGGCGACAAC	GTCGGCTTCA	ACGTGAAGAA	CGTGTGCGTG	-750
	AAGGACATCC	GCCGTGGCAA	CGTGTGCGGC	AACTCGAAGA	ACGACCCGCC	800
	GAAGGAGGCG	GCCGACTTCA	CGGCGCAGGT	GATCGTGCTG	AACCACCCCG	850
	GCCAGATCAG	CAACGGCTAC	GCGCCGGTGC	TGGA CTGCCA	CACGAGCCAC	900
5	ATTGCGTGCC	GCTTCGCGGA	AATCGAGTCC	AAGATCGACC	GCCGCTCCGG	950
	CAAGGAGCTG	GAGAAGAACC	CCAAGGCGAT	CAAGTCTGGC	GATGCCGCGA	1000
	TCGTGAAGAT	GGTGCCGCAG	AAGCCGATGT	GCGTGGAGGT	GTTCAACGAC	1050
	TACGCGCCGC	TGGGCCGCTT	TGCCGTGCGC	GACATGCGCC	AAACCGTTGC	1100
	CGTC					1104

## 2) INFORMATION FOR SEQ ID NO: 516

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1106 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Leishmania tropica*

(B) STRAIN: ATCC 30815

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 516

	TACGCGTGGG	TGCTCGACAA	GCTGAAGGCG	GAGCGCGAGC	GCGGCATCAC	50
30	GATCGACATT	GCGCTGTGGA	AGTTCGAGTC	GCCCAAGTCC	GTGTTCACGA	100
	TCATCGATGC	GCCCGGCCAC	CGCGACTTCA	TCAAGAACAT	GATCACGGGC	150
	ACGTCGCAGG	CGGACGCCGC	CATCCTGATG	ATCGACTCGA	CGCATGGTGG	200
	CTTCGAGGCT	GGCATCTCGA	AGGACGGCCA	GACCCGCGAG	CACGCGCTGC	250
	TTGCCTTCAC	KCTTGCGCTG	AAGCAGATGG	TGGTGTGCTG	CAACAAGATG	300
35	GACGACAAGA	CGGTGACGTA	CGCGCAGTCG	CGCTACGATG	AGATCAGCAA	350
	GGAGGTGGGC	GCGTACCTGA	AGCGCGTGGG	CTACAACCCG	GAGAAGGTGC	400
	GCTTCATCCC	GATCTCGGGC	TGGCAGGGCG	ACAACATGAT	CGAGAAGTCG	450
	GACAACATGC	CGTGGTACAA	GGGTCCACAG	CTGCTGGACG	CGCTCGACAT	500
	GCTGGAGCCG	CCGGTGCGCC	CGGTGGACAA	GCCGCTGCGC	CTGCCCCTGC	550
40	AGGACGTGTA	CAAGATCGGC	GGTATCGGGA	CGGTGCCCGT	GGGGCGCGTG	600
	GAGACCGGCA	TCATGAAGCC	GGGCGACGTG	GTGACGTTCT	CGCCCGCCAA	650
	CGTGACGACT	GAGGTGAAGT	CGATCGAGAT	GCACCACGAG	CAGCTGGCGG	700
	AGGCGCAGCC	CGGCGACAAC	GTCGGCTTCA	ACGTGAAGAA	CGTGTGCGGTG	750
	AAGGACATCC	GCCGTGGTAA	CGTGTGCGGC	AACTCGAAGA	ACGACCCGCC	800
45	GAAGGAGGCG	GCCGACTTCA	CGGCGCAGGT	GATCGTGCTG	AACCACCCCG	850
	GCCAGATCAG	CAACGGCTAC	GCGCCGGTGC	TGGA CTGCCA	CACGAGCCAC	900
	ATTGCGTGCC	GCTTCGCGGA	AATCGAGTCC	AAGATCGACC	GCCGCTCCGG	950
	CAAGGAGCTG	GAGAAGAACC	CCAAGGCGAT	CAAGTCTGGC	GATGCCGCGA	1000
	TCGTGAAGAT	GGTGCCGCAG	AAGCCGATGT	GCGTGGAGGT	GTTCAACGAC	1050
50	TACGCGCCGC	TGGGCCGCTT	TGCCGTGCGC	GACATGCGCC	AAACCGTTGC	1100
	CGTCGG					1106

## 2) INFORMATION FOR SEQ ID NO: 517

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1099 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

5 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Leishmania donovani*

(B) STRAIN: ATCC 50212

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 517

10 TACGCGTGGG TGCTCGACAA GCTGAAGGCG GAGCGCGAGC GCGGCATCAC 50  
 GATCGACATT GCGCTGTGGA AGTTCGAGTC GCCCAAGTCC GTGTTACGA 100  
 TCATCGATGC GCCCGGCCAC CGCGACTTCA TCAAGAACAT GATCACGGGC 150  
 ACGTCGCAGG CGGACGCCGC CATCCTGATG ATCGACTCGA CGCATGGTGG 200  
 15 CTTGAGGCT GGCATCTCGA AGGACGGCCA GACCCGCGAG CACGCGCTGC 250  
 TTGCCTTCAC GCTTGCGGTG AAGCAGATGG TGGTGTGCTG CAACAAGATG 300  
 GACGACAAGA CCGTGACGTA CGCGCAGTCG CGCTACGATG AGATCAGCAA 350  
 GGAGGTGGGC GCGTACCTGA AGCGCGTGGG CTACAACCCG GAGAAGGTGC 400  
 GCTTCATCCC GATCTCGGGC TGGCAGGGCG ACAACATGAT CGAGAGGTTCG 450  
 20 GACAACATGC CGTGGTACAA GGGTCCCACG CTGCTGGACG CGCTCGACAT 500  
 GCTGGAGCCG CCGGTGCGCC CGGTGGACAA GCCGCTGCGC CTGCCCCCTGC 550  
 AGGACGTGTA CAAGATCGGC GGTATCGGGA CTGTGCCCGT GGGCCGCGTG 600  
 GAGACCGGCA TCATGAAGCC GGGCGACGTG GTGACGTTTCG CGCCCGCCAA 650  
 CGTGACGACT GAGGTGAAGT CGATCGAGAT GCACCACGAG CAGCTGGCGG 700  
 25 AGGCGCAGCC CGGCGACAAC GTCGGCTTCA ACGTGAAGAA CGTGTGCGTG 750  
 AAGGACATCC GCCGTGGCAA CGTGTGCGGC AACTCGAAGA ACGACCCGCC 800  
 GAAGGAGGCG GCCGACTTCA CGGCGCAGGT GATCGTGCTG AACCACCCCG 850  
 GCCAGATCAG CAACGGCTAC GCGCCGGTGC TGGACTGCCA CACGAGCCAC 900  
 ATTGCGTGCC GCTTCGCGGA AATCGAGTCC AAGATCGACC GCCGCTCCCG 950  
 30 CAAGGAGCTG GAGAAGAACC CCAAGGCGAT CAAGTCTGGC GATGCCGCGA 1000  
 TCGTGAAGAT GGTGCCGCAG AAGCCGATGT GCGTGGAGGT GTTCAACGAC 1050  
 TACGCGCCGC TGGGCCGCTT TGCCGTGCGC GACATGCGCC AAACCGTTG 1099

35

2) INFORMATION FOR SEQ ID NO: 518

(i) SEQUENCE CHARACTERISTICS:

40 (A) LENGTH: 1098 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

45

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Leishmania infantum*

(B) STRAIN: MOU

50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 518

55 TACGCGTGGG TGCTCGACAA GCTGAAGGCG GAGCGCGAGC GCGGCATCAC 50  
 GATCGACATT GCGCTGTGGA AGTTCGAGTC GCCCAAGTCC GTGTTACGA 100  
 TCATCGATGC GCCCGGCCAC CGCGACTTCA TCAAGAACAT GATCACGGGC 150  
 ACGTCGCAGG CGGACGCCGC CATCCTGATG ATCGACTCGA CGCATGGTGG 200  
 CTTGAGGCT GGCATCTCGA AGGACGGCCA GACCCGCGAG CACGCGCTGC 250  
 TTGCCTTCAC GCTTGCGGTG AAGCAGATGG TGGTGTGCTG CAACAAGATG 300  
 GACGACAAGA CCGTGACGTA CGCGCAGTCG CGCTACGATG AGATCAGCAA 350  
 GGAGGTGGGC GCGTACCTGA AGCGCGTGGG CTACAACCCG GAGAAGGTGC 400  
 60 GCTTCATCCC GATCTCGGGC TGGCAGGGCG ACAACATGAT CGAGAGGTTCG 450



	GACAACATGC	CGTGGTACAA	GGGTCCCACG	CTGCTGGACG	CGCTCGACAT	500
	GCTGGAGCCG	CCGGTGCGCC	CGGTGGACAA	GCCGCTGCGC	CTGCCCCTGC	550
	AGGACGTGTA	CAAGATCGGC	GGTATCGGGA	CTGTGCCCCG	GGGCCGCGTG	600
	GAGACCGGCA	TCATGAAGCC	GGGCGACGTG	GTGACGTTTC	CGCCCCGCCAA	650
5	CGTGACGACT	GAGGTGAAGT	CGATCGAGAT	GCACCACGAG	CAGCTGGCGG	700
	AGGCGCAGCC	CGGCGACAAC	GTGCGCTTCA	ACGTGAAGAA	CGTGTGCGTG	750
	AAGGACATCC	GCCGTGGCAA	CGTGTGCGGC	AACTCGAAGA	ACGACCCGCC	800
	GAAGGAGGCG	GCCGACTTCA	CGGCGCAGGT	GATCGTGCTG	AACCACCCCG	850
	GCCAGATCAG	CAACGGCTAC	GCGCCGGTGC	TGGACTGCCA	CACGAGCCAC	900
10	ATTGCGTGCC	GCTTCGCGGA	AATCGAGTCC	AAGATCGACC	GCCGCTCCGG	950
	CAAGGAGCTG	GAGAAGAACC	CCAAGGCGAT	CAAGTCTGGC	GATGCCGCGA	1000
	TCGTGAAGAT	GGTGCCGCAG	AAGCCGATGT	GCGTGGAGGT	GTTCAACGAC	1050
	TACGCGCCGC	TGGGCCGCTT	TGCCGTGCGC	GACATGCGCC	AAACCGTT	1098

15

## 2) INFORMATION FOR SEQ ID NO: 519

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1071 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Leishmania enriettii*

(B) STRAIN: ATCC 50120

30

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 519

	CTCGACAAGC	TGAAGGCGGA	GCGCGAGCGC	GGCATCACGA	TCGACATTGC	50
	GCTGTGGAAG	TTCGAGTCGC	CCAAGTCTGT	GTTCACGATC	ATCGATGCGC	100
35	CCGGCCACCG	CGACTTTCATC	AAGAACATGA	TCACCGGCAC	GTGCGAGGCC	150
	GACGCCGCCA	TCCTGATGAT	CGACTCGACC	CAGGGCGGCT	TCGAGGCTGG	200
	CATCTCGAAG	GACGGCCAGA	CCGCGAGCA	CGCGCTGCTC	GCCTTCACGC	250
	TTGGTGTGAA	GCAGATGGTG	GTGTGCTGCA	ACAAGATGGA	CGACAAGACG	300
	GTGCAGTACT	CGCAGGCGCG	CTACGAGGAG	ATCAGCAAGG	AGGTGGGCGC	350
40	GTACCTGAAG	CGCGTCGGCT	ACAACCCGGA	GAAGGTGCGC	TTCATCCCGA	400
	TCTCGGGCTG	CGAGGCGGAC	AACATGATCG	ACAAGTCGGA	CAGCATGCCG	450
	TGGTACAAGG	GGCCACGCT	GCTGGACGCG	CTCGACATGC	TGGAGGCGCC	500
	GGTGCGCCCC	GTGGACAAGC	CGCTGCGCCT	GCCCCGTCAG	GACGTGTACA	550
	AGATCGGCGG	TATCGGGACG	GTGCCCCTGG	GCCGCGTGGA	GACCGGCATC	600
45	ATGAAGCCTG	GCGACGTGGT	GACGTTTGCG	CCCGCCAACG	TGACGACGGA	650
	GGTGAAGTCG	ATCGAGATGC	ACCACGAGCA	GCTGGCGGAG	GCGGTGCCCG	700
	GCGACAACGT	CGGCTTCAAC	GTGAAGAACG	TGTCGGTGAA	GGACATCCGC	750
	CGTGGTAACG	TGTGCGGCAA	CTCGAAGAAC	GACCCGCCGA	AGGAGGCGGC	800
	CGACTTCACG	GCGCAGGTGA	TCGTGCTGAA	CCACCCTGGC	CAGATCAGCA	850
50	ACGGCTACGC	GCCGGTGCTG	GACTGCCACA	CGAGCCACAT	CGCGTGCCGC	900
	TTCGCGGATA	TCGAGTCCAA	GATCGACCGC	CGCTCTGGCA	AGGAGCTGGA	950
	GAAGAACCCC	AAGGCGATCA	AGTCCGGCGA	TGCGGCCATC	GTGAAGATGG	1000
	TGCCGCAGAA	GCCGATGTGC	GTGGAGGTGT	TCAACGACTA	CCCGCCGCTG	1050
	GGGCGCTTCG	CTGTGCGCGA	C			1071

55

## 2) INFORMATION FOR SEQ ID NO: 520

(i) SEQUENCE CHARACTERISTICS:

320

(A) LENGTH: 1071 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

5

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Leishmania gerbilli*  
 (B) STRAIN: ATCC 50121

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 520

	CTCGACAAGC	TGAAGGCGGA	GCGCGAGCGC	GGCATCACGA	TCGACATTGC	50
15	GCTGTGGAAG	TTCGAGTCGC	CCAAGTCCGT	GTTCACGATC	ATCGATGCGC	100
	CCGGCCACCG	CGACTTCATC	AAGAACATGA	TCACGGGCAC	GTCGCAGGCG	150
	GACGCCGCCA	TCCTGATGAT	CGACTCGACG	CATGGTGGCT	TCGAGGCTGG	200
	CATCTCGAAG	GACGGCCAGA	CCC GCGAGCA	CGCGCTGCTT	GCCTTCACTC	250
	TTGGCGTGAA	GCAGATGGTG	GTGTGCTGCA	ACAAGATGGA	CGACAAGACG	300
20	GTGACGTACG	CGCAGTCGCG	CTACGATGAG	ATCAGCAAGG	AGGTGGGCGC	350
	GTACCTGAAG	CGCGTGGGCT	ACAACCCGGA	GAAGGTGCGC	TTCATCCCGA	400
	TCTCGGGCTG	GCAGGGCGAC	AACATGATCG	AGAAGTCGGA	CAACATGCCG	450
	TGGTACAAGG	GTCCACGCT	GCTGGACGCG	CTCGACATGC	TGGAGCCGCC	500
	GGTGCGCCCC	GTGGACAAGC	CGCTGCGCCT	GCCCCTGCAG	GACGTGTACA	550
25	AGATCGGCGG	TATCGGGACG	GTGCCCCGTGG	GCCGCGTGGA	GACCGGCATC	600
	ATGAAGCCGG	GCGACGTGGT	GACGTTGCGC	CCCGCCAACG	TGACGACTGA	650
	GGTGAAGTCG	ATCGAGATGC	ACCACGAGCA	GCTGGCGGAG	GCGCAGCCCG	700
	GCGACAACGT	CGGCTTCAAC	TGAAGAAGC	TGTCGGTGAA	GGACATCCGC	750
	CGTGGGTAACG	TGTGCGGCAA	CTCGAAGAAG	GACCCGCCGA	AGGAGGCGGC	800
30	CGACTTCACG	GCGCAGGTGA	TCGTGCTGAA	CCACCCCGGC	CAGATCAGCA	850
	ACGGCTATGC	GCCGGTGCTG	GACTGCCACA	CGAGCCACAT	TGCGTGCCGC	900
	TTCGCGGAAA	TCGAGTCCAA	GATCGACCGC	CGCTCCGGCA	AGGAGCTGGA	950
	GAAGAACCCC	AAGGCGATCA	AGTCTGGCGA	TGCCGCGATC	GTGAAGATGG	1000
	TGCCGCGAGAA	GCCGATGTGC	GTGGAGGTGT	TCAACGACTA	CGCGCCGCTG	1050
35	GGCCGCTTTG	CCGTGCGCGA	C			1071

2) INFORMATION FOR SEQ ID NO: 521

40

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1114 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

45

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Leishmania hertigi*  
 (B) STRAIN: ATCC 50125

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 521

55	TCGTTCAAGT	ACGCGTGGGT	GCTCGACAAG	CTGAAGGCGG	AGCGCGAGCG	50
	CGGTATCACG	ATCGACATTG	CGCTGTGGAA	GTTCGAGTCG	CCCAAGTCGG	100
	TGTTACAGAT	CATCGATGCG	CCCGGCCACC	GCGACTTCAT	CAAGAACATG	150
	ATCACCGGCA	CGTCGCAGGC	GGATGCTGCC	ATTCTGATGA	TCGATTTCGAC	200
	GCAGGGTGGC	TTGAGGGCTG	GCATCTCGAA	GGACGGCCAG	ACGCGCGAGC	250
60	ACGCGCTGCT	GGCCTTCACG	CTGGGCGTGA	AGCAGATGGT	TGTGTGCTGC	300

	AACAAGATGG	ACGACAAGAC	GGTGCAGTAC	GCGCAGGCGC	GCTACGAGGA	350
	GATCAGCAAG	GAGGTGGGCG	CGTACCTGAA	GCGCGTGGGC	TACAACCCGG	400
	AGAAGGTGCG	CTTCATCCCG	ATCTCGGGCT	GGCAGGGCGA	CAACATGATC	450
	GAGAAGTCCG	ACAACATGTC	GTGGTACAAG	GGTCCCACGC	TGCTGGAGGC	500
5	GCTGGACATG	CTGGAGGCGC	CGGTGCGCCC	GGTGGACAAG	CCGCTGCGCC	550
	TGCCCCCTGCA	GGACGTGTAC	AAGATCGGCG	GCATTGGCAC	GGTGCCGGTG	600
	GGCCGTGTGG	AGACCGGCAT	CATGAAGCCC	GGCGACGTGG	TGACGTTTCG	650
	GCCCCGCCAAC	GTGACGACGG	AGGTGAAGTC	GATCGAGATG	CACCACGAGC	700
	AGCTGCAGGA	GGCTGTGCCC	GGCGACAACG	TCGGCTTCAA	CGTGAAGAAC	750
10	GTGTCTGGTGA	AGGACATCCG	CCGTGGTAAC	GTGTGTGGCA	ACTCGAAGAA	800
	CGACCCGCGG	AAGGAGGCGG	CTGACTTCAC	GGCGCAGGTG	ATCGTGCTGA	850
	ACCACCCCGG	CCAGATCAGC	AACGGCTACG	CGCCGGTGCT	GGACTGCCAC	900
	ACCAGCCACA	TCGCGTGCCG	CTTCGCGGAC	ATCGAGTCGA	AGATCGACCG	950
	CCGCTCCGGC	AAGGAGCTGG	AGAAGAACCC	CAAGTCCATC	AAGTCCGGCG	1000
15	ACGCCGCCAT	CGTGAAGATG	GTGCCGCGA	AGCCGATGTG	CGTGGAGGTG	1050
	TTCAACGACT	ACCCGCCGCT	GGGCCGCTTT	GCGGTGCGCG	ACATGCGCCA	1100
	AACCGTTGCC	GTCG				1114

20

## 2) INFORMATION FOR SEQ ID NO: 522

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1106 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

30

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Leishmania major*  
 (B) STRAIN: ATCC 50122

35

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 522

	TACGCGTGGG	TGCTCGACAA	GCTGAAGGCG	GAGCGCGAGC	GCGGCATCAC	50
	GATCGACATT	GCGCTGTGGA	AGTTCGAGTC	GCCCAAGTCC	GTGTTACGA	100
	TCATCGATGC	GCCCCGCCAC	CGCGACTTCA	TCAAGAACAT	GATCACGGGC	150
40	ACGTGCGAGG	CGGACGCCGC	CATTCTGATG	ATCGACTCGA	CGCATGGCGG	200
	CTTCGAGGCT	GGCATCTCGA	AGGACGGCCA	GACCCGCGAG	CACGCGCTGC	250
	TTGCCTTCAC	TCTTGCGGTG	AAGCAGATGG	TGGTGTGCTG	CAACAAGATG	300
	GACGACAAGA	CGGTGACGTA	CGCGCAGTCR	CGCTACGATG	AGATCAGCAA	350
	GGAGGTGGGC	GCGTACCTGA	AGCGCGTGGG	CTACAACCCG	GAGAAGGTGC	400
45	GCTTCATCCC	GATCTCGGGC	TGGCAGGGCG	ACAACATGAT	CGAGAAGTCG	450
	GACAACATGC	CGTGGTACAA	GGGTCCCACG	CTGCTGGACG	CGCTCGACAT	500
	GCTGGAGCCG	CCGGTGCGCC	CGGTGGACAA	GCCGCTGCGC	CTGCCCCCTGC	550
	AGGACGTGTA	CAAGATCGGC	GGTATCGGGA	CGGTGCCCGT	GGGCCGCGTG	600
	GAGACCGGCA	TCATGAAGCC	GGGCGACGTG	GTGACGTTTCG	CGCCCCGCCAA	650
50	CGTGACGACT	GAGGTGAAGT	CGATCGAGAT	GCACCACGAG	CAGCTGGCGG	700
	AGGCGCAGCC	CGGCGACAAC	GTCGGCTTCA	ACGTGAAGAA	CGTGTCTGGT	750
	AAGGACATCC	GCCGTGGTAA	CGTGTGCGGC	AACTCGAAGA	ACGACCCGCC	800
	GAAGGAGGCG	GCCGACTTCA	CGGCGCAGGT	GATCGTGCTG	AACCACCCCG	850
	GCCAGATCAG	CAACGGCTAT	GCGCCGGTGC	TGGACTGCCA	CACGAGCCAC	900
55	ATTGCGTGCC	GCTTCGCGGA	AATCGAGTCC	AAGATCGACC	GCCGCTCCGG	950
	CAAGGAGCTG	GAGAAGAACC	CCAAGGCGAT	CAAGTCTGGC	GATGCCGCGA	1000
	TCGTGAAGAT	GGTGCCGCGA	AAGCCGATGT	GCGTGGAGGT	GTTCAACGAC	1050
	TACGCGCCGC	TGGGCCGCTT	TGCCGTGCGC	GACATGCGCC	AAACCGTTGC	1100
	CGTCCG					1106

60

## 2) INFORMATION FOR SEQ ID NO: 523

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1105 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Leishmania amazonensis*  
 (B) STRAIN: ATCC 50131

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 523

TACGCGTGGG	TGCTCGACAA	GCTGAAGGCG	GAGCGCGAGC	GCGGCATCAC	50
GATCGACATT	GCGCTGTGGA	AGTTCGAGTC	GCCGAAGTCC	GTGTTACGA	100
TCATCGATGC	GCCCGGCCAC	CGCGACTTCA	TCAAGAACAT	GATCACGGGC	150
ACGTCGCAGG	CGGACGCGGC	CATCCTGATG	ATCGACTCGA	CGCATGGTGG	200
CTTCGAGGCT	GGCATCTCGA	AGGACGGCCA	GACCCGCGAG	CACGCGCTGC	250
TTGCCTTCAC	TCTTGGCGTG	AAGCAGATGG	TGGTGTGCTG	CAACAAGATG	300
GACGACAAGA	CGGTGATGTA	CGCGCAGTCG	CGCTACGATG	AGATCAGCAA	350
GGAGGTGAGC	GCGTACCTGA	AGCGCGTGGG	CTACAACCCG	GAGAAGGTGC	400
GCTTCATCCC	GATCTCGGGG	TGGCAGGGCG	ACAACATGAT	CGACAAGTCG	450
GACAACATGC	CGTGGTACAA	GGGTCCACG	CTGCTGGACG	CGCTCGACAT	500
GCTGGAGCCG	CCGGTGCGCC	CGGTGGACAA	GCCGCTGCGC	CTGCCCCCTGC	550
AGGACGTGTA	CAAGATCGGC	GGTATCGGGA	CGGTGCCCGT	GGGCCGCGTG	600
GAGACCGGGA	TCATGAAGCC	GGGCGACGTG	GTGACGTTCG	CGCCCCGCCAA	650
CGTGACGACT	GAGGTGAAGT	CGATCGAGAT	GCACCACGAG	CAGCTGGCGG	700
AGGCGCAGCC	CGGCGACAAC	GTCGGCTTCA	ACGTGAAGAA	CGTGTCGGTG	750
AAGGACATCC	GCCGTGGTAA	CGTGTGCGGC	AACTCGAAGA	ACGACCCGCC	800
GAAGGAGGCG	GCCGACTTCA	CGGCGCAGGT	GATCGTGCTG	AACCACCCCG	850
GCCAGATCAG	CAACGGCTAC	GCGCCGGTGC	TGGACTGCCA	CACGAGCCAC	900
ATCGCGTGCC	GCTTCGCGGA	GATCGAGTCC	AAGATCGACC	GCCGCTCCGG	950
CAAGGAGCTG	GAGAAGAACC	CCAAGGCGAT	CAAGTCTGGC	GACGCCGCGA	1000
TCGTGAAGAT	GGTGCCGCAG	AAGCCGATGT	GCGTGGAGGT	GTTCAACGAC	1050
TACGCGCCGC	TGGGCCGCTT	TGCCGTGCGC	GACATGCGCC	AAACCGTTGC	1100
CGTCG					1105

## 2) INFORMATION FOR SEQ ID NO: 524

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1098 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Leishmania mexicana*  
 (B) STRAIN: ATCC 50156

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 524

	TACGCGTG	GGG	TGCTCGACAA	GCTGAAGGCG	GAGCGCGAGC	GCGGCATCAC	50
	GATCGACATT	GCGCTGTGGA	AGTTTCGAGTC	GCCGAAGTCC	GTGTTTCACGA	100	
	TCATCGATGC	GCCCCGGCCAC	CGCGACTTCA	TCAAGAACAT	GATCACGGGC	150	
	ACGTCGCAGG	CGGACGCGGC	CATCCTGATG	ATCGACTCGA	CGCATGGTGG	200	
5	CTTCGAGGCT	GGCATCTCGA	AGGACGGCCA	GACCCGCGAG	CACGCGCTGC	250	
	TTGCCTTCAC	TCTTGCGCTG	AAGCAGATGG	TGGTGTGCTG	CAACAAGATG	300	
	GACGACAAGA	CGGTGATGTA	CGCGCAGTCG	CGCTACGATG	AGATCAGCAA	350	
	GGAGGTGAGC	GCGTACCTGA	AGCGCGTGGG	CTACAACCCG	GAGAAGGTGC	400	
	GCTTCATCCC	GATCTCGGGG	TGGCAGGGCG	ACAACATGAT	CGACAAGTCG	450	
10	GACAACATGC	CGTGGTACAA	GGGTCCACG	CTGCTGGACG	CGCTCGACAT	500	
	GCTGGAGCCG	CCGGTGCGCC	CGGTGGACAA	GCCGCTGCGC	CTGCCCCCTGC	550	
	AGGACGTGTA	CAAGATCGGC	GGTATCGGGA	CGGTGCCCGT	GGGCCGCGTG	600	
	GAGACCGGGA	TCATGAAGCC	GGGCGACGTG	GTGACGTTTCG	CGCCCCGCCAA	650	
	CGTGACGACT	GAGGTGAAGT	CGATCGAGAT	GCACCACGAG	CAGCTGGCGG	700	
15	AGGCGCAGCC	CGGCGACAAC	GTCGGCTTCA	ACGTGAAGAA	CGTGTGCGTG	750	
	AAGGACATCC	GCCGTGGTAA	CGTGTGCGGC	AACTCGAAGA	ACGACCCGCC	800	
	GAAGGAGGCG	GCCGACTTCA	CGGCGCAGGT	GATCGTGCTG	AACCACCCCG	850	
	GCCAGATCAG	CAACGGCTAC	GCGCCGGTGC	TGGACTGCCA	CACGAGCCAC	900	
	ATCGCGTGCC	GCTTCGCGGA	GATCGAGTCC	AAGATCGACC	GCCGCTCCGG	950	
20	CAAGGAGCTG	GAGAAGAACC	CCAAGGCGAT	CAAGTCTGGC	GACGCCGCGA	1000	
	TCGTGAAGAT	GGTGCCGCAG	AAGCCGATGT	GCGTGGAGGT	GTTCAACGAC	1050	
	TACGCGCCGC	TGGGCCGCTT	TGCCGTGCGC	GACATGCGCC	AAACCGTT	1098	

25

## 2) INFORMATION FOR SEQ ID NO: 525

## (i) SEQUENCE CHARACTERISTICS:

- 30 (A) LENGTH: 1081 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

35

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Leishmania tarentolae*  
 (B) STRAIN: II WT

40

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 525

	GCTGAAGGCG	GAGCGCGAGC	GCGGCATCAC	GATCGACATT	GCGCTGTGGA	50
	AGTTTCGAGTC	GCCCAAGTCG	GTGTTTCACGA	TCATCGATGC	GCCCCGGCCAC	100
	CGCGACTTCA	TCAAGAACAT	GATCACGGGC	ACGTCGCAGG	CGGACGCGGC	150
45	CATCCTGATG	ATCGACTCGA	CGCACGGTGG	GTTTCGAGGCT	GGCATCTCGA	200
	AGGACGGGCA	GACGCGCGAG	CACGCGCTGC	TTGCCTTCAC	TCTTGCGCTG	250
	AAGCAGATGG	TTGTGTGCTG	CAACAAGATG	GACGACAAGA	CGGTGATGTA	300
	CGCGCAGTCG	CGCTACGATG	AGATCAGCAA	GGAGGTGGGC	GCGTACCTGA	350
	AGCGCGTGGG	CTACAACCCG	GAGAAGGTGC	GCTTCATCCC	GATCTCGGGC	400
50	TGGCAGGGCG	ACAACATGAT	CGAGAAGTCG	GACAACATGC	CGTGGTACAA	450
	GGGTCCACG	CTGCTGGACG	CGCTCGACAT	GCTGGAGGCG	CCGGTGCGCC	500
	CGGTGGACAA	GCCGCTGCGC	CTGCCCCCTGC	AGGACGTGTA	CAAGATCGGC	550
	GGCATCGGCA	CGGTGCCCCGT	GGGCCGCGTG	GAGACCGGCA	TCATGAAGCC	600
	GGGCGACGTG	GTGACGTTTCG	CGCCCCGCGAA	CGTGACGACG	GAGGTGAAGT	650
55	CGATCGAGAT	GCACCACGAG	CAGCTGGCGG	AGGCGCAGCC	CGGCGACAAC	700
	GTCGGCTTCA	ACGTGAAGAA	CGTGTGCGTG	AAGGACATCC	GCCGTGGGAA	750
	CGTGTGCGGT	AACTCGAAGA	ACGACCCGCC	GAAGGAGGCC	GCCGACTTCA	800
	CGGCGCAGGT	GATCGTGCTG	AACCACCCCG	GCCAGATCAG	CAACGGCTAC	850
	GCGCCGGTGC	TGGACTGCCA	CACGAGCCAC	ATCGCGTGCC	GTTTCGCGGA	900
60	CATCGAGTCC	AAGATTGACC	GCCGCTCCGG	CAAGGAGCTG	GAGAAGAACC	950

CCAAGGCGAT	CAAGTCCGGC	GATGCCGCGA	TCGTGAAGAT	GGTGCCGCGAG	1000
AAGCCGATGT	GCGTGGAGAT	GTTCAACGAC	TACGCGCCGC	TTGGCCGCTT	1050
TGCTGTGCGC	GACATGCGCC	AAACCGTTGC	C		1081

5

## 2) INFORMATION FOR SEQ ID NO: 526

## (i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 1102 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

15 (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Leishmania tropica*  
 (B) STRAIN: ATCC 50129

20

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 526

AAATACGCGT	GGGTGCTCGA	CAAGCTGAAG	GCGGAGCGCG	AGCGCGGCAT	50
CACGATCGAC	ATTGCGCTGT	GGAAGTTCGA	GTCGCCCAAG	TCCGTGTTCA	100
25 CGATCATCGA	TGCGCCCGGC	CACCGCGACT	TCATCAAGAA	CATGATCACG	150
GGCACGTCGC	AGCGGGACGC	CGCCATCCTG	ATGATCGACT	CGACGCATGG	200
TGGCTTCGAG	GCTGGCATCT	CGAAGGACGG	CCGACCCCGC	GAGCACGCGC	250
TGCTTGCTT	CACKCTTGGC	GTGAAGCAGA	TGGTGGTGTG	CTGCAACAAG	300
ATGGACGACA	AGACGGTGAC	GTACGCGCAG	TCGCGCTACG	ATGAGATCAG	350
30 CAAGGAGGTG	GGCGCGTACC	TGAAGCGCGT	GGGCTACAAC	CCGGAGAAGG	400
TGCGCTTCAT	CCCGATCTCG	GGCTGGCAGG	GCGACAACAT	GATCGAGAAG	450
TCGGACAACA	TGCCGTGGTA	CAAGGGTCCC	ACGCTGCTGG	ACGCGCTCGA	500
CATGCTGGAG	CCGCCGGTGC	GCCCGGTGGA	CAAGCCGCTG	CGCCTGCCCC	550
TGCAGGACGT	GTACAAGATC	GGCGGTATCG	GGACGGTGCC	CGTGGGGCGC	600
35 GTGGAGACCG	GCATCATGAA	GCCGGGCGAC	GTGGTGACGT	TCGCGCCCGC	650
CAACGTGACG	ACTGAGGTGA	AGTCGATCGA	GATGCACCAC	GAGCAGCTGG	700
CGGAGGCGCA	GCCCGGCGAC	AACGTCGGCT	TCAACGTGAA	GAACGTGTCT	750
GTGAAGGACA	TCCGCCGTGG	TAACGTGTGC	GGCAACTCGA	AGAACGACCC	800
GCCGAAGGAG	GCGGCCGACT	TCACGGCGCA	GGTGATCGTG	CTGAACCACC	850
40 CCGGCCAGAT	CAGCAACGGC	TACGCGCCGG	TGCTGGACTG	CCACACGAGC	900
CACATTGCGT	GCCGCTTCGC	GGAAATCGAG	TCCAAGATCG	ACCGCCGCTC	950
CGGCAAGGAG	CTGAGAGAAG	ACCCCAAGGC	GATCAAGTCT	GGCGATGCCG	1000
CGATCGTGAA	GATGGTGCCG	CAGAAGCCGA	TGTGCGTGGA	GGTGTTC AAC	1050
GACTACGCGC	CGCTGGGCCG	CTTTGCCGTG	CGCGACATGC	GCCAAACCGT	1100
45 TG					1102

## 2) INFORMATION FOR SEQ ID NO: 527

50

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1105 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 55 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- 60 (A) ORGANISM: *Neospora caninum*  
 325

(B) STRAIN: Suarez-4

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 527

5	GGACRAACTT	AAAGCTGAAC	GTGAGCGTGG	TATCACCATT	GATATCTCCC	50
	TGTGGAAATT	TGAGACCAGC	AAGTACTATG	TTACCATCAT	TGATGCCCCA	100
	GGACACAGAG	ACTTCATCAA	AAACATGATT	ACAGGCACAT	CCCAGGCTGA	150
	CTGTGCTGTC	CTGATTGTTG	CTGCTGGTGT	TGGTGAATTT	GAAGCCGGTA	200
	TCTCCAAGAA	CGGGCAGACC	CGTGAGCATG	CCCTTNTGGC	TTACACCGTG	250
10	GGTGTGAAAC	AACTAATTGT	TGGCGTTAAC	AAAAGGGATT	CCACTGAGCC	300
	ACCCTATAGC	CARAAGAGAT	ACGARGAAAT	TGTTAAGGAA	GTCAGCMCCT	350
	AYNTTAAAAA	AATTGGYTAC	AACCCCGACA	CAGTANCATT	TGKGCCAATT	400
	TNTGGCTGGA	ATGGTGACAA	CATGCTGGAN	CCAAGTGCTA	ATATGCCATG	450
	GTTCAAGGGA	TGGAAGTCM	CCCGTAAGGA	CGGCAATGCC	AGKGGAAACCM	500
15	CCCTGCTTGA	AGCTYTGGAT	TGCATTYTGC	CACCAAYTTG	CCCAACTGAC	550
	AAACCCTTGC	GTTTGCCTYT	CCAGGATGTC	TATAAAATTG	GKGGTATTGG	600
	TACTGTCCCT	GTGGGTCGTG	TGGAGACTGG	TGTTCTCAA	CCTGGCATGG	650
	TGGTCACCTT	TGCTCCAGTC	AATGTAACAA	CTGAAGTGAA	GTCTGTAGAA	700
	ATGCACCATG	AAGCATTGAG	TGAAGCCCTT	CCTGGGGACA	ATGTGGGCTT	750
20	CAATGTCAAG	AACGTGTCTG	TCAAAGATGT	CCGTCGTGGC	AATGTGGCTG	800
	GTGACAGCAA	AAATGATCCA	CCCATGGAAG	CTGCTGGCTT	CACAGCTCAG	850
	GTGATTATTT	TGAACCATCC	AGGCCAAATC	AGTGCTGGAT	ATGCACCTGT	900
	GCTGGATTGT	CACACAGCTC	ACATTGCTTG	CAAGTTTGCT	GAGCTGAAGG	950
	AGAAGATTGA	TCGTCTGTTCT	GGGAAAAAGC	TGGAAGATGG	CCCTAAATTC	1000
25	TTGAAATCTG	GTGACGCTGC	CATCGTTGAT	ATGGTTCCTG	GCAAGCCCAT	1050
	GTGTGTCGAG	AGCTTCTCTG	ATTATCCTCC	CCTGGGCCGT	TTTGCTGTGC	1100
	GTGAC					1105

30

2) INFORMATION FOR SEQ ID NO: 528

(i) SEQUENCE CHARACTERISTICS:

	(A)	LENGTH: 935 bases
35	(B)	TYPE: Nucleic acid
	(C)	STRANDEDNESS: Double
	(D)	TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

40

(vi) ORIGINAL SOURCE:

	(A)	ORGANISM: <i>Trichomonas vaginalis</i>
	(B)	STRAIN: ATCC 30001

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 528

	GCACATCCCA	GGCTGATGCT	GCTATCCTTG	TCATCGACTC	CACACTCGGT	50
	GGYTTCGAAG	CCGGTATCGC	TGAACAAGGC	CAGACACGTG	AACACGCTCT	100
	TCTTGCCCTTC	ACACTCGGCA	TCAAGCAGGT	CATTGTGCGC	GTCAACAAGA	150
50	TGGATGACAA	GACAGTCAAC	TACAACAAGG	CYCGTTTCGA	CGAAATCACA	200
	GCCGAAATGA	CACGCATCCT	TACAGGCATC	GGCTACAAGC	CAGAAATGTT	250
	CCGCTTCGTC	CCAATCTCCG	GCTGGGCTGG	CGACAACATG	ACAGAGAAGT	300
	CTCCAAACAT	GCCATGGTAC	AATGGCCCAT	ACCTTCTTGA	AGCCCTCGAT	350
	TCCCTTCAGC	CACCAAAGCG	CCCATTGCGC	AAGCCACTCC	GTCTTCCACT	400
55	CCAGGATGTC	TACAAGATCA	ACGGTATCGG	TACAGTTCCA	GTCGGCCGTG	450
	TCGAATCCGG	CACAATGAAG	CCAGGCATGA	TCGTAACTT	CGCCCCATCC	500
	ACAGTTACAG	CTGAAGTTAA	GTCCATCGAA	ATGCACCACG	AATCCCTTCC	550
	AGAGGTCTCT	CCAGGTGACA	ACATCGGCTT	CAACGTCAAG	AACGTTTCCA	600
	CAGCTGATGT	CAAGCGTGGC	TACGTGCTTG	GTGATACAAA	GCGTGACCCA	650
60	CCAGTCGAAT	GCGCTTCCTT	CACAGCTCAR	ATGATCATCT	CCAACCACCC	700

	AGGCAAGATC	CACGCCGGCT	ACCAGCCAGT	TTTCGACTGC	CACACAGCTC	750
	ACATCGCCTG	CAAGTTCGAC	AAGCTCATCC	AGCGTATCGA	TCGTCCGSCAC	800
	GGCAAGAAGG	CTACAGAGAA	CCCAGAATAC	ATTGAGAAGG	ATGATGCCGC	850
	TATCGTCGAG	GTTGTCCCAT	CCAAGCCACT	CGTCGTGCGAG	TCCTTCCAGG	900
5	AGTACCCACC	ACTCGGCCGT	TTCGCCATCC	GTGAT		935

## 2) INFORMATION FOR SEQ ID NO: 529

10

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1065 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 15 (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- 20 (A) ORGANISM: *Trypanosoma brucei* subsp. *brucei*  
 (B) STRAIN: EATRO795

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 529

25	AAGCTGAAGG	CTGAGCGCGA	ACGTGGTATC	ACGATCGACA	TTGCACTGTG	50
	GAAATTTCGAG	TCACCCAAGT	CTGTCTTCAC	TATTATTGAT	GCTCCTGGGC	100
	ACCGTGACTT	CATCAAGAAC	ATGATCACCG	GCACATCGCA	AGCCGACGCA	150
	GCCATCCTCA	TCATTGCCTC	TGCGCAGGGT	GAGTTCGAGG	CTGGTATCTC	200
	CAAGGATGGA	CAGACCCGCG	AGCACGCGTT	GCTGGCCTTC	ACTTTGGGTG	250
30	TGAAGCAGAT	GGTTGTGTGC	TGCAACAAGA	TGGACGACAA	GACTGTGAAC	300
	TACGGACAGG	AGCGGTATGA	CGAGATTGTG	AAGGAGGTGT	CTGCTTACAT	350
	CAAGAAGGTT	GGGTACAACG	TGGAGAAGGT	GCGCTTCGTC	CCCATCTCCG	400
	GATGGCAGGG	CGACAACATG	ATTGAGAAAT	CCGAGAAGAT	GCCATGGTAC	450
	AAGGGTCCAA	CGCTCCTGGA	GGCACTAGAC	ATGCTGGAGC	CACCACTGCG	500
35	TCCGAGCGAC	AAGCCCCTGC	GTCTGCCACT	GCAGGACGTG	TACAAGATCG	550
	GTGGTATTGG	CACCGTGCCC	GTTGGTCGTG	TGGAGACCGG	CGTGATGAAG	600
	CCTGGTGATG	TGGTGACGTT	TGCCCCCGCC	AACGTGACGA	CCGAGGTGAA	650
	ATCGATCGAG	ATGCACCACG	AGCAGCTCGC	TGAGGCGACC	CCCGGTGACA	700
	ACGTGGGCTT	TAACGTGAAG	AACGTTTCTG	TAAAGGACAT	CCGCCGTGGC	750
40	AACGTCTGCG	GTAACACCAA	GAACGACCCC	CCAAAGGAGG	CCGCCGACTT	800
	CACGGCACAG	GTGATCATCC	TGAACCACCC	CGGACAGATT	GGAAACGGTT	850
	ATGCGCCCCG	GCTGGACTGC	CACACATCGC	ACATTGCCTG	CAAGTTCGCG	900
	GAGATCGAGT	CGAAGATCGA	CCGTCGCTCT	GGCAAGGAGC	TGGAGAAGGC	950
	TCCCAAGTCG	ATCAAGTCTG	GCGACGCCGC	GATCGTGCGC	ATGGTGCCGC	1000
45	AGAAGCCTAT	GTGCGTGGAG	GTCTTCAACG	ACTACGCGCC	ACTCGGCCGC	1050
	TTTGCCGTGC	GTGAC				1065

## 50 2) INFORMATION FOR SEQ ID NO: 530

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1297 bases  
 (B) TYPE: Nucleic acid  
 55 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

60



(A) ORGANISM: *Crithidia rasciculata*  
 (B) STRAIN: ATCC 11745

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 530

```

5   TTCGCGGAGG GCGTGCCGCC GGTGCTGACG GCGCTGGACG TGACGGAGGA      50
    CCTCGGCCGC GACGAGCCGC TGACGCTGGA GATTGTGCAG CACTTGGACG      100
    CGAACACCGG CCGCTGCATT GCCATGCAGA CGACGGATCT GCTGAAGCTG      150
    AAGTCGAAGG TTGTGTCGAC GGGCGGCAAC ATCTCCGTGC CGGTTGGCCG      200
10  CGAGACGCTG GGCCGCATCT TCAACGTGCT CGGCGACGCG ATCGACCAGC      250
    GCGGTGTGGT GGGCGAGAAG ATGCGCATGC CGATCCACGC CGAGGCCGCC      300
    AAGCTGGCGG ACCAGGCCGC GGAGGACGCG ATTCTGACGA CCGGCATCAA      350
    GGTGATCGAC CTGATTCTGC CGTACTGCAA GGGTGGCAAG ATCGGGCTGT      400
    TCGGCGGTGC TGGTGTGGGC AAGACTGTGA TCATCATGGA GCTGATCAAC      450
15  AACGTGGCCA AGGGCCACGG TGGTTTCTCC GTGTTGCGCC GCGTTGGCGA      500
    GCGCACCCGC GAGGGCACGG ATCTGTACCT GGAGATGATG CAGTCGAAGG      550
    TCATTGACCT GAAGGGCGAG TCGAAGTGCG TGCTGGTGTA CGGCCAGATG      600
    AACGAGCCCC CGGGTGCGCG TGCGCGTGTT GCGCAGTCTG CGCTGACGAT      650
    GCGGGAGTAC TTCCGTGACG TGGAGGGCCA GAACGTGCTG CTGTTTCATCG      700
20  ACAACATCTT CCGCTTCACC CAGGCCAACT CCGAGGTGTC CGCCCTGCTG      750
    GGCCGCATTC CCGCCGCCGT GGGCTACCAG CCGACGCTTG CCGAGGATCT      800
    TGGTATGCTG CAGGAGCGCA TTACGTGCGAC GACGAAGGGC TCGATTACGT      850
    CTGTGCAGGC CGTGTACGTG CCGGCCGATG ATATCACGGA TCCGGCGCCG      900
    GCGACGACCT TCTCGCACCT GGATGCGACG ACGGTGCTGG ACCGCGCGGT      950
25  TGCCGAGTCT GGCATCTACC CCGCCGTGAA CCCGCTGGAG TGCGCGTCGC      1000
    GTATCATGGA CCCCAGATGT ATCGACGTGG ACCACTACAA CGTTGCGCAG      1050
    GATATCGTGC AGATGCTGAC CAAGTACAAG GAGCTGCAGG ATATCATTGC      1100
    CGTGCTGGGT ATCGACGAGC TGAGCGAGGA GGACAAGCTT GTGTTGGACC      1150
    GCGCTCGCAA GGTGACGCGC TTCCTGTGCG AGCCGTTCCA GGTGGCCGAG      1200
30  GTGTTACACG GCATGACGGG CCACTACGTG CAGCTGGAGG ACACAGTGGA      1250
    GTCGTTCTCT GGCCTGCTGA TGGGCTCGTA CGACCAGATC CCGGAGA      1297
  
```

## 35 2) INFORMATION FOR SEQ ID NO: 531

## (i) SEQUENCE CHARACTERISTICS:

```

    (A) LENGTH: 1298 bases
    (B) TYPE: Nucleic acid
40  (C) STRANDEDNESS: Double
    (D) TOPOLOGY: Linear
  
```

## (ii) MOLECULE TYPE: Genomic DNA

## 45 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Leishmania tropica*  
 (B) STRAIN: ATCC 30816

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 531

```

50  CTTCTCGGAG GCGTGCCGC CCGTGCTGAC GGCGCTGGAT GTGACGGAGG      50
    ACCTTGGCCG CGATGAGCCG CTGACGCTGG AGATCGTGCA GCACTTGGAC      100
    GCGAACACGG GCCGCTGCAT TGCGATGCAG ACGACGGACC TGCTGAAGCT      150
    GAAGTCGAAG GTCGTGTCGA CCGGCGGCAA CATCTCTGTG CCGGTGGGCC      200
55  GTGAGACGCT GGGCCGCATC TTCAAYGTTT TGGGCGACGC GATCGACCAG      250
    CGCGGCCCCG TGGGCGAGAA GATGCGCATG GCGATCCACG CCGAGGCCCC      300
    GAAGCTGGCG GATCAGGCCG CGGAGGACAC GATCCTGACG ACCGGCATCA      350
    AGGTGATCGA CCTGATTCTG CCCTACTGCA AGGGTGGCAA GATCGGCCTG      400
    TTCGGCGGTG CCGGTGTGGG CAAGACTGTG ATCATCATGG AGCTGATCAA      450
60  CAACGTGCGG AAGGGCCACG GCGGTTTCTC CGTGTTTGCC GCGTTGGCG      500
  
```

	AGCGCACGCG	CGAGGGCAGC	GACCTGTACC	TGGAGATGAT	GCAGTGAAG	550
	GTGATTGACC	TGAAGGGCGA	GTCGAAGTGY	GTGCTTGTGT	ATGGGCAGAT	600
	GAACGAGCCC	CCGGGTGCGC	GCGCGCGCGT	TGCGCAGTCT	GCGCTGACGA	650
	TGGCGGAGTA	CTTCCGCGAC	GTGGAGGGCC	AGAACGTGCT	GCTGTTTCATC	700
5	GACAACATCT	TCCGCTTCAC	GCAGGCGAAC	TCCGAGGTGT	CTGCGCTGCT	750
	GGGCCGCATT	CCGGCCGCCG	TGGGCTACCA	GCCGACGCTT	GCGGAGGATC	800
	TTGGTATGCT	GCAGGAGCGC	ATCACGTCGA	CAACGAAGGG	GTCGATCACG	850
	TCCGTGCAGG	CCGTGTACGT	GCCAGCGGAT	GATATCACGG	ATCCCGCGCC	900
	CGCGACGACG	TTCTCGCACC	TGGACGCGAC	GACTGTGCTG	GACCGCGCGG	950
10	TGGCGGAGTC	GGGCATCTAC	CCTGCCGTGA	ACCCGCTGGA	GTGCGCGTCG	1000
	CGTATCATGG	ACCCTGATGT	GATCGATGTG	GACCACTACA	ACGTTGCGCA	1050
	GGATATCGTG	CAGATGCTGA	CCAAGTACAA	GGAGCTGCAG	GATATCATTG	1100
	CGGTGCTTGG	CATCGACGAG	CTGAGCGAGG	AAGACAAGGT	TGTTGTGGAC	1150
	CGCGCGCGCA	AGGTGACCCG	GTTCTGTGCG	CAGCCGTTCC	AGGTTGCGGA	1200
15	GGTGTTCACG	GGCATGACGG	GCCACTACGT	GCAGCTGGTC	GACACGGTGG	1250
	AGTCGTTCTC	TGGCCTGCTG	ATGGGGTCGT	ACGACCAGAT	CCCGGAGA	1298

## 20 2) INFORMATION FOR SEQ ID NO: 532

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1297 bases  
 (B) TYPE: Nucleic acid  
 25 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

## 30 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Leishmania aethiopica*  
 (B) STRAIN: ATCC 50119

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 532

35	TTCTCGGAGG	GCGTGCCGCC	CGTGCTGACG	GCGCTGGATG	TGACGGAGGA	50
	CCTTGGCCGC	GATGAGCCGC	TGACGCTGGA	GATCGTGCAG	CACTTGGACG	100
	CGAACACCGG	CCGCTGCATT	GCGATGCAGA	CGACGGACCT	GCTGAAGCTG	150
	AAGTCGAAGG	TTGTGTGCAC	CGGCGGCAAC	ATCTCTGTGC	CGGTGGGCCG	200
40	TGAGACGCTG	GGCCGCATCT	TCAACGTTCT	GGGCGACGCG	ATCGACCAGC	250
	GCGGCCCCGT	GGGCGAGAAG	ATGCGCATGG	CGATCCACGC	CGAGGCCCCA	300
	AAGCTGGCGG	ATCAGGCCGC	GGAGGACACG	ATCCTGACGA	CCGGCATCAA	350
	GTGTATCGAC	CTGATTCTGC	CCTACTGCAA	GGGTGGCAAG	ATCGGCCTGT	400
	TCCGCGGTGC	CGGTGTGGGC	AAGACTGTGA	TCATCATGGA	GCTGATCAAC	450
45	AACGTCGCGA	AGGGCCACGG	TGGTTTCTCC	TGTTTGGCCG	GCGTTGGCGA	500
	GCGCACGCGC	GAGGGCACGG	ACCTGTACCT	GGAGATGATG	CAGTCGAAGG	550
	TGATTGACCT	GAAGGGCGAG	TCGAAGTGCG	TGCTTGTGTA	CGGGCAGATG	600
	AACGAGCCCC	CGGGTGCGCG	GCGCGCGGTT	GCGCAGTCTG	CGCTGACGAT	650
	GGCGGAGTAC	TTCCGCGACG	TGGAGGGCCA	GAACGTGCTG	CTGTTCATCG	700
50	ACAACATCTT	CCGCTTCACG	CAGGCGAACT	CCGAGGTGTC	TGCGCTGCTG	750
	GGCCGCATTC	CAGCCGCCGT	GGGCTACCAG	CCGACGCTTG	CGGAGGATCT	800
	TGGTATGCTG	CAGGAGCGCA	TCACGTCGAC	AACGAAGGGG	TCGATCACGT	850
	CCGTGCAGGC	CGTGTACGTG	CCAGCGGATG	ATATCACGGA	TCCCGCGCCC	900
	GCGACGACGT	TCTCGCACCT	GGACGCGACG	ACTGTGCTGG	ACCGCGCGGT	950
55	GGCGGAGTCG	GGCATCTACC	CTGCCGTGAA	CCCGCTGGAG	TGCGCGTCGC	1000
	GTATCATGGA	CCCCGACGTG	ATCGATGTGG	ACCACTACAA	CGTTGCGCAG	1050
	GATATCGTGC	AGATGCTGAC	CAAGTACAAG	GAGCTGCAGG	ATATCATTGC	1100
	GGTGCTTGGC	ATCGACGAGC	TGAGCGAGGA	AGACAAGGTT	GTTGTGGACC	1150
	GCGCGCGCAA	GGTGACCCGG	TTCCTGTGCG	AGCCGTTCCT	GGTTGCGGAG	1200
60	GTGTTACAGG	GCATGACGGG	CCACTACGTG	CAGCTGGTCG	ACACGGTGGG	1250

GTCGTTCTCT GGCCTGCTGA TGGGGTCGTA CGACCAGATC CCGGAGA 1297.

5 2) INFORMATION FOR SEQ ID NO: 533

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1298 bases  
 (B) TYPE: Nucleic acid  
 10 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

15 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Leishmania donovani*  
 (B) STRAIN: ATCC 50212

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 533

20 CTTCTCGGAG GGCCTGCCGC CCGTACTGAC GGCGCTGGAT GTGACGGAGG 50  
 ACCTTGGCCG CGATGAGCCG CTGACGCTGG AGATCGTGCA GCACTTGGAT 100  
 GCGAACACCG GCCGCTGCAT TGCATGTCAG ACGACGGACC TGCTGAAGCT 150  
 GAAGTCGAAG GTTGTGTCGA CCGGCGGCAA CATCTCTGTG CCGGTGGGCC 200  
 25 GTGAGACGCT GGGCCGCATC TTCAACGTTT TGGGCGACGC GATCGACCAG 250  
 CGCGGCCCCG TGGGCGAGAA GATGCGCATG GCGATCCACG CCGAGGCCCC 300  
 GAAGCTGGCG GACCAGGCCG CGGAGGACAC GATCCTGACG ACCGGCATCA 350  
 AGGTGATCGA CCTCATTCTG CCCTACTGCA AGGGCGGCAA GATCGGCCCTG 400  
 TTCGGCGGTG CCGGTGTGGG CAAGACTGTG ATCATCATGG AGCTGATCAA 450  
 30 CAACGTCGCG AAGGGCCACG GTGGCTTCTC CGTGTGTTGCC GCGGTTGGCG 500  
 AGCGCACGCG CGAGGGCACG GACCTATACC TGGAGATGAT GCAGTCGAAG 550  
 GTGATTGACC TGAAGGGCGA GTCGAAGTGC GTGCTTGTGT ACGGGCAGAT 600  
 GAACGAGCCC CCGGGTGCGC GCGCGCGCGT TCGCGAGTCT GCGCTGACGA 650  
 TGGCGGAGTA CTTCCGCGAC GTGGAGGGCC AGAACGTGCT GCTGTTTCATC 700  
 35 GACAACATCT TCCGCTTCAC GCAGGCGAAC TCCGAGGTGT CTGCGCTGCT 750  
 GGGCCGCATT CCGGCCGCCG TGGGCTACCA GCCGACGCTT GCCGAGGATC 800  
 TTGGTATGCT GCAGGAGCGC ATCACATCGA CGACGAAGGG GTCGATCACG 850  
 TCCGTGCAGG CCGTGTACGT GCCGGCGGAT GATATCACGG ATCCCGCGCC 900  
 CGCGACGACG TTCTCGCACC TGGACGCGAC GACTGTGCTG GACCGCGCGG 950  
 40 TGGCGGAGTC GGGCATCTAC CCTGCCGTGA ACCCGCTGGA GTGCGCGTCG 1000  
 CGTATCATGG ACCCCGATGT GATCGATGTG GACCACTACA ACGTTGCGCA 1050  
 GGATATCGTG CAGATGCTGA CCAAGTACAA GGAGCTGCAG GATATCATTG 1100  
 CGGTGCTTGG CATCGACGAG CTGAGCGAGG AGGACAAGGT TGTGGTGGAC 1150  
 CGCGCGCGCA AGGTGACCCG GTTCCTGTG CAGCCGTTCC AGGTTGCGGA 1200  
 45 GGTGTTTCAG GGCATGACGG GCCACTACGT GCAGCTGGCC GACACGGTGG 1250  
 AGTCGTTCTC TGGCCTGCTG ATGGGGTCGT ACGACCAGAT CCCGGAGA 1298

50 2) INFORMATION FOR SEQ ID NO: 534

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1298 bases  
 (B) TYPE: Nucleic acid  
 55 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

60 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Leishmania infantum*

(B) STRAIN: MOU

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 534

```

5      CTTCTCGGAG GGC GTGCCGC CCGTACTGAC GGC GTGGAT GTGACGGAGG      50
      ACCTTGGCCG CGATGAGCCG CTGACGCTGG AGATCGTGCA GCACTTGGAT      100
      GCGAACACCG GCCGCTGCAT TGC GATGCAG ACGACGGACC TGCTGAAGCT      150
      GAAGTCGAAG GTTGTGTCTGA CCGGCGGCAA CATCTCTGTG CCGGTGGGCC      200
10     GTGAGACGCT GGGCCGCATC TTCAACGTTT TGGGCGACGC GATCGACCAG      250
      CGCGGCCCCG TGGGCGAGAA GATGCGCATG GCGATCCACG CCGAGGCCCC      300
      AAAGCTGGCG GACCAGGCCG CGGAGGACAC GATCCTGACG ACCGGCATCA      350
      AGGTGATCGA CCTCATTTCTG CCCTACTGCA AGGGCGGCAA GATCGGCCTG      400
      TTCGGCGGTG CCGGTGTGGG CAAGACTGTG ATCATCATGG AGCTGATCAA      450
15     CAACGTCGCG AAGGGCCACG GTGGCTTCTC CGTGTTTGCC GGC GTTGCG      500
      AGCGCACGCG CGAGGGCACG GACCTATACC TGGAGATGAT GCAGTCGAAG      550
      GTGATTGACC TGAAGGGCGA GTCGAAGTGC GTGCTTGTGT ACGGGCAGAT      600
      GAACGAGCCC CCGGGTGC GC GCGCGCGCGT TGC GAGTCT GCGCTGACGA      650
      TGGCGGAGTA CTTCCGCGAC GTGGAGGGCC AGAACGTGCT GCTGTTTCATC      700
20     GACAACATCT TCCGCTTCAC GCAGGCGAAC TCCGAGGTGT CTGCGCTGCT      750
      GGGCCGCATT CCGGCCGCCG TGGGCTACCA GCCGACGCTT GCCGAGGATC      800
      TTGGTATGCT GCAGGAGCGC ATCACATCGA CGACGAAGGG GTCGATCACG      850
      TCCGTGCAGG CCGTGTACGT GCCGGCGGAT GATATCACTG ATCCCGCGCC      900
      CGCGACGACG TTCTCGCACC TGGACGCGAC GACTGTGCTG GACCGCGCGG      950
25     TGGCGGAGTC GGGCATCTAC CCTGCGGTGA ACCCGCTGGA GTGCGCGTCG      1000
      CGTATCATGG ACCCCGATGT GATCGATGTG GACCACTACA ACGTTGCGCA      1050
      GGATATCGTG CATGCTGA CCAAGTACAA GGAGCTGCAG GATATCATTG      1100
      CGGTGCTTGG CATCGACGAG CTGAGCGAGG AGGACAAGGT TGTGGTGGAC      1150
      CGCGCGCGCA AGGTGACCCG GTTCCTGTG CAGCCGTTCC AGGTTGCGGA      1200
30     GGTGTTACG GGCATGACGG GCCACTACGT GCAGCTGGCC GACACGGTGG      1250
      AGTCGTTCTC TGGCCTGCTG ATGGGGTCGT ACGACCAGAT CCCGGAGA      1298

```

## 35 2) INFORMATION FOR SEQ ID NO: 535

## (i) SEQUENCE CHARACTERISTICS:

```

      (A) LENGTH: 1301 bases
      (B) TYPE: Nucleic acid
40     (C) STRANDEDNESS: Double
      (D) TOPOLOGY: Linear

```

## (ii) MOLECULE TYPE: Genomic DNA

## 45 (vi) ORIGINAL SOURCE:

```

      (A) ORGANISM: Leishmania gerbilli
      (B) STRAIN: ATCC 50121

```

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 535

```

50     GCACTTCTCG GAGGGCGTGC CGCCCGTGCT GACGGCGCTG GATGTGACGG      50
      AGGACCTTGG CCGCGATGAG CCGCTGACGC TGGAGATCGT GCAGCACTTG      100
      GACGCGAACA CCGGCCGCTG CATTGCGATG CAGACGACGG ACCTGCTGAA      150
      GCTGAAGTCG AAGGTTGTGT CGACCGGTGG CAACATCTCT GTGCCGGTGG      200
55     GCCGTGAGAC GCTGGGCCGC ATCTTCAACG TTCTGGGCGA TCGATCGAC      250
      CAGCGCGGCC CCGTGGGCGA GAAGATGCGC ATGGCGATCC ACGCCGAGGC      300
      CCCGAAGCTG GCGGATCAGG CCGCGGAGGA CACGATCCTG ACGACCGGCA      350
      TCAAGGTGAT CGACCTGATT CTGCCCTACT GCAAGGGTGG CAAGATCGGY      400
      CTGTTGCGCG GTGCCGGTGT GGCAAGACT GTGATCATCA TGGAGCTGAT      450
60     CAACAACGTC GCGAAGGGCC ACGGTGGTTT CTCCGTGTTT GCCGGCGTTG      500

```

	GCGAGCGCAC	GCGCGAGGGC	ACGGACCTGT	ACCTGGAGAT	GATGCAAGTCG	550
	AAGGTGATTG	ACCTGAAGGG	CGAGTCGAAG	TGCGTGCTTG	TGTACGGGCA	600
	GATGAACGAG	CCCCCGGGTG	CGCGCGCGCG	CGTTGCGCAG	TCTGCGCTGA	650
	CGATGGCGGA	GTACTTCCGC	GACGTGGAGG	GCCAGAACGT	GCTGCTGTTC	700
5	ATCGACAACA	TCTTCCGCTT	CACGCAGGCG	AACTCCGAGG	TGTCCGCGCT	750
	GCTGGGCCGC	ATTCCGGCCG	CCGTGGGCTA	CCAGCCGACG	CTTGCGGAGG	800
	ATCTTGGTAT	GCTGCAGGAG	CGCATCACGT	CGACAACGAA	GGGGTCGATC	850
	ACGTCCGTGC	AGGCCGTGTA	CGTGCCAGCG	GATGATATCA	CGGATCCCGC	900
	GCCCCGACG	ACGTTCTCGC	ACCTTGACGC	GACGACTGTG	CTGGACCGCG	950
10	CGGTGGCGGA	GTCGGGCATC	TACCTTGCCG	TGAACCCGCT	GGAGTGCGCG	1000
	TCGCGTATCA	TGGACCCCGA	TGTGATCGAT	GTGGACCACT	ACAACGTTGC	1050
	GCAGGATATC	GTGCAGATGC	TGACCAAGTA	CAAGGAGCTG	CAGGACATCA	1100
	TTGCGGTGCT	TGGCATCGAC	GAGCTGAGCG	AGGAAGACAA	GGTTGTGGTG	1150
	GACCGCGCGC	GCAAGGTGAC	CCGGTTCCTG	TCGCAGCCGT	TCCAGGTTGC	1200
15	GGAGGTGTTT	ACGGGCATGA	CGGGCCACTA	CGTGCAGCTG	GTCGACACGG	1250
	TGGAGTCGTT	CTCTGGCTTG	CTGATGGGGT	CGTACGACCA	GATCCCGGAG	1300
	A					1301

20

## 2) INFORMATION FOR SEQ ID NO: 536

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1298 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

30

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Leishmania hertigi*  
 (B) STRAIN: ATCC 50125

35

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 536

	CTTCGCGGAG	GGCGTGCCGC	CGGTGCTGAC	GTCGCTGGAT	GTGACGGAGA	50
	ACCTCGGCCG	CGATGAGCCG	CTGACGCTGG	AGATTGTGCA	GCACTTGGAC	100
	GCGAACACCG	GTCGCTGCAT	TGCGATGCAG	ACGACGGACC	TGCTGAAGCT	150
40	GAAGTCGAAG	GTCGTGTCGA	CCGGTGGCAA	CATCTCTGTG	CCTGTTGGCC	200
	GCGAGACGCT	GGGTCGCATC	TTCAACGTGC	TTGGCGATGC	GATTGACCAG	250
	CGCGGCCCTG	TGGGTGAGAA	GATGCGCATG	GCGATCCACG	CCGAGGCGCC	300
	GAAGCTGGCG	GATCAGGCGG	CAGAGGACAC	GATCCTGACG	ACCGGCATCA	350
	AGGTGATCGA	TCTTATTCTG	CCGTACTGCA	AGGGTGGTAA	GATCGGTCTG	400
45	TTCGGTGGTG	CCGGTGTAGG	CAAGACTGTG	ATTATTATGG	AGCTGATCAA	450
	TAACGTGGCG	AAGGGCCACG	GTGGGTTTTC	CGTGTTTGCT	GGCGTGGGCG	500
	AGCGCACGCG	CGAGGGCACT	GACCTGTACC	TGGAGATGAT	GCAGTCGAAG	550
	GTGATTGACC	TGAAGGGCGA	ATCAAAGTGC	GTGCTTGTGT	ACGGACAGAT	600
	GAACGAGCCC	CCGGGTGCGC	GTGCGCGCGT	TGCGCAGTCT	GCGCTGACGA	650
50	TGGCCGAGTA	CTTCCGCGAT	GTGGAGGGCC	AGAACGTGCT	GCTGTTTCATT	700
	GACAACATCT	TCCGCTTCAC	GCAGGCGAAC	TCCGAGGTGT	CTGCGCTGCT	750
	GGGTGCGATT	CCTGCCGCCG	TGGGCTACCA	GCCGACGCTT	GCGGAGGATC	800
	TGGGCATGCT	GCAGGAGCGC	ATTACGTCGA	CGACGAAGGG	CTCGATTACG	850
	TCTGTGCAGG	CCGTGTACGT	GCCTGCGGAT	GATATCACGG	ACCCGGCGCC	900
55	CGCGACGACG	TTCTCGCACC	TGGACGCGAC	GACTGTGCTG	GACCGTGCGG	950
	TGGCAGAGTC	GGGCATTTAC	CCTGCGGTGA	ACCCGCTGGA	GTGCGCGTCG	1000
	CGTATCATGT	ACCCCGATGT	CATCGATGTG	GACCACTACA	ACGTTGCGCA	1050
	GGATATCGTG	GAGATGCTGA	CCAAGTACAA	GGAGCTGCAG	GATATCATTA	1100
	CCGTGCTTGG	TATCGACGAG	CTGAGCGAGG	AGGACAAGGT	TGTGGTGGAC	1150
60	CGCGCGCGCA	AGGTGACCCG	GTTCTGTGTCG	CAGCCGTTCC	AGGTTGCGGA	1200

GGTGTTCACCT GGCATGACGG GTCACTACGT TCAGCTGGAG GACACGGTGG 1250  
 AGTCGTTCTC TGGCCTACTG ATGGGGTCAT ACGACCAGAT CCCGGAGA 1298

5

## 2) INFORMATION FOR SEQ ID NO: 537

## (i) SEQUENCE CHARACTERISTICS:

10

- (A) LENGTH: 1297 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

15

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Leishmania major*
- (B) STRAIN: ATCC 50122

20

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 537

CTTCTCGGAG GCGGTGCCGC CCGTGCTGAC GGCGCTGGAT GTGACGGAGG 50  
 ACCTTGGCCG TGATGAGCCG CTGACGCTGG AGATCGTGCA GCACTTGGAC 100  
 GCGAACACCG GCCGCTGCAT TGCGATGCAG ACGACGGACC TGCTGAAGCT 150  
 25 GAAGTCGAAG GTTGTGTCTGA CCGGCGGCAA CATCTCTGTG CCGGTGGGCC 200  
 GTGAGACGCT GGGCCGCATC TTCAACGTTT TGGGCGATGC GATCGACCAG 250  
 CGCGGCCCGG TGGCGGAGAA GATGCGCATG GCGATCCACG CCGAGGCCCC 300  
 GAAGCTGGCG GATCAGGCCG CAGAGCACAC GATCCTGACG ACCGGCATCA 350  
 AGGTGATCGA CTTGATCCTG CCCTACTGCA AGGGTGGCAA GATCGGCCCTG 400  
 30 TTCGGCGGGT CCGGTGTGGG CAAGACTGTG ATCATCATGG AGCTGATCAA 450  
 CAATGTTCGG AAGGGCCACG GTGGTTTCTC CGTGTTTGCC GGCGTTGGCG 500  
 AGCGCACGCG CGAGGGCACG GACCTGTACC TGGAGATGAT GCAGTCGAAG 550  
 GTGATTGACC TGAAGGGCGA GTCGAAGTGC GTGCTTGTGT ACGGGCAGAT 600  
 GAACGAGCCC CCGGGTGCAG GCGCGCGCGT TGCAGAGTCT GCGCTGACGA 650  
 35 TGGCGGAGTA CTTCCGCGAC GTGGAGGGCC AGAACGTGCT GCTGTTTCATC 700  
 GACAACATCT TCCGCTTCAC GCAGGCGAAC TCCGAGGTGT CCGCGCTGCT 750  
 GGGCCGCATT CCGGCCGCCG TGGGCTACCA GCCGACGCTT GCGGAGGATC 800  
 TTGGTATGCT GCAGGAGCGC ATCACGTCGA CAACGAAGGG GTCGATCACG 850  
 TCCGTGCAGG CCGTGTACGT GCCAGCGGAT GATATCACGG ATCCCGCGCC 900  
 40 CGCGACGACG TTCTCGCACC TGGATGCGAC GACTGTGCTG GACCGCGCGG 950  
 TGGCGGAGTC GGGCATCTAC CCTGCCGTGA ACCCGCTGGA GTGCGCGTGG 1000  
 CGTATCATGG ACCCCGATGT GATCGATGTG GACCACTACA ACGTTGCGCA 1050  
 GGATATCGTG CAGATGCTGA CCAAGTACAA GGAGCTGCAG GACATCATTG 1100  
 CCGTGCTTGG CATCGACGAG CTGAGCGAGG AAGACAAGGT TGTGGTGGAC 1150  
 45 CGCGCGCGCA AGGTGACCCG GTTCCTGTG CAGCCGTTCC AGGTTGCGGA 1200  
 GGTGTTTACG GGCATGACGG GCCACTACGT GCAGCTGGTC GACACGGTGG 1250  
 AGTCGTTCTC TGGCCTGCTG ATGGGGTCGT ACGACCAGAT CCCGGAG 1297

50

## 2) INFORMATION FOR SEQ ID NO: 538

## (i) SEQUENCE CHARACTERISTICS:

55

- (A) LENGTH: 1297 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

60

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Leishmania amazonensis*  
 (B) STRAIN: ATCC 50131

## 5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 538

	TTCTCGGAGG	GCGTGCCGCC	CGTGCTGACG	GCGCTGGATG	TGACGGAGGA	50
	CCTTGGCCGC	GATGAGCCGC	TGACGCTGGA	GATCGTGACG	CACCTGGACG	100
	CGAACACCGG	CCGCTGCATT	GCGATGCAGA	CGACGGACCT	GTGAAGCTG	150
10	AAGTCGAAGG	TTGTGTTCGAC	CGGCGGCAAC	ATCTCTGTGC	CGGTGGGCCG	200
	TGAGACGCTG	GGCCGCATCT	TCAACGTGCT	GGGCGACGCG	ATCGACCAGC	250
	GCGGCCCCGT	GGGTGAGAAG	ATGCGCATGG	CGATCCACGC	CGAGGCCCCG	300
	AAGCTGGCGG	ATCAGGCCGC	GGAGGACACG	ATCCTGACGA	CCGGCATCAA	350
	GGTGATCGAC	CTGATTCTGC	CCTACTGCAA	GGGTGGCAAG	ATCGGCCTGT	400
15	TTGGTGGCGC	CGGTGTGGGC	AAGACCGTGA	TCATCATGGA	GTTGATTAAAC	450
	AACGTCGCGA	AGGGCCACGG	TGGTTTCTCG	GTGTTTGCCG	GCGTTGGCGA	500
	GCGCACGCGC	GAGGGCACGG	ACCTGTACCT	GGAGATGATG	CAGTCGAAGG	550
	TGATTGACCT	GAAGGGCGAG	TCGAAGTGCG	TGCTTGTGTA	CGGGCAGATG	600
	AACGAGCCCC	CGGGTGCGCG	CGCGCGCGTT	GCGCAGTCTG	CGCTGACGAT	650
20	GGCGGAGTAC	TTCCGAGACG	TGGAGGGCCA	GAATGTGCTG	CTGTTTCATCG	700
	ACAACATCTT	CCGCTTCACG	CAGGCGAACT	CCGAGGTGTC	TGCGCTGCTG	750
	GGCCGCATTC	CGGCCGCCGT	GGGCTACCAG	CCGACGCTTG	CGGAGGATCT	800
	TGGTATGCTG	CAGGAGCGCA	TCACGTCGAC	GACGAAGGGG	TCGATCACGT	850
	CCGTGCAGGC	CGTGTACGTG	CCTGCGGATG	ATATCACGGA	TCCGGCGCCC	900
25	GCGACGACGT	TCTCGCACCT	GGACGCGACG	ACTGTGCTGG	ACCGCGCGGT	950
	GGCGGAGTCG	GGGATCTACC	CTGCCGTGAA	CCCCTGGAG	TGCGCGTCGC	1000
	GTATCATGGA	CCCCGATGTG	ATCGACGTGG	ACCACTACAA	CGTTGCGCAG	1050
	GATATCGTGC	AGATGCTGAC	CAAGTACAAG	GAGCTGCAGG	ATATCATTGC	1100
	GGTGCTTGGT	ATCGACGAGC	TGAGCGAGGA	GGACAAGGTC	GTGGTGGACC	1150
30	GCGCGCGCAA	GGTGACCCGG	TTCCTGTCTG	AGCCGTTCCA	GGTTGCGGAG	1200
	GTGTTTCACG	GATGACGGG	CCACTACGTG	CAGCTGGCCG	ACACGGTGGA	1250
	GTCGTTCTCT	GGGCTGCTGA	TGGGGTCGTA	CGACCAGATC	CCGGAGA	1297

35

## 2) INFORMATION FOR SEQ ID NO: 539

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Single  
 (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: DNA

45

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 539

CCITACATCC TBGTYGCICT IAACAAG

27

50

## 2) INFORMATION FOR SEQ ID NO: 540

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Single  
 (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 540

GGDGCITCYT CRTCGWAITC CTG

23

5

2) INFORMATION FOR SEQ ID NO: 541

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 23 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 541

GTKGAAATGT TCCGCAAGCT GCT

23

20

2) INFORMATION FOR SEQ ID NO: 542

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 24 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 542

CGGAARTAGA ACTGSGGACG GTAG

24

35

2) INFORMATION FOR SEQ ID NO: 543

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 23 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 543

ATCTTAGTAG TTTCTGCTGC TGA

23

50

2) INFORMATION FOR SEQ ID NO: 544

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 23 bases

(B) TYPE: Nucleic acid

335

60



- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 544

AYGTTGTCGC CMGGCATTC CAT

23

10

2) INFORMATION FOR SEQ ID NO: 545

(i) SEQUENCE CHARACTERISTICS:

15

- (A) LENGTH: 26 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

20

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 545

TACATCCTBG TYGCICTIAA CAAGTG

26

25

2) INFORMATION FOR SEQ ID NO: 546

(i) SEQUENCE CHARACTERISTICS:

30

- (A) LENGTH: 23 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

35

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 546

40 CCRCGICCGG TRATGGTGAA GAT

23

2) INFORMATION FOR SEQ ID NO: 547

45

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

50

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 547

55

GTACAGTTGC TTCAGGACGT ATC

23

60 2) INFORMATION FOR SEQ ID NO: 548

336

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 21 bases  
(B) TYPE: Nucleic acid  
5 (C) STRANDEDNESS: Single  
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 548  
ACGTTTCGATT TCATCACGTT G 21

15 2) INFORMATION FOR SEQ ID NO: 549

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 24 bases  
20 (B) TYPE: Nucleic acid  
(C) STRANDEDNESS: Single  
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 549  
GAACGTGATA CTGACAAACC TTTA 24

30 2) INFORMATION FOR SEQ ID NO: 550

(i) SEQUENCE CHARACTERISTICS:  
35 (A) LENGTH: 20 bases  
(B) TYPE: Nucleic acid  
(C) STRANDEDNESS: Single  
(D) TOPOLOGY: Linear

40 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 550  
45 GAAGAAGAAC ACCAACGTTG 20

2) INFORMATION FOR SEQ ID NO: 551

50 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 25 bases  
(B) TYPE: Nucleic acid  
(C) STRANDEDNESS: Single  
55 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 551  
60 GAAGAAAAA TCTTCGAACT GGCTA 25

## 2) INFORMATION FOR SEQ ID NO: 552

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: DNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 552

TACACGGCCG GTGACTACG

19

## 2) INFORMATION FOR SEQ ID NO: 553

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: DNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 553

GGCCGTGTTG AACGTGGTCA AATCA

25

## 2) INFORMATION FOR SEQ ID NO: 554

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: DNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 554

GTTCTTACA TCGTTGTTTT TCTC

24

## 2) INFORMATION FOR SEQ ID NO: 555

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 555

5 TCTCGAACTT TCTCTATGTA TGCA

24

2) INFORMATION FOR SEQ ID NO: 556

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 21 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 556

CGGCGCNATC YTS GTTGTTG C

21

2) INFORMATION FOR SEQ ID NO: 557

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 22 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 557

CCMAGGCATR ACCATCTCGG TG

22

2) INFORMATION FOR SEQ ID NO: 558

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 558

TCITTYAART AYG CITGGGT

20

2) INFORMATION FOR SEQ ID NO: 559

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 23 bases

- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

5 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 559

CCGACRGCRA YIGTYTGICK CAT

23

2) INFORMATION FOR SEQ ID NO: 560

15 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

20

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 560

25 GAYTTCATYA ARAAYATGAT YAC

23

2) INFORMATION FOR SEQ ID NO: 561

30

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

35

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 561

40

ACIGTICGGC CRCCCTCAG GAT

23

2) INFORMATION FOR SEQ ID NO: 562

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

50

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 562

CARATGRAYG ARCCICCI GG IGYIMGIATG

30

60

## 2) INFORMATION FOR SEQ ID NO: 563

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: DNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 563

GGYTGRTAIC CIACIGCIGA IGGCAT

26

## 2) INFORMATION FOR SEQ ID NO: 564

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: DNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 564

TAYGGICARA TGAAYGARCC ICCIGGIAA

29

## 2) INFORMATION FOR SEQ ID NO: 565

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: DNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 565

GGYTGRTAIC CIACIGCIGA IGGDAT

26

## 2) INFORMATION FOR SEQ ID NO: 566

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: DNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 566

5 2) INFORMATION FOR SEQ ID NO: 567

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 26 bases  
(B) TYPE: Nucleic acid  
(C) STRANDEDNESS: Single  
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 567

TCRTCIGCIG GIACRTAIAY IGCYTG

26

20 2) INFORMATION FOR SEQ ID NO: 568

(i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 23 bases  
(B) TYPE: Nucleic acid  
(C) STRANDEDNESS: Single  
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 568

RTIATIGGIG CIGTIRTIGA YGT

23

35 2) INFORMATION FOR SEQ ID NO: 569

(i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 23 bases  
(B) TYPE: Nucleic acid  
(C) STRANDEDNESS: Single  
(D) TOPOLOGY: Linear

45 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 569

RTIRTIGGIS CIGTIRTIGA TAT

23

50

2) INFORMATION FOR SEQ ID NO: 570

55 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 bases  
(B) TYPE: Nucleic acid  
(C) STRANDEDNESS: Single  
(D) TOPOLOGY: Linear

60

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 570

5 RTIRYIGGIC CIGTIRTIGA YGT

23

2) INFORMATION FOR SEQ ID NO: 571

10

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 23 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

15

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 571

20

RTIRTIGGIC CIGTIRTIGA TGT

23

25 2) INFORMATION FOR SEQ ID NO: 572

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 bases

(B) TYPE: Nucleic acid

30

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 572

RTIRTIGGIS CIGTIRTIGA

20

40

2) INFORMATION FOR SEQ ID NO: 573

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 bases

45

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 573

CCICCIACCA TRTARAAIGC

20

55

2) INFORMATION FOR SEQ ID NO: 574

(i) SEQUENCE CHARACTERISTICS:

60

(A) LENGTH: 23 bases

343



(B) TYPE: Nucleic acid  
(C) STRANDEDNESS: Single  
(D) TOPOLOGY: Linear

5 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 574

10 ATIGCIATGG AYGGIACIGA RGG

23

2) INFORMATION FOR SEQ ID NO: 575

15 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 25 bases  
(B) TYPE: Nucleic acid  
(C) STRANDEDNESS: Single  
(D) TOPOLOGY: Linear

20

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 575

25 TIACCATTTC AGTACCTTCT GGTA

25

2) INFORMATION FOR SEQ ID NO: 576

30

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 26 bases  
(B) TYPE: Nucleic acid  
(C) STRANDEDNESS: Single  
(D) TOPOLOGY: Linear

35

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 576

40

AACTTCRTCA AGAAGGTYGG TTACAA

26

2) INFORMATION FOR SEQ ID NO: 577

45

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 bases  
(B) TYPE: Nucleic acid  
(C) STRANDEDNESS: Single  
(D) TOPOLOGY: Linear

50

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 577

55

CATGATTGAA CCATCCACCA

20

60

## 2) INFORMATION FOR SEQ ID NO: 578

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: DNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 578

CATGATTGAA GCTTCCACCA

20

## 2) INFORMATION FOR SEQ ID NO: 579

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: DNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 579

GAAGGCCGTG CTGGTGAGAA

20

## 2) INFORMATION FOR SEQ ID NO: 580

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: DNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 580

GCTAAACCAG CTACAATCAC TCCAC

25

## 2) INFORMATION FOR SEQ ID NO: 581

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: DNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 581

5 2) INFORMATION FOR SEQ ID NO: 582

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 28 bases  
(B) TYPE: Nucleic acid  
10 (C) STRANDEDNESS: Single  
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 582

TTTCAACTTC GTCGTTGACA CGAACAGT

28

20

2) INFORMATION FOR SEQ ID NO: 583

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 35 bases  
25 (B) TYPE: Nucleic acid  
(C) STRANDEDNESS: Single  
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 583

CAACTGCTTT TTGGATATCT TCTTTAATAC CAACG

35

35

2) INFORMATION FOR SEQ ID NO: 584

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 bases  
40 (B) TYPE: Nucleic acid  
(C) STRANDEDNESS: Single  
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 584

ACATGACACA TCTAAAACAA

20

50

2) INFORMATION FOR SEQ ID NO: 585

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 bases  
55 (B) TYPE: Nucleic acid  
(C) STRANDEDNESS: Single  
(D) TOPOLOGY: Linear

60

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 585

5 ACCACATACT GAATTCAAAG 20

2) INFORMATION FOR SEQ ID NO: 586

10

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

15

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 586

20

CAGAAGTATA CGTATTATCA 20

2) INFORMATION FOR SEQ ID NO: 587

25

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 bases

(B) TYPE: Nucleic acid

30

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 587

35

CGTATTATCA AAAGACGAAG 20

2) INFORMATION FOR SEQ ID NO: 588

40

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 bases

45

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 588

TCTTCTCAAA CTATCGTCCA 20

2) INFORMATION FOR SEQ ID NO: 589

55

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 bases

60

- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

5 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 589

GCACGAAACT TCTAAAACAA

20

2) INFORMATION FOR SEQ ID NO: 590

15 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

20

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 590

25 TATACGTATT ATCTAAAGAT

20

2) INFORMATION FOR SEQ ID NO: 591

30

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

35

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 591

40

TCCTGGTTCT ATTACACCAC

20

45 2) INFORMATION FOR SEQ ID NO: 592

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

50

(ii) MOLECULE TYPE: DNA

55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 592

CAAAGCTGAA GTATACGTAT

20

60

## 2) INFORMATION FOR SEQ ID NO: 593

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: DNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 593

TTCACCTAACT ATCGCCCACA

20

## 2) INFORMATION FOR SEQ ID NO: 594

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: DNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 594

ATTGGTATCC ATGACACTTC

20

## 2) INFORMATION FOR SEQ ID NO: 595

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: DNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 595

TTAAAGCAGA CGTATACGTT

20

## 2) INFORMATION FOR SEQ ID NO: 596

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: DNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 596

5 2) INFORMATION FOR SEQ ID NO: 597

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 20 bases  
(B) TYPE: Nucleic acid  
(C) STRANDEDNESS: Single  
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 597

ATTGGTATCA AAGAACTTC

20

20

2) INFORMATION FOR SEQ ID NO: 598

(i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 20 bases  
(B) TYPE: Nucleic acid  
(C) STRANDEDNESS: Single  
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 598

AATTACACCT CACACAAAAT

20

35

2) INFORMATION FOR SEQ ID NO: 599

(i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 20 bases  
(B) TYPE: Nucleic acid  
(C) STRANDEDNESS: Single  
(D) TOPOLOGY: Linear

45 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 599

CGGTGAAGAA ATCGAAATCA

20

50

2) INFORMATION FOR SEQ ID NO: 600

(i) SEQUENCE CHARACTERISTICS:

- 55 (A) LENGTH: 20 bases  
(B) TYPE: Nucleic acid  
(C) STRANDEDNESS: Single  
(D) TOPOLOGY: Linear

60

350

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 600

5 ATGCAAGAAG AATCAAGCAA

20

2) INFORMATION FOR SEQ ID NO: 601

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 601

GTTTCACGTG ATGATGTACA

20

2) INFORMATION FOR SEQ ID NO: 602

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 602

AAGTTGAAGT TGTTGGTATT

20

2) INFORMATION FOR SEQ ID NO: 603

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 603

GGTATTAAAG ACGAAACATC

20

2) INFORMATION FOR SEQ ID NO: 604

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 bases

351



- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

5 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 604

GGTGATGAAG TAGAAATCGT

20

2) INFORMATION FOR SEQ ID NO:605

15 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

20

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 605

25 GAAATGTTCC GTAAATTATT

20

2) INFORMATION FOR SEQ ID NO:606

30

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

35

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 606

40

ATTAGACTAC GCTGAAGCTG

20

45 2) INFORMATION FOR SEQ ID NO: 607

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 821 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

50

(ii) MOLECULE TYPE: Genomic DNA

55 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus faecalis*
- (B) STRAIN: ATCC 29212

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 607

60

	CGGAGCTATC	TTAGTAGTTT	CTGCTGCTGA	TGGTCCTATG	CCTCAAACAC	50
	GTGAACATAT	CTTATTATCA	CGTAACGTTG	GTGTACCATA	CATCGTTGTA	100
	TTCTTAAACA	AAATGGATAT	GGTTGATGAC	GAAGAATTAT	TAGAATTAGT	150
	AGAAATGGAA	GTTCGTGACT	TATTATCAGA	ATACGATTTC	CCAGGCGATG	200
5	ATGTTCCAGT	TATCGCAGGT	TCTGCTTTGA	AAGCTTTAGA	AGGCGACGAG	250
	TCTTATGAAG	AAAAAATCTT	AGAATTAATG	GCTGCAGTTG	ACGAATATAT	300
	CCCAACTCCA	GAACGTGATA	CTGACAAACC	ATTCATGATG	CCAGTCGAAG	350
	ACGTATTCTC	AATCACTGGA	CGTGGTACTG	TTGCTACAGG	ACGTGTTGAA	400
	CGTGGTGAAG	TTCGCGTTGG	TGACGAAGTT	GAAATCGTTG	GTATTAAAGA	450
10	CGAAACATCT	AAAACAACTG	TTACAGGTGT	TGAAATGTTT	CGTAAATTAT	500
	TAGACTACGC	TGAAGCAGGC	GACAACTTCG	GTGCTTTATT	ACGTGGTGTA	550
	GCACGTGAAG	ATATCGAACG	TGGACAAGTA	TTAGCTAAAC	CAGCTACAAT	600
	CACTCCACAC	ACAAAATTCA	AAGCTGAAGT	ATACGTATTA	TCAAAAGAAG	650
	AAGGCGGACG	TCACACTCCA	TTCTTCACTA	ACTACCGTCC	TCAATTCTAC	700
15	TTCCGTACAA	CAGACGTTAC	TGGTGTTGTA	GAATTGCCAG	AAGGTACTGA	750
	AATGGTAATG	CCTGGTGATA	ACGTTGCTAT	GGACGTTGAA	TTAATTCACC	800
	CAATCGCTAT	CGAAGACGGA	A			821

20 2) INFORMATION FOR SEQ ID NO: 608

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 751 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus faecium*  
 (B) STRAIN: ATCC 19434

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 608

	CGGAGCTATC	TTGGTAGTTT	CTGCTGCTGA	CGGCCCAATG	CCTCAAACCTC	50
	GTGAACACAT	CCTATTGTCT	CGTCAAGTTG	GTGTTCTTAA	CATCGTTGTA	100
	TTCTTGAACA	AAGTAGACAT	GGTTGATGAC	GAAGAATTAC	TAGAATTAGT	150
40	TGAAATGGAA	GTTCGTGACC	TATTAACAGA	ATACRAATTC	CCTGGTGRCG	200
	ATGTTCTCTGT	AGTTGCTGGA	TCAGCTTTGA	AAGCTCTAGA	AGGCGACGCT	250
	TCATACGAAG	AAAAAATTCT	TGAATTAATG	GCTGCAGTTG	ACGAATACAT	300
	CCCAACTCCA	GAACGTGACA	ACGACAAACC	ATTCATGATG	CCAGTTGAAG	350
	ACGTGTTCTC	AATTACTGGA	CGTGGTACTG	TTGCTACAGG	TCGTGTTGAA	400
45	CGTGGACAAG	TTCGCGTTGG	TGACGAAGTT	GAAGTTGTTG	GTATTGCTGA	450
	AGAAACTTCA	AAAACAACAG	TTACTGGTGT	TGAAATGTTT	CGTAAATTGT	500
	TAGACYACGC	TGAAGCTGGA	GACRACATTG	GTGCTTTACT	ACGTGGTGTT	550
	GCACGTGAAG	ACATCCAACG	TGGACAAGTT	TTAGCTAAAC	CAGGTACAAT	600
	CACACCTCRT	ACAAAATTCT	CTGCAGAAGT	ATACGTGTTG	ACAAAAGAAG	650
50	AAGGTGGACG	TCATACTCCA	TTCTTCACTA	ACTACCGTCC	ACAATTCTAC	700
	TTCCGTACAA	CTGACGTAAC	AGGTGTTGTT	GAATTACCAG	AAGGAACTGA	750
	A					751

55 2) INFORMATION FOR SEQ ID NO: 609

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 751 bases  
 (B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

5

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Enterococcus gallinarum*

(B) STRAIN: ATCC 49573

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 609

	CGGTGCGATC	TTAGTAGTAT	CTGCTGCTGA	CGGTCCTATG	CCTCAAACCTC	50
	GTGAACACAT	CTTGTTATCA	CGTAACGTTG	GCGWACCATA	CATCGTTGTT	100
	TTCTTGAACA	AAATGGATAT	GGTTGAYGAC	GAAGAATTGC	TAGAATTAGT	150
15	TGAAATGGAA	GTTTCGTGACC	TATTGTCTGA	ATATGACTTC	CCAGGCGACG	200
	ATGTTCTCTGT	AATCGCCGGT	TCTGCTTTGA	AAGCTCTTGA	AGGAGATCCT	250
	TCATACGAAG	AAAAAATCAT	GGAATTGATG	GCTGCAGTTG	ACGAATACGT	300
	TCCAACCTCCA	GAACGTGATA	CTGACAAACC	ATTCATGATG	CCAGTCGAAG	350
	ACGTATTCTC	AATCACTGGA	CGTGGTACTG	TTGCTACAGG	CCGTGTTGAA	400
20	CGTGGACAAG	TTCGCGTTGG	TGATGAAGTA	GAAATCGTTG	GTATTGCTGA	450
	CGAAACTGCT	AAAACAACTG	TAACAGGTGT	TGAAATGTTT	CGTAAATTGT	500
	TAGACTATGC	TGAAGCAGGG	GATAACATTG	GTGCATTGCT	ACGTGGGGTT	550
	GCTCGTGAAG	ACATCCAACG	TGGACAAGTA	TTGGCTAAAG	CTGGTACRAT	600
	CACACCTCAT	ACAAAATTCA	AAGCTGAAGT	TTATGTTTTG	ACAAAAGAAG	650
25	AAGGTGGRCG	TCACACTCCA	TTCTTCACTA	ACTACCGTCC	TCAGTTCTAC	700
	TTCCGTACAA	CTGACGTAAC	TGGTGTGTGT	GAATTACCAG	AAGGAACTGA	750
	A					751

30

2) INFORMATION FOR SEQ ID NO: 610

(i) SEQUENCE CHARACTERISTICS:

35	(A) LENGTH: 891 bases
	(B) TYPE: Nucleic acid
	(C) STRANDEDNESS: Double
	(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

40

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Haemophilus influenzae* Rd

(B) STRAIN: KW20

(C) ACCESSION NUMBER: extracted from U32739

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 610

	AATATGATTA	CTGGTGCGGC	ACAAATGGAT	GGTGCTATTT	TAGTAGTAGC	50
	AGCAACAGAT	GGTCCTATGC	CACAAACTCG	TGAACACATC	TTATTAGGTC	100
50	GCCAAGTAGG	TGTTCCATAC	ATCATCGTAT	TCTTAAACAA	ATGCGACATG	150
	GTAGATGACG	AAGAGTTATT	AGAATTAGTC	GAAATGGAAG	TTCGTGAACT	200
	TCTATCTCAA	TATGACTTCC	CAGGTGACGA	TACACCAATC	GTACGTGGTT	250
	CAGCATTACA	AGCGTTAAAC	GGCGTAGCAG	AATGGGAAGA	AAAAATCCTT	300
	GAGTTAGCAA	ACCACTTAGA	TACTTACATC	CCAGAACCAG	AACGTGCGAT	350
55	TGACCAACCG	TTCCTTCTTC	CAATCGAAGA	TGTGTTCTCA	ATCTCAGGTC	400
	GTGGTACTGT	AGTAACAGGT	CGTGTAGAAC	GAGGTATTAT	CCGTACAGGT	450
	GATGAAGTAG	AAATCGTCGG	TATCAAAGAT	ACAGCGAAAA	CTACTGTAAC	500
	GGGTGTTGAA	ATGTTCCGTA	AATTACTTGA	CGAAGGTCGT	GCAGGTGAAA	550
	ACATCGGTGC	ATTATTACGT	GGTACCAAAC	GTGAAGAAAT	CGAAGCTGGT	600
60	CAAGTATTAG	CGAAACCAGG	TTCAATCACA	CCACACACTG	ACTTCGAATC	650

	AGAAGTGTAC	GTATTATCAA	AAGATGAAGG	TGGTCGTCAT	ACTCCATCTCT	700
	TCAAAGGTTA	CCGTCCACAA	TTCTATTTCC	GTACAACAGA	CGTGACTGGT	750
	ACAATCGAAT	TACCAGAAGG	CGTGGAAATG	GTAATGCCAG	GCGATAACAT	800
	CAAGATGACA	GTAAGCTTAA	TCCACCCAAT	TGCGATGGAT	CAAGGTTTAC	850
5	GTTTCGCAAT	CCGTGAAGGT	GGCCGTACAG	TAGGTGCAGG	C	891

## 2) INFORMATION FOR SEQ ID NO: 611

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 818 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus epidermidis*  
 (B) STRAIN: ATCC 14990

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 611

25	CGGCGGTATC	TTAGTTGTAT	CTGCTGCTGA	CGGTCCAATG	CCACAAACTC	50
	GTGAACACAT	CTTATTATCA	CGTAACGTTG	GTGTACCAGC	ATTAGTTGTA	100
	TTCTTAAACA	AAGTTGACAT	GGTAGACGAC	GAAGAATTAT	TAGAATTAGT	150
	TGAAATGGAA	GTTTCGTGACT	TATTAAGCGA	ATATGACTTC	CCAGGTGACG	200
	ATGTACCTGT	AATCGCTGGT	TCTGCATTAA	AAGCATTAGA	AGGCGATGCT	250
30	GAATACGAAC	AAAAAATCTT	AGACTTAATG	CAAGCAGTTG	ATGATTACAT	300
	TCCAACCTCA	GAACGTGATT	CTGACAAACC	ATTCATGATG	CCAGTTGAGG	350
	ACGTATTCTC	AATCACTGGT	CGTGGTACTG	TTGCTACAGG	CCGTGTTGAA	400
	CGTGGTCAAA	TCAAAGTTGG	TGAAGAAGTT	GAAATCATCG	GTATGCACGA	450
	AACTTCTAAA	ACAACGTGTA	CTGGTGTAGA	AATGTTCCGT	AAATTATTAG	500
35	ACTACGCTGA	AGCTGGTGAC	AACATCGGTG	CTTTATTACG	TGGTGTTGCA	550
	CGTGAAGACG	TACAACGTGG	TCAAGTATTA	GCTGCTCCTG	GTTCTATTAC	600
	ACCACACACA	AAATTCAAAG	CTGAAGTATA	CGTATTATCT	AAAGATGAAG	650
	GTGGACGTCA	CACTCCATTC	TTCACCTAAT	ATCGCCCACA	ATTCTATTTT	700
	CGTACTACTG	ACGTAACTGG	TGTTGTAAAC	TTACCAGAAG	GTACAGAAAT	750
40	GGTTATGCCT	GGCGACAACG	TTGAAATGAC	AGTTGAATTA	ATCGCTCCAA	800
	TCGCTATCGA	AGACGGAA				818

## 2) INFORMATION FOR SEQ ID NO: 612

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 825 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Salmonella choleraesuis* subsp. *choleraesuis*  
 serotype Paratyphi A  
 (B) STRAIN: ATCC 9150

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 612

	GGCGCGATCC	TGGTTGTTGC	TGCGACTGAC	GGCCCGATGC	CGCAGACCCG	50
	TGAGCACATC	CTGCTGGGTC	GTCAGGTAGG	CGTTCGGTAC	ATCATCGTGT	100
	TCCTGAACAA	ATGCGACATG	GTTGATGACG	AAGAGCTGCT	GGAAGTGGTT	150
5	GAAATGGAAG	TTCGTGAACT	TCTGTCTCAG	TACGACTTCC	CGGGCGACGA	200
	CACGCCGATC	GTTTCGTGGT	CTGCTCTGAA	AGCGCTGGAA	GGCGACGCAG	250
	AGTGGAAGC	GAAAATCATC	GAAGTGGCTG	GCTTCCTGGA	TTCTTACATC	300
	CCGGAACCAG	AGCGTGCGAT	TGACAAGCCG	TTCCTGCTGC	CGATCGAAGA	350
	CGTATTCTCC	ATCTCCGGTC	GTGGTACCGT	TGTTACCGGT	CGTGTAGAAC	400
10	GCGGTATCAT	CAAAGTGGGC	GAAGAAGTTG	AAATCGTTGG	TATCAAAGAG	450
	ACTCAGAAAGT	CTACCTGTAC	TGGCGTTGAA	ATGTTCCGCA	AACTGCTGGA	500
	CGAAGGCCGT	GCCGGTGAGA	ACGTAGGTGT	TCTGCTGCGT	GGTATCAAAC	550
	GTGAAGAAAT	CGAACGTGGT	CAGGTACTGG	CTAAGCCGGG	CACCATCAAG	600
	CCGCACACCA	AGTTCGAATC	TGAAGTGTAC	ATTCTGTCCA	AAGATGAAGG	650
15	CGGCCGTCAT	ACTCCGTTCT	TCAAAGGCTA	CCGTCCGCAG	TTCTACTTCC	700
	GTACTACTGA	CGTGACTGGC	ACCATCGAAC	TGCCGGAAGG	CGTAGAGATG	750
	GTAATGCCGG	GCGACAACAT	CAAAATGGTT	GTTACCCTGA	TCCACCCGAT	800
	CGCAATGGAC	GACGGTCTGC	GTTTC			825

20

## 2) INFORMATION FOR SEQ ID NO: 613

## (i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 778 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

## 30 (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Serratia ficaria*  
 (B) STRAIN: ATCC 33105

35

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 613

	GGCGCTATCC	TGGTTGTTGC	TGCGACTGAC	GGCCCAATGC	CTCAGACCCG	50
	TGAGCACATC	CTGCTGGGTC	GYCAGGTTGG	CGTTCCTTTC	ATCATCGTRT	100
40	TCATGAACAA	ATGCGACATG	GTTGATGATG	AAGAGCTGCT	GGAAGTGGTA	150
	GAAATGGAAG	TTCGCGAACT	GCTGTCCGCT	TACGACTTCC	CTGGCGATGA	200
	CCTGCCGGTG	ATTCGCGGTT	CCGCGCTGAA	AGCGCTGGAA	GGCGAAGCCG	250
	AGTGGAAGC	TAAAATCATC	GAGCTGCTG	AMCMSCTGGA	TACTTACATC	300
	CCAGAACCAG	AGCGCGCTAT	CGACAAGCCG	TTCCTGCTGC	CAATCGAAGA	350
45	CGTATTCTCC	ATCTCCGGTC	GTGGTACCGT	GGTTACCGGT	CGTGTGAGC	400
	GCGGTATCAT	CAAAGTTGGC	GAAGAAGTTG	AAATCGTTGG	TATCAAAGAC	450
	ACCGTCAAGT	CTACCTGTAC	CGGCGTTGAA	ATGTTCCGCA	AACTGCTGGA	500
	CGAAGGCCGT	GCCGGTGAGA	ACGTAGGTGT	TCTGCTGCGT	GGTATCAAGC	550
	GTGAAGACAT	CGAACGTGGT	CAGGTTCTGG	CTAAACCAGG	TTCCATCAAG	600
50	CCGCACACCC	AGTTCGATTC	AGAAGTGTAC	ATCCTGAGCA	AAGAAGAAGG	650
	TGGTCGTCAC	ACKCCATTCT	TCAAAGGCTA	CCGTCCACAG	TTCTACTTCC	700
	GTACTACTGA	CGTGACCGGT	ACCATCGAAC	TGCCAGAAGG	CGTTGAGATG	750
	GTAATGCCTG	GCGACAACGT	GAACATGA			778

55

## 2) INFORMATION FOR SEQ ID NO: 614

## (i) SEQUENCE CHARACTERISTICS:

- 60 (A) LENGTH: 653 bases

356

- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

5 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus malodoratus*
- (B) STRAIN: ATCC 43197

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 614

	GTGCGATCTT	AGTAGTATCA	GCTACTGATG	GTCCAATGCC	TCAAACCTCGT	50
	GAACACATTT	TGTTATCACG	TCAAGTTGGT	GTAAAGCACT	TGATCGTTTT	100
15	CTTGAACAAA	GTAGATTTAG	TTGATGACGA	AGAATTGATC	GACTTAGTTG	150
	AAATGGAAGT	ACGTGAATTA	CTTTCTGAAT	ATGGTTTCCC	AGGTGATGAT	200
	ATTCCAGTGC	TTAAAGGTTT	TGCTTTGAAA	GCATTAGAAG	GCGATCCAGA	250
	ACAAGAACAA	GTTATTCTTG	ATTTGATGGA	TACCGTTGAT	GAATATATCC	300
	CAACACCTGA	ACGTGACAAT	GACAAACCGT	TCTTGTTACC	AGTTGAGGAT	350
20	GTTTTCTCGA	TCACAGGACG	TGGTACTGTA	GCTTCTGGTC	GTATCGACCG	400
	TGGCGAAGTT	AAAGTCGGCG	ATGAAATTGA	AATCATCGGG	ATCAAACCTG	450
	AAGTTCAAAA	AGCAATCGTT	ACTGGACTTG	AAATGTTCCG	TAAAACATTG	500
	GATTATGGTG	AAGCTGGCGA	TAACGTTGGG	GTTCTATTAC	GTGGGATTAC	550
	ACGTGATGAA	ATCGAACGTG	GCCAAGTATT	AGCTAAACCA	GGTTCAATCA	600
25	CACCACATAC	TAAGTTCAAA	GCCGAAGTAT	ATGTGTTGAC	GAAAGAAGAA	650
	GGT					653

30 2) INFORMATION FOR SEQ ID NO: 615

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 829 bases
- (B) TYPE: Nucleic acid
- 35 (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

40 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus durans*
- (B) STRAIN: ATCC 19432

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 615

45

	CCATTCTAGT	TGTATCTGCA	ACAGATGGAC	CAATGCCACA	AACACGTGAA	50
	CATATTTTAT	TGTCACGTCA	AGTAGGTGTT	AAATATTTGA	TCGTCTTCTT	100
	GAACAAAATC	GACTTAGTAG	ATGATGAAGA	ATTGATTGAT	CTTGTCGAAA	150
	TGGAAGTTTCG	TGAATTATTA	AGCGAATATG	GTTTCCCAGG	TGACGATACA	200
50	CCAGTCATCA	AAGGTTTCAGC	ATTAAAAGCT	TTACAAGGAG	ATCCTGATGC	250
	AGAAGCAGCT	ATCATGGAAT	TGATGGATAC	TGTTGATGAA	TATATCCCAA	300
	CACCAGAACG	TGATACAGAC	AAACCATTAT	TGTTACCAGT	GGAAGATGTC	350
	TTCTCAATCA	CAGGTCGTGG	GACTGTTGCT	TCAGGTCGTA	TCGATCGTGG	400
	TGCAGTTCGT	GTAGGTGATG	AAATCGAAAT	CGTCGGTATC	AAACCTGAAA	450
55	CACAAAAGC	TGTTGTAAC	GGGGTCGAAA	TGTTCCGCAA	GACATTAGAC	500
	TATGGTGAAG	CAGGAGATAA	CGTTGGGGTA	TTGTTACGTG	GTATCCAACG	550
	TGAAGATATC	GAACGTGGAC	AAGTAATCGC	AAAACCAGGT	TCAATCACAC	600
	CACATACAAA	ATTCAAAGCA	GAAGTGTACG	TATTGACAAA	AGAAGAAGGT	650
	GGACGTCATA	CACCATTTCTT	CAATAACTAT	CGTCCACAAT	TCTACTTCCG	700
60	TACAACTGAC	GTAAC	TGGAA	CAATCGTTT	ACCTGGAGGC	750

TTATGCCTGG AGATAACGTA ACGATCGACG TTGAATTGAT CCATCCAGTT 800  
GCCATCGAAA ACGGAACAAC TTTCTCTAT 829

5

## 2) INFORMATION FOR SEQ ID NO: 616

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 669 bases  
(B) TYPE: Nucleic acid  
(C) STRANDEDNESS: Double  
(D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus pseudoavium*  
(B) STRAIN: ATCC 49372

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 616

	GGTGCAATTT	TAGTAGTATC	TGCTACTGAT	GGCCCAATGC	CACAAACACG	50
	TGAACATATC	TTGTTATCAC	GTCAAGTAGG	GGTTAAACAC	TTAATCGTCT	100
	TCTTGAACAA	AGTTGATTTA	GTTGATGATG	AAGAATTGAT	CGATTTAGTT	150
25	GAAATGGAAG	TTCGGGAATT	GCTTTCTGAA	TATGGTTTCC	CAGGCGATGA	200
	TATTCCAGTA	CTTAAAGGTT	CTGCTTTGAA	AGCTTTAGAA	GGCGATCCTG	250
	AACAAGAACA	AGTAATCCTT	GACTTGATGG	ATACGGTTGA	TGAATACATC	300
	CCAACGCCTG	AACGTGATAC	TGACAAACCA	TTCTTGTTAC	CAGTCGAAGA	350
	TGTCTTCTCA	ATCACAGGAC	GTGGTACGGT	TGCATCTGGT	CGTATCGATC	400
30	GTGGGGAAGT	TAAAGTCGGT	GATGAAGTTG	AAATCATCGG	GATCAAACCT	450
	GAAGTGCAAA	AAGCTGTCGT	AACTGGACTA	GAAATGTTCC	GTAAGACATT	500
	GGATTACGGT	GAAGCTGGCG	ATAACGTTGG	GGTTCTATTA	CGTGGGATTA	550
	CTCGTGATGA	AATCGAACGT	GGACAAGTAT	TAGCTAAACC	AGGTTCAATC	600
	ACTCCACATA	CGAAATTCAG	TGCAGAAGTT	TATGTATTGA	CGAAAGAAGA	650
35	AGGTGGCCGT	CATACGCCA				669

## 2) INFORMATION FOR SEQ ID NO: 617

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 835 bases  
(B) TYPE: Nucleic acid  
(C) STRANDEDNESS: Double  
(D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus dispar*  
(B) STRAIN: ATCC 51266

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 617

55	CGGGGCAATT	TTAGTTGTAT	CTGCAACTGA	TGGCCCAATG	CCACAAACAC	50
	GTGAACACAT	TTTGTTAGCT	CGTCAAGTAG	GGGTAAATA	TTAATCGTC	100
	TTCTTGAACA	AAACAGATTT	AGTTGATGAT	GAAGAATTAT	TGGAAC TAGT	150
	TGAAATGGAA	GTTCTGTGAAT	TATTAAATGA	ATACAATTTT	CCTGGCGATG	200
	ATATTCCTGT	TATTCGCGGA	TCTGCTTTAA	AAGCATTAGA	AGGCGATCCA	250
60	GAACAAGAAG	AAGTAATTAT	GAAC TTGATG	GATACTGTGG	ATGAATATAT	300

	CCCAACTCCA	GAACGTGACA	ATGATAAACC	ATTCTTGTTA	CCAGTGAAG	350
	ATGTCTTCAC	AATTACTGGT	CGTGGTACTG	TTGCTTCAGG	TCGTATCGAC	400
	CGTGGTAAAG	TCAACGTTGG	TGATGAAATT	GAAATTATCG	GAATTAAACC	450
	AGAAACACAA	AAAGCTGTTG	TAACCGGTTT	GGAAATGTTC	CGTAAACTTT	500
5	TGGATTATGG	TGAAGCTGGT	GATAACGTTG	GGGTCTTATT	ACGTGGGATT	550
	ACTCGTGATG	AAGTAGAACG	TGGTCAAGTA	TTAGCAAAAC	CAGGTTCCAT	600
	TACACCGCAT	ACCAAATTTA	AAGGTGAAGT	TTATATCTTA	ACAAAAGAAG	650
	AAGGTGGACG	TCATACTCCT	TTCTTTAATA	ACTATCGTCC	TCAATTTTAT	700
	TTCCGTACAA	CTGATGTGAC	TGGTAACATC	GCATTACCTG	AAGGAACCTG	750
10	AATGGTAATG	CCTGGTGATA	ATGTAACAAT	TGAAGTTGAA	TTGATTCATC	800
	CAATCGCCGT	TGAAAAAGGG	ACTACTTTCT	CAATT		835

## 15 2) INFORMATION FOR SEQ ID NO: 618

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 673 bases  
 (B) TYPE: Nucleic acid  
 20 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

## 25 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus avium*  
 (B) STRAIN: ATCC 14025

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 618

30	GGTGCAATCC	TAGTAGTATC	AGCTACTGAT	GGTCCAATGC	CGCAAACACG	50
	TGAACATATT	TTGCTATCAC	GGCAAGTGGG	TGTTAAACAC	TTAATCGTAT	100
	TTTTAAACAA	AGTTGATTTA	GTCGATGATG	AAGAATTGAT	CGATCTAGTT	150
	GAAATGGAAG	TCCGTGAATT	ACTTTCTGAA	TATGGTTTCC	CAGGTGACGA	200
35	TATTCCAGTT	CTCAAAGGTT	CAGCTTTGAA	AGCATTAGAA	GGCGATCCTG	250
	AACAAGAACA	AGTAATCCTT	GATTTAATGG	ATACAGTTGA	CGAATATATC	300
	CCAACTCCAG	AACGTGACAC	TGACAAGCCA	TTCTTGTTAC	CAGTCGAAGA	350
	TGTATTTTCT	ATCACTGGTC	GTGGGACTGT	AGCGTCTGGA	CGGATTGATC	400
	GTGGTGAAGT	TAAAGTCGGC	GATGAAGTTG	AAATCATCGG	GATCAAACCT	450
40	GAAATTCAAA	AAGCAGTCGT	AACTGGACTT	GAAATGTTCC	GTAAAACCTT	500
	AGATTATGGT	GAAGCTGGCG	ATAACGTTGG	GGTTCCTATTA	CGTGGGATTA	550
	CACGTGATGA	AATCGAACGT	GGTCAAGTCT	TAGCTAAACC	AGGTTCAATC	600
	ACACCACATA	CAAAATTCAG	TGCAGAAGTT	TACGTATTGA	CGAAAGAAGA	650
45	AGGTGGACGT	CATACACCAT	CTT			673

## 2) INFORMATION FOR SEQ ID NO: 619

## 50 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1713 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 55 (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Saccharomyces cerevisiae*  
 60 (C) ACCESSION NUMBER: K00428



## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 619

5	TTTCATATTT	TTAAGGATTT	TGTTTTAGCA	CCCATCCGAC	CTCAGTCAAT	50
	ATATCCTTTC	GCGACCAGGC	TTTCCTCCCT	TTTGCTGCTA	ACTGGTTACA	100
	GATTTTCCTA	TTTTTGGTCA	TTTTTATCTT	TGAAACTGAT	TAAGCTGAAA	150
	AAATTTGAGC	TTCTTTGTTG	TAAACTATTT	TGTGCTTTCA	GTTTTATTCT	200
	AGCTCGACAA	AGGTAACAGA	CAAAAATGTC	AGCTTTATTA	CCAAGATTAC	250
	TCACAAGAAC	AGCTTTTAAA	GCTTCTGGGA	AACTTCTGAG	GCTCTCTTCA	300
10	GTAATTTCTA	GGACCTTTTC	TCAAACACT	ACTTCCTATG	CAGCTGCTTT	350
	TGATCGTTCC	AAACCGCATG	TAAATATAGG	TACGATCGGC	CATGTTGATC	400
	ATGGGAAGAC	AACTTTAACC	GCAGCCATTA	CGAAAACGTT	AGCCGCAAAA	450
	GGTGGTGCCA	ACTTCTTGGA	CTATGCTGCC	ATCGATAAGG	CTCCGGAAGA	500
	AAGAGCTCGT	GGTATTACAA	TTTCTACTGC	ACACGTGGAA	TACGAAACGG	550
15	CCAAGAGACA	TTATTCTCAC	GTCGACTGTC	CAGGCCACGC	TGATTACATC	600
	AAGAATATGA	TTACCGGTGC	TGCTCAAATG	GATGGTGCTA	TCATTGTTGT	650
	AGCTGCTACC	GATGGACAAA	TGCCCCAAAC	TAGAGAACAT	TTACTTTTGG	700
	CCAGACAAGT	TGGTGTCCAA	CATATTGTCG	TTTTTGTTAA	CAAGGTTGAT	750
	ACCATTGATG	ATCCAGAAAT	GTTAGAGTTA	GTCGAAATGG	AAATGAGAGA	800
20	ACTTTTAAAC	GAATATGGGT	TTGACGGTGA	TAATGCTCCA	ATTATCATGG	850
	GTTCTGCCCT	TTGCGCTTTG	GAAGGTCGCC	AACCTGAAAT	TGGGGAGCAG	900
	GCCATCATGA	AACTTTTGGA	TGCAGTGGAT	GAGTATATTC	CTACACCTGA	950
	AAGAGATTTG	AACAAGCCTT	TCTTGATGCC	CGTTGAAGAT	ATCTTCTCTA	1000
	TCTCCGGTAG	AGGTACTGTG	GTCAGTGGTC	GTGTGGAAAG	GGGTAATTTA	1050
25	AAGAAAGGTG	AGGAATTGGA	AAATGTTGGT	CACAACTCCA	CCCCATTGAA	1100
	AACAACAGTT	ACTGGTATTG	AAATGTTTAG	AAAGGAATTG	GACTCTGCTA	1150
	TGGCAGGTGA	CAATGCCGGT	GTTTTACTTA	GAGGTATCAG	GAGAGATCAA	1200
	TTGAAGAGAG	GTATGGTCTT	AGCTAAGCCA	GGTACCGTTA	AAGCCCATAC	1250
	AAAGATTCTA	GCCTCTTTGT	ACATTTTATC	CAAAGAGGAA	GGTGGTAGAC	1300
30	ATTCTGGGTT	TGGTGAAAAC	TACAGACCAC	AAATGTTTAT	AAGAACAGCT	1350
	GATGTTACAG	TTGTGATGAG	ATTTCTTAAG	GAGGTTGAAG	ATCATTCTAT	1400
	GCAAGTTATG	CCAGGTGACA	ATGTTGAAAT	GGAATGTGAT	TTGATCCATC	1450
	CTACCCCAT	AGAAGTTGGT	CAACGTTTCA	ATATCAGAGA	GGGTGGAAGA	1500
	ACTGTTGGTA	CCGGTCTAAT	CACACGTATT	ATTGAATAGA	CTTATTGATG	1550
35	CAACTGGAGT	ATATTTCTAT	ATATTCTGTT	CATTTCCCTT	CTCATAATAT	1600
	ATACTTGTTT	CGTTAAAATT	TTATACGTGT	AAATAAAGTG	CCATAAATTT	1650
	TTCAGCTTTA	CTTTTGGTAG	AGTCCTGCTA	GCACTAGATT	TTACAATTTT	1700
	ATGTGCACAC	ACC				1713

40

## 2) INFORMATION FOR SEQ ID NO: 620

## (i) SEQUENCE CHARACTERISTICS:

- |    |     |                      |
|----|-----|----------------------|
| 45 | (A) | LENGTH: 18 bases     |
|    | (B) | TYPE: Nucleic acid   |
|    | (C) | STRANDEDNESS: Single |
|    | (D) | TOPOLOGY: Linear     |

50 (ii) MOLECULE TYPE: DNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 620

ATTGGTG CAT TGCTACGT

55

18

## 2) INFORMATION FOR SEQ ID NO: 621

## (i) SEQUENCE CHARACTERISTICS:

60

360

- (A) LENGTH: 751 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

5

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus faecium*  
 (B) STRAIN: ATCC 19434

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 621

15	TGGTGCAATC	TTAGTTGTTT	CTGCAACTGA	CGGTCCGATG	CCTCAAACAC	50
	GTGAACACAT	TTTATTGTCA	CGCCAAGTTG	GTGTAAAATA	CCTGATTGTT	100
	TTCTTGAACA	AAGTTGATTT	AGTCGATGAT	GAAGAATTGA	TCGATTGTTG	150
	AGAAATGGAA	GTTTCGCGAGT	TATTGAGCGA	ATATGGTTTC	CCAGGCGATG	200
	ACACTCCTGT	GATCAAAGGT	TCCGCATTAA	AAGCATTGCA	AGGCGATCCA	250
	GATGCTGAAG	CTGCTATTAT	GGAATTGATG	GATACAGTAG	ATGAATATAT	300
20	CCCAACACCA	GAACGTGATA	CAGATAAACC	ATTACTATTG	CCAGTGAAG	350
	ACGTCTTCTC	AATTACAGGT	CGAGGAACTG	TTGCCCTCAGG	TCGTATTGAT	400
	CGTGGTGCTG	TTCGTGTCGG	TGATGAGGTA	GAGATCGTAG	GGATCAAACC	450
	TGAAACACAA	AAAGCAGTTG	TAACAGGTGT	AGAAATGTTC	CGTAAAACGT	500
	TAGATTACGG	GGAAGCTGGG	GATAACGTAG	GCGTGTTGTT	ACGGGGGATC	550
25	CAACGTGACG	ATATCGAACG	TGGACAAGTA	CTTGCTAAAC	CAGGTTCCAT	600
	TACTCCACAT	ACAAAATTCA	AAGCAGAAGT	GTACGTGTTG	ACAAAAGAAG	650
	AAGGTGGACG	TCATACTCCA	TTCTTCAACA	ACTATCGTCC	ACAGTTCTAC	700
	TTCCGCACAA	CTGATGTTAC	AGGAACAATC	ACATTGCCAG	AAGATACAGA	750
30	A					751

2) INFORMATION FOR SEQ ID NO: 622

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 750 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

40

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Saccharomyces cerevisiae*  
 (B) STRAIN: ATCC 13264

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 622

50	GTCAAATGGG	ACGAATCCAG	ATTCCAAGAA	ATTGTCAAGG	AAACCTCCAA	50
	CTTTATCAAG	AAGGTTGGTT	ACAACCCAAA	GACTGTTCCA	TTCGTCCCAA	100
	TCTCTGGTTG	GAACGGTGAC	AACATGATTG	AAGCTACCAC	CAACGCTCCA	150
	TGGTACAAGG	GTTGGGAAAA	GGAAACCAAG	GCCGGTGTCG	TCAAGGGTAA	200
	GACTTTGTTG	GAAGCCATTG	ACGCCATTGA	ACAACCATCT	AGACCAACTG	250
	ACAAGCCATT	GAGATTGCCA	TTGCAAGATG	TTTACAAGAT	TGGTGGTATT	300
55	GGTACTGTGC	CAGTCGGTAG	AGTTGAAACC	GGTGTCATCA	AGCCAGGTAT	350
	GGTTGTTACT	TTCGCCCCAG	CTGGTGTTAC	CACTGAAGTC	AAGTCCGTTG	400
	AAATGCATCA	CGAACAATTG	GAACAAGGTG	TTCCAGGTGA	CAACGTTGGT	450
	TTCAACGTCA	AGAACGTTTC	CGTTAAGGAA	ATCAGAAGAG	GTAACGTCTG	500
	TGGTGACGCT	AAGAACGATC	CACCAAAGGG	TTGCGCTTCT	TTCAACGCTA	550
60	CCGTCATTGT	TTTGAACCAT	CCAGGTCAAA	TCTCTGCTGG	TTACTCTCCA	600

361

GTTTTGGATT	GTCACACTGC	TCACATTGCT	TGTAGATTCG	ACGAATTGTT	650
GGAAAAGAAC	GACAGAAGAT	CTGGTAAGAA	GTTGGAAGAC	CATCCAAAGT	700
TCTTGAAGTC	CGGTGACGCT	GCTTTGGTCA	AGTTCGTTCC	ATCTAAGCCA	750

5

## 2) INFORMATION FOR SEQ ID NO: 623

## (i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 1269 bases  
(B) TYPE: Nucleic acid  
(C) STRANDEDNESS: Double  
(D) TOPOLOGY: Linear

## 15 (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Cryptococcus neoformans*  
(B) STRAIN: ATCC 44104

20

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 623

TCTTGAAAGC	TTAAGGCCGA	GCGAGAGCGA	GGTATCACCA	TCGACATTGC	50
TCTTTGGAAG	TTCGAGACCC	CCAGGTACCA	GGTCACCGTC	ATTGACGCCC	100
CCGGTCACCG	AGACTTCATC	AAGAACATGA	TCACCGGTAC	CTCCCAGGCT	150
GACTGTGCCA	TCCTCATCAT	TGCCACCGGT	ATCGGTGAGT	TCGAGGCCGG	200
TATCTCCAAG	GACGGTCAGA	CCCGAGACA	CGCCCTCCTC	GCCTTCACCC	250
TCGGTGTCTAG	GCAGCTCATT	GTTGCTTGCA	ACAAGATGGA	CACCTGCAAG	300
TGGTCCGAGG	ACCGATTCAA	CGAAATCGTC	AAGGAGACCA	ACGGTTTCAT	350
CAAGAAGGTT	GGTTACAACC	CCAAGGCTGT	CCCCTTCGTC	CCCATCTCTG	400
GTTGGCACGG	TGACAACATG	TTGGAGGAGA	CCACCAAGTC	AGTGAATCCG	450
CTTCTACGTG	ATGAGATGTT	TTTCTGACTT	TCCGTGCAGC	ATGCCCTGGT	500
ACAAGGGATG	GACCAAGGAG	ACCAAGTCTG	GTGTTTCCAA	GGGTAAGACC	550
CTCCTCGAGG	CCATCGACGC	CATCGAGCCC	CCTACCCGAC	CCACCGACAA	600
35 GCCCTTCCGT	CTCCCTCTCC	AGGACGTCTA	CAAGATCGGT	GGTATCGGCA	650
CAGTCCCTGT	CGGCCGAGTC	GAGACCGGTG	TCATCAAGGC	CGGTATGTTG	700
TCTCATCTCT	CTTGTCTCGT	AACATGCGTC	TCGTAACATG	CGCTTACTTC	750
ATTTTCAGGT	ATGGTCGTCA	AGTTCGCCCC	CACCAACGTC	ACCACTGAAG	800
TCAAGTCCGT	TGAGATGCAC	CACGAGCAGA	TCCCCGAGGG	TCTTCCCCGGA	850
40 GACAACGTTG	GTTTCAACGT	CAAGAACGTT	TCCATCAAGG	ACATCCGACG	900
AGGTAACGTC	TGTGGTGACT	CCAAGAACGA	CCCCCTATG	GAGGCTGCTT	950
CTTTCAACGC	CCAGGTTATC	GTCCTTAACC	ACCCTGGTCA	GATCGGTGCC	1000
GGTTACACCC	CCGTTCTCGA	CTGTCACACT	GCCCGTAAGC	CTGACCCAAT	1050
ACCTCCAACA	TACCTTTGAA	GCTGACCCTT	TCTAGACATT	GCCTGCAAGT	1100
45 TTGCTGAGTT	GATCGAGAAG	ATTGACCGAC	GAACCGGTAA	GGTCATGGAG	1150
GCCGCCCCCA	AGTTCGTCAA	GTCTGGTGAC	GCCGCCATTG	TCAAGCTTGT	1200
TGCCCAGAAG	CCCCTCTGTG	TTGAGACCTA	CGCCGACTAC	CCCCCTCTTG	1250
GTCGATTTCG	CGTCCGAGA				1269

50

## 2) INFORMATION FOR SEQ ID NO: 624

## (i) SEQUENCE CHARACTERISTICS:

- 55 (A) LENGTH: 753  
(B) TYPE: Nucleic acid  
(C) STRANDEDNESS: Double  
(D) TOPOLOGY: Linear

## 60 (ii) MOLECULE TYPE: Genomic DNA

362

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Candida albicans*

(B) STRAIN: ATCC 36801

5

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 624

	TCTGTCAAAT	GGGACAAAAA	CAGATTTGAA	GAAATCATCA	AGGAAACCTC	50
	CAACTTCGTC	AAGAAGGTTG	GTTACAACCC	AAAGACTGTT	CCATTCGTTC	100
10	CAATCTCTGG	TTGGAATGGT	GACAACATGA	TTGAACCATC	CACCAACTGT	150
	CCATGGTACA	AGGGTTGGGA	AAAGGAAACC	AAATCCGGTA	AAGTTACTGG	200
	TAAGACCTTG	TTAGAAGCTA	TTGACGCTAT	TGAACCACCA	ACCAGACCAA	250
	CCGACAAACC	ATTGAGATTG	CCATTGCAAG	ATGTTTACAA	GATCGGTGGT	300
	ATTGGTACTG	TGCCAGTCGG	TAGAGTTGAA	ACTGGTATCA	TCAAAGCCGG	350
15	TATGGTTGTT	ACTTTCGCC	CAGCTGGTGT	TACCACTGAA	GTCAAATCCG	400
	TTGAAATGCA	TCACGAACAA	TTGGCTGAAG	GTGTTCCAGG	TGACAATGTT	450
	GGTTTCAACG	TTAAGAACGT	TTCCGTTAAA	GAAATTAGAA	GAGGTAACGT	500
	TTGTGGTGAC	TCCAAGAACG	ATCCACCAAA	GGGTGTGAC	TCTTTC AATG	550
	CCCAAGTCAT	TGTTTTGAAC	CATCCAGGTC	AAATCTCTGC	TGGTTACTCT	600
20	CCAGTCTTGG	ATTGTCACCC	TGCCACATT	GCTTGTAAT	TCGACACTTT	650
	GGTTGAAAAG	ATTGACAGAA	GAAGTGGTAA	GAAATTGGAA	GAAAATCCAA	700
	AATTCGTCAA	ATCCGGTGAT	GCTGCTATCG	TCAAGATGGT	CCCAACCAAA	750
	CCA					753

25

## 2) INFORMATION FOR SEQ ID NO: 625

## (i) SEQUENCE CHARACTERISTICS:

30

(A) LENGTH: 26 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

35

## (ii) MOLECULE TYPE: DNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 625

	CGTTGAAGAC	ACGACCCAAA	GTATCC	26
--	------------	------------	--------	----

40

## 2) INFORMATION FOR SEQ ID NO: 626

## (i) SEQUENCE CHARACTERISTICS:

45

(A) LENGTH: 26 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

50

## (ii) MOLECULE TYPE: DNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 626

55	TACCACCTTT	TAAGTAAGGT	GCTAAT	26
----	------------	------------	--------	----

60

## 2) INFORMATION FOR SEQ ID NO: 627

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: DNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 627

ATTGTCTATA AAAATGGCGA TAAGTC

26

## 2) INFORMATION FOR SEQ ID NO: 628

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: DNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 628

AAAATGGCGA TAAGTCACAA AAAGTA

26

## 2) INFORMATION FOR SEQ ID NO: 629

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: DNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 629

AAGTTCCATC TCAACAAGGT CAATA

25

## 2) INFORMATION FOR SEQ ID NO: 630

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: DNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 630

CGGAGCTATC CTAGTCGTTT CA

22

## 2) INFORMATION FOR SEQ ID NO: 631

5 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 26 bases  
(B) TYPE: Nucleic acid  
(C) STRANDEDNESS: Single  
(D) TOPOLOGY: Linear  
10 (ii) MOLECULE TYPE: DNA  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 631  
15 CAGACCAACY GAIAARCCAT TRAGAT 26

## 2) INFORMATION FOR SEQ ID NO: 632

20 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 23 bases  
(B) TYPE: Nucleic acid  
(C) STRANDEDNESS: Single  
25 (D) TOPOLOGY: Linear  
(ii) MOLECULE TYPE: DNA  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 632  
30 CCCTTTGGTG GRTCSTKCTT GGA 23

## 2) INFORMATION FOR SEQ ID NO: 633

35 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 26 bases  
(B) TYPE: Nucleic acid  
40 (C) STRANDEDNESS: Single  
(D) TOPOLOGY: Linear  
(ii) MOLECULE TYPE: DNA  
45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 633  
CAGACCAACY GAIAARCCIT TRAGAT 26

## 2) INFORMATION FOR SEQ ID NO: 634

50 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 26 bases  
55 (B) TYPE: Nucleic acid  
(C) STRANDEDNESS: Single  
(D) TOPOLOGY: Linear  
(ii) MOLECULE TYPE: DNA  
60

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 634

AACACYGTCA GRRCIATTGC YATGGA

26

5

2) INFORMATION FOR SEQ ID NO: 635

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 26 bases  
(B) TYPE: Nucleic acid  
(C) STRANDEDNESS: Single  
(D) TOPOLOGY: Linear

15 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 635

20 AAACCRGTIA RRGCRCTCT IGCTCT

26

2) INFORMATION FOR SEQ ID NO: 636

25 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 bases  
(B) TYPE: Nucleic acid  
(C) STRANDEDNESS: Single  
(D) TOPOLOGY: Linear

30

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 636

35 ACTGGYGTTG AIATGTTCCG YAA

23

2) INFORMATION FOR SEQ ID NO: 637

40

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 bases  
(B) TYPE: Nucleic acid  
(C) STRANDEDNESS: Single  
(D) TOPOLOGY: Linear

45

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 637

50

ACGTCAGTIG TACGGAARTA GAA

23

55 2) INFORMATION FOR SEQ ID NO: 638

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 bases  
(B) TYPE: Nucleic acid  
(C) STRANDEDNESS: Single

60

366

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 638

CCAATGCCAC AAACICGTGA RCACAT

26

10

2) INFORMATION FOR SEQ ID NO: 639

(i) SEQUENCE CHARACTERISTICS:

15 (A) LENGTH: 28 bases  
(B) TYPE: Nucleic acid  
(C) STRANDEDNESS: Single  
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 639

TTTACGGAAC ATTTCWACAC CWGTIACA

28

25

2) INFORMATION FOR SEQ ID NO: 640

(i) SEQUENCE CHARACTERISTICS:

30 (A) LENGTH: 23 bases  
(B) TYPE: Nucleic acid  
(C) STRANDEDNESS: Single  
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 640

TCCATGGTIT WYGGICARAT GAA

23

40

2) INFORMATION FOR SEQ ID NO: 641

(i) SEQUENCE CHARACTERISTICS:

45 (A) LENGTH: 26 bases  
(B) TYPE: Nucleic acid  
(C) STRANDEDNESS: Single  
(D) TOPOLOGY: Linear

50

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 641

55 TGATAACCWA CIGCIGAIGG CATACG

26

60

2) INFORMATION FOR SEQ ID NO: 642



## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: DNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 642

GGCGTIGGIG ARCGIACICG TGA

23

## 2) INFORMATION FOR SEQ ID NO: 643

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: DNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 643

ACTGGIGTIG ARATGTTCCG YAA

23

## 2) INFORMATION FOR SEQ ID NO: 644

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: DNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 644

ACGTCIGTIG TICKGAARTA GAA

23

## 2) INFORMATION FOR SEQ ID NO: 645

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: DNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 645

ACGTCIGTIG TICKGAARTA RAA

23

## 2) INFORMATION FOR SEQ ID NO: 646

5 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 23 bases  
(B) TYPE: Nucleic acid  
(C) STRANDEDNESS: Single  
(D) TOPOLOGY: Linear  
10 (ii) MOLECULE TYPE: DNA  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 646  
15 ATCGACAAGC CITTCTIAT GSC 23

## 2) INFORMATION FOR SEQ ID NO: 647

20 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 26 bases  
(B) TYPE: Nucleic acid  
(C) STRANDEDNESS: Single  
25 (D) TOPOLOGY: Linear  
(ii) MOLECULE TYPE: DNA  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 647  
30 ACGTCCGTSG TRCGGAAGTA GAACTG 26

## 2) INFORMATION FOR SEQ ID NO: 648

35 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 26 bases  
(B) TYPE: Nucleic acid  
40 (C) STRANDEDNESS: Single  
(D) TOPOLOGY: Linear  
(ii) MOLECULE TYPE: DNA  
45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 648  
ACGTCSGTSG TRCGGAAGTA GAACTG 26

## 2) INFORMATION FOR SEQ ID NO: 649

50 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 26 bases  
55 (B) TYPE: Nucleic acid  
(C) STRANDEDNESS: Single  
(D) TOPOLOGY: Linear  
(ii) MOLECULE TYPE: DNA  
60

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 649

GTCCTATGCC TCARACWCGI GAGCAC

26

5

2) INFORMATION FOR SEQ ID NO: 650

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 23 bases  
(B) TYPE: Nucleic acid  
(C) STRANDEDNESS: Single  
(D) TOPOLOGY: Linear

15 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 650

20 TTACGGAACA TYTCAACACC IGT

23

2) INFORMATION FOR SEQ ID NO: 651

25 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 bases  
(B) TYPE: Nucleic acid  
(C) STRANDEDNESS: Single  
(D) TOPOLOGY: Linear

30

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 651

35 TGACGACCAC CITCYTCYTT YTTCA

25

2) INFORMATION FOR SEQ ID NO: 652

40 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 bases  
(B) TYPE: Nucleic acid  
(C) STRANDEDNESS: Single  
(D) TOPOLOGY: Linear

45

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 652

50

CCWAYAGTIY KICCICCYTC YCTIATA

27

55 2) INFORMATION FOR SEQ ID NO: 653

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 bases  
(B) TYPE: Nucleic acid  
(C) STRANDEDNESS: Single

60

370

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 653

GAYTTCATIA ARAAYATGAT

20

10

2) INFORMATION FOR SEQ ID NO: 654

(i) SEQUENCE CHARACTERISTICS:

15

(A) LENGTH: 20 bases  
(B) TYPE: Nucleic acid  
(C) STRANDEDNESS: Single  
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 654

TACAARATYK GIGGTATYGG

20

25

2) INFORMATION FOR SEQ ID NO: 655

(i) SEQUENCE CHARACTERISTICS:

30

(A) LENGTH: 20 bases  
(B) TYPE: Nucleic acid  
(C) STRANDEDNESS: Single  
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 655

CCRATACCIC MRATYTTGTA

20

40

2) INFORMATION FOR SEQ ID NO: 656

(i) SEQUENCE CHARACTERISTICS:

45

(A) LENGTH: 22 bases  
(B) TYPE: Nucleic acid  
(C) STRANDEDNESS: Single  
(D) TOPOLOGY: Linear

50

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 656

55 AATTAATGGC TGCAGTTGAY GA

22

60

2) INFORMATION FOR SEQ ID NO: 657

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 657

TTGTCCACGT TCGATRTCTT CA

## 2) INFORMATION FOR SEQ ID NO: 658

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 658

GATYTAGTCG ATGATGAAGA ATT

## 2) INFORMATION FOR SEQ ID NO: 659

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 659

GCTTTTTGIG TTTCWGGTTT RAT

## 2) INFORMATION FOR SEQ ID NO: 660

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 660

GTAGAATTGA GGACGGTAGT TAG

## 2) INFORMATION FOR SEQ ID NO: 661

- 5 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 23 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Single  
 (D) TOPOLOGY: Linear

10

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 661

15 GTAGAAAYTGT GGWCGATART TRT

23

## 2) INFORMATION FOR SEQ ID NO: 662

20

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 832 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

25

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

30

- (A) ORGANISM: *Corynebacterium diphtheriae*  
 (B) STRAIN: ATCC 27010

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 662

35	CGGCGCAATC CTCGTTGTTG CTGCCACCGA CGGCCCAATG CCTCAGACCC	50
	GTGAGCACGT TCTGCTCGCT CGCCAGGTCG GCGTTCCTTA CATCCTCGTT	100
	GCTCTGAACA AGTGCACAT GGTGATGAT GAGGAAATCA TCGAGCTCGT	150
	CGAGATGGAG ATCCTGAGC TGCTCGCTGA GCAGGATTAC GACGAAGAGG	200
	CTCCAATCAT CCACATCTCC GCACTGAAGG CTCTTGAGGG CGACGAGAAG	250
40	TGGACCCAGT CCATCATCGA CCTCATGCAG GCTTGCKATG ATTCCATCCC	300
	AGACCCAGAG CGTGAGACCG ACAAGCCATT CCTCATGCCT ATCGAGGACA	350
	TCTTCACCAT CACCGGCCGC GGTACCGTTG TTACCGGCCG TGTGAGCGT	400
	GGCTCCCTGA AGGTCAACGA GGACGTCGAG ATCATCGGTA TCCGCGAGAA	450
	KGCTACCACC ACCACCGTTA CCGGTATCGA GATGTTCCGT AAGCTTCTCG	500
45	ACTACACCGA GGCTGGCGAC AACTGTGGTC TGCTTCTCCG TGGCGTTAAG	550
	CGCGAAGACG TTGAGCGTGG CCAGGTTGTT GTTAAGCCAG GCGCTTACAC	600
	CCCTCACACC GAGTTCGAGG GCTCTGTCTA CGTTCTGTCC AAGGACGAGG	650
	GTGGCCGCCA CACCCATTTC TTCGACAACT ACCGCCACA GTTCTACTTC	700
	CGCACCACCG ACGTTACCGG TGTGTGAAG CTTCTGAGG GCACCGAGAT	750
50	GGTCATGCCT GCGGACAACG TCGACATGTC CGTCACCCTG ATCCAGCCTG	800
	TCGCTATGGA TGAGGGCCTG CGCTTCGCTA TC	832

## 55 2) INFORMATION FOR SEQ ID NO: 663

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 1192 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Single

60

373

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

5 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Candida catenulata*

(B) STRAIN: ATCC 10565

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 663

```

10 AACGGCGAGC AAGACTTGGT GTTGGAGGTT TCTCAGCACT TGGGTGAGAA      50
   CACCGTGCCT ACCATTGCCA TGGACGGTAC CGAGGGTTTG GTGAGAGGTA      100
   CCGCTGTCAC TGACACCGGT GCTCCCATCT CGGTCCCCGT TGGTCAGGGT      150
   ACCTTGGGCC GGATCATCAA CGTTGTCGGT GAGCCCATCG ACGAGCGTGG      200
15 TCCCATCCAG TGCAAGCAGA GAAACCCCAT TCACGCCGAG CCCCCGTCTT      250
   TCACCGAGCA GTCCGTCGAG GCTGAGGTGT TGGAGACCGG TATCAAGGTT      300
   GTCGACTTGT TGGCTCCCTA CGCCCGTGGT GGTAAGATTG GTCTTTTCGG      350
   TGGTGCCGGT GTCGGTAAGA CCGTGTTTCAT CCAGGAGTTG ATTAACAACA      400
   TTGCCAAGGC CCACGGTGGT TTCTCCGTGT TCACTGGTGT CCGTGAGCGT      450
20 ACTCGTGAGG GTAACGACTT GTACCGTGAA ATGAAGGAGA CCGGTGTCAT      500
   CAACTTGGAG GGCGACTCCA AGGTGGCCTT GGTGTTCCGG CAGATGAACG      550
   AGCCCCCGGG GGCTCGTGCC CGTGTCGCCT TGACCGGTTT GACCATTGCC      600
   GAGTACTTCC GTGACGAGGA AGGCCAGGAC GTGTTGTTGT TCGTTGACAA      650
   CATTTTCAGA TTCACCCAGG CCGGTTCCGA GGTGTCGGCG TTGTTGGGTC      700
25 GTATCCCCTC CGCCGTCGGT TACCAGCCCA CTTTGGCCAC CGACATGGGT      750
   TTGTTGCAGC AGAGAATTAC CACCACCAAG AAGGGTTCCG TCACCTCTGT      800
   GCAGGCCGTG TACGTCCCTG CCGATGACTT GACTGACCCT GCCCCGCCA      850
   CCACTTTCGC TCACTTGGAC GCCACCACCG TGTTGTCGCG TGGTATCTCC      900
   GAGTTGGGTA TCTACCCCGC CGTCGACCCC TTGGACTCCA AGTCGAGATT      950
30 GTTGGACGTC GAGGTTGTTG GCCAGGAGCA CTACGACGTC GCCACCGGTG      1000
   TCCAGGAGTG CTTGCAGGCC TACAAGTCGT TGCAGGACAT CATTGCCATT      1050
   TTGGGTATGG ACGAGTTGTC CGAGCAGGAC AAGTTGACCG TCGAGAGAGC      1100
   CCGTAAGATC CAGCGTTTCT TGTCGCAGCC CTTCGCTGTC GCCGAGGTTT      1150
   TCACTGGTAT CCCCGGTAGA TTGGTGAGAT TGCAGGACAC CG              1192
35

```

2) INFORMATION FOR SEQ ID NO: 664

40 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 29 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

45 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 664

50 AAYATGATIA CIGGIGCIGC ICARATGGA

29

2) INFORMATION FOR SEQ ID NO: 665

55 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1377 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

60 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 5 (A) ORGANISM: *Saccharomyces cerevisiae*  
(C) ACCESSION NUMBER: extracted from X00779

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 665

10	ATGGGTAAAG	AGAAGTCTCA	CATTAACGTT	GTCGTTATCG	GTCATGTCGA	50
	TTCTGGTAAG	TCTACCACTA	CCGGTCATTT	GATTTACAAG	TGTGGTGGTA	100
	TTGACAAGAG	AACCATCGAA	AAGTTCGAAA	AGGAAGCCGC	TGAATTAGGT	150
	AAGGGTTCTT	TCAAGTACGC	TTGGGTTTTG	GACAAGTTAA	AGGCTGAAAG	200
	AGAAAGAGGT	ATCACTATCG	ATATTGCTTT	GTGGAAGTTC	GAAACTCCAA	250
15	AGTACCAAGT	TACCGTTATT	GATGCTCCAG	GTCACAGAGA	TTTCATCAAG	300
	AACATGATTA	CTGGTACTTC	TCAAGCTGAC	TGTGCTATCT	TGATTATTGC	350
	TGGTGGTGTG	GGTGAATTTC	AAGCCGGTAT	CTCTAAGGAT	GGTCAAACCA	400
	GAGAACACGC	TTTGTTGGCT	TTCACCTTGG	GTGTTAGACA	ATTGATTGTT	450
	GCTGTCAACA	AGATGGACTC	CGTCAAATGG	GACGAATCCA	GATTCCAAGA	500
20	AATTGTCAAG	GAAACCTCCA	ACTTTATCAA	GAAGGTTGGT	TACAACCCAA	550
	AGACTGTTCC	ATTCGTCCCA	ATCTCTGGTT	GGAACGGTGA	CAACATGATT	600
	GAAGCTACCA	CCAACGCTCC	ATGGTACAAG	GGTTGGGAAA	AGGAAACCAA	650
	GGCCGGTGTG	GTCAAGGGTA	AGACTTTGTT	GGAAGCCATT	GACGCCATTG	700
	AACAACCATC	TAGACCAACT	GACAAGCCAT	TGAGATTGCC	ATTGCAAGAT	750
25	GTTTACAAGA	TTGGTGGTAT	TGGTACTGTG	CCAGTCGGTA	GAGTTGAAAC	800
	CGGTGTCATC	AAGCCAGGTA	TGGTTGTTAC	TTTTGCCCCA	GCTGGTGTTA	850
	CCACTGAAGT	CAAGTCCGTT	GAAATGCATC	ACGAACAATT	GGAACAAGGT	900
	GTTCCAGGTG	ACAACGTTGG	TTTCAACGTC	AAGAACGTTT	CCGTTAAGGA	950
	AATCAGAAGA	GGTAACGTCT	GTGGTGACGC	TAAGAACGAT	CCACCAAAGG	1000
30	GTTGCGCTTC	TTTCAACGCT	ACCGTCATTG	TTTTGAACCA	TCCAGGTCAA	1050
	ATCTCTGCTG	GTTACTCTCC	AGTTTTGGAT	TGTCACACTG	CTCACATTGC	1100
	TTGTAGATTG	GACGAATTGT	TGGAAAAGAA	CGACAGAAGA	TCTGGTAAGA	1150
	AGTTGGAAGA	CCATCCAAAG	TTCTTGAAGT	CCGGTGACGC	TGCTTTGGTC	1200
	AAGTTCGTTG	CATCTAAGCC	AATGTGTGTT	GAAGCTTTCA	GTGAATACCC	1250
35	ACCATTAGGT	AGATTGCTG	TCAGAGACAT	GAGACAAACT	GTCGCTGTCG	1300
	GTGTTATCAA	GTCTGTTGAC	AAGACTGAAA	AGGCCGCTAA	GGTTACCAAG	1350
	GCTGCTCAAA	AGGCTGCTAA	GAAATAA			1377

40

2) INFORMATION FOR SEQ ID NO: 666

(i) SEQUENCE CHARACTERISTICS:

- 45 (A) LENGTH: 1536 bases  
(B) TYPE: Nucleic acid  
(C) STRANDEDNESS: Double  
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

50

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Saccharomyces cerevisiae*  
(C) ACCESSION NUMBER: extracted from M12082

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 666

	ATGGTTTTTG	CAAGACTATA	TACTGCTACA	TCCCGTGCTG	CTTTTAAAGC	50
	AGCCAAACAA	TCCGCTCCGC	TTCTATCCAC	TTCGTGGAAA	AGATGTATGG	100
	CCTCAGCTGC	TCAATCTACT	CCAATCACCG	GTAAAGTTAC	CGCTGTCATT	150
60	GGTGCCATTG	TTGACGTTCA	TTTTGAACAA	TCAGAGTTGC	CCGCTATTTT	200

375



	GAACGCTTTA	GAAATTAAAA	CACCTCAAGG	TAAGTTGGTT	TTGGAAGTTG	250
	CTCAACATTT	GGGTGAAAAC	ACTGTCAGAA	CCATTGCTAT	GGATGGTACC	300
	GAAGGTTTGG	TCCGTGGTGA	AAAGGTTCTT	GACACTGGTG	GCCCTATCTC	350
	CGTCCCAGTT	GGGAGAGAAA	CTTTAGGGAG	AATCATCAAC	GTTATCGGTG	400
5	AACCTATTGA	TGAAAGAGGT	CCAATTAAGT	CCAAACTAAG	AAAGCCAATT	450
	CACGCAGACC	CTCCTAGTTT	TGCAGAACAA	TCTACTTCGG	CTGAAATTTT	500
	GGAAACAGGT	ATCAAAGTCG	TCGATCTATT	AGCTCCTTAT	GCCAGAGGTG	550
	GTAAGATTGG	TCTTTTCGGT	GGTGCAGGTG	TCGGTAAGAC	TGTGTTCAAT	600
	CAAGAATTGA	TTAACAATAT	CGCCAAGGCC	CATGGTGGTT	TTTCCGTTTT	650
10	CGCCGGTGTT	GGTGAAAGGA	CCAGAGAGGG	TAATGACTTG	TACCGTGAAA	700
	TGAAGGAAAC	TGGAGTCATT	AACTTGGAAG	GTGAATCCAA	GGTCGCCTTA	750
	GTTTTTCGGT	AAATGAACGA	ACCTCCAGGA	GCCAGAGCCA	GAGTCGCTTT	800
	AACCTGGTTT	ACGATCGCTG	AATATTTTCT	AGATGAAGAA	GGTCAAGACG	850
	TCTTGTTGTT	TATCGACAAT	ATCTTTAGAT	TTACTCAAGC	TGGTTCAGAA	900
15	GTCTCTGCCC	TTTTGGGTCG	TATTCCATCT	GCCGTCGGTT	ATCAACCAAC	950
	TTTGGCCACT	GATATGGGTC	TCTTACAAGA	AAGAATTACC	ACCACAAAGA	1000
	AGGGTTCTGT	CACTTCTGTG	CAAGCCGTTT	ATGTTCCAGC	CGATGATTTA	1050
	ACAGATCCGT	CTCCGTCCAC	ATCTTTTGCC	CATTTGGACG	CATCATCCGT	1100
	CTTGTCGAAG	GGTATTTTCT	AATTAGGTAT	TTACCCTGCA	GTGGATCCAT	1150
20	TGGATTCTAA	ATCAAGGTTA	TTGGATGCCG	CCGTTGTCGG	TCAAGAACAT	1200
	TATGACGTCG	CCTCCAAGGT	TCAAGAAACT	TTACAGACCT	ATAAATCTTT	1250
	ACAAGATATC	ATTGCTATTT	TGGGTATGGA	TGAATTGTCC	GAACAAGATA	1300
	AACTAACTGT	CGAAAGGGCA	AGAAAGATTC	AAAGATTCTT	ATCTCAACCA	1350
	TTTGCTGTCT	CCGAAGTCTT	TACTGGTATC	CCAGGTAAAT	TAGTGAGATT	1400
25	AAAGGACACC	GTTGCCTCGT	TCAAAGCCGT	TTTGGAAGGT	AAATACGATA	1450
	ATATACCAGA	ACATGCTTTC	TATATGGTTG	GTGGTATTGA	AGATGTTGTT	1500
	CGTAAAGCTG	AAAAGTTAGC	CCGTGAAGCC	AACTAG		1536

30

## 2) INFORMATION FOR SEQ ID NO: 667

## (i) SEQUENCE CHARACTERISTICS:

35

- (A) LENGTH: 1293 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

40

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Trypanosoma cruzi*
- (B) STRAIN: Y

45

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 667

	CGGAAGGCGT	GCCGCCGGTG	TTAACTGCTT	TGGATGTGGT	GGAAAACTT	50
	GGCCGTGACG	AGCCCTTGAC	ACTTGAAATT	GTACAGCACT	TGGACGCCCA	100
	CACCGGCCGT	TGCATTGCGA	TGCAGACGAC	AGATCTGCTT	AAGCTGAAAT	150
50	CGAAGGTAGT	CTCGAGTGGC	GGGAACATTT	CTGTGCCTGT	GGGTCGGGAG	200
	ACACTTGGCA	GAATCTTCAA	TGTGCTGGGC	GATGCCATTG	ACCAGCGCGG	250
	CCATGTTGGA	GAGAAGCAAC	GCATGCCTAT	TCACGCTGTG	GCACCAAAGT	300
	TGGCGGATCA	GGCGGCAGAG	GACACCATTC	TCACAACGGG	TATCAAGGTG	350
	ATTGATCTGA	TTTTGCCCTA	CTGCAAGGGT	GGGAAGATTG	GTCTTTTTTG	400
55	TGGTGCTGGC	GTGGGCAAGA	CGGTATTAT	CATGGAACCT	ATTAACAACG	450
	TTGCCAAGGG	CCATGGTGGG	TTCTCCGTCT	TTGCGGGTGT	TGGTGAACGC	500
	ACGCGTGAGG	GGACGGATCT	TTACCTGGAG	ATGATGCAAT	CCAAAGTTAT	550
	TGACCTGAAG	GGTGACTCGA	AGTGTGTGTT	GGTGATGGT	CAGATGAACG	600
	AGCCTCCGGG	TGCCCCGTGCT	CGTGTGGCGC	AGTCTGCCTT	GACAATGGCC	650
60	GAGTACTTCC	GTGATGTGGA	AGGGCAAGAC	GTGTTGCTTT	TTATCGACAA	700

	CATTTTCCGC	TTTACGCAGG	CAAACCTCTGA	GGTGTCTAGCG	CTGTTGGGTC	750
	GTATTCCCGC	TGCCGTCGGC	TACCAGCCTA	CCCTTGCTGA	GGATCTTGGG	800
	CAGTTGCAGG	AGCGCATTAC	GTCCACGACA	AAAGGTTCCA	TTACCTCTGT	850
	GCAGGCTGTG	TACGTGCCAG	CCGATGATAT	TACCGACCCT	GCGCCAGCAA	900
5	CGACCTTTTC	CCACCTCGAT	GCCACGACGG	TGCTGGACCG	TGCCGTTGCC	950
	GAATCCGGCA	TTTACCCCGC	TGTCAACCCA	CTGGAGTGTG	CCTCGCGTAT	1000
	CATGGACCCG	GATGTAATCA	GCGTTGACCA	CTACAACGTG	GCGCAGGATG	1050
	TGGTGCAGAT	GCTTACCAAG	TACAAGGAGC	TGCAGGATAT	CATTGCGGTG	1100
	CTTGGCATTG	ATGAGCTCAG	TGAGGAGGAT	AAACTTATCG	TGGACCGTGC	1150
10	GCGTAAGGTG	ACAAAGTTTC	TCTCCCAGCC	TTTCCAGGTG	GCGGAGGTGT	1200
	TTACTGGCAT	GACAGGCCAC	TACGTGCAGC	TGGAGGAGAC	CATTGAGTCT	1250
	TTTTCCGGCC	TGTTGATGGG	CACATATGAT	CAGGTGCCGG	AGA	1293

15

## 2) INFORMATION FOR SEQ ID NO: 668

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1191 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
- (A) ORGANISM: *Corynebacterium glutamicum*
- (C) ACCESSION NUMBER: X77034

## 30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 668

	GTGGCAAAGG	CGAAGTTCGA	GCGTACCAAG	CCCCACGTAA	ACATCGGCAC	50
	CATCGGTCAC	GTTGACCACG	GTAAGACCAC	CACCACCGCG	GCTATCACCA	100
	AGGTTCTGGC	TGACACTTAC	CCTGAGCTCA	ACGAGGCTTT	CGCCTTTCGAC	150
35	TCCATCGATA	AGGCTCCTGA	GGAGAAGGAG	CGTGGCATCA	CGATCAACAT	200
	CTCCACGTT	GAGTACCAGA	CTGAAAAGCG	CCACTACGCA	CACGTTGACG	250
	CTCCAGGCCA	CGCCGACTAC	ATCAAGAACA	TGATTACCGG	CGCTGCTCAG	300
	ATGGACGGCG	CAATCCTCGT	TGTTGCTGCT	ACCGACGGCC	CAATGCCTCA	350
	GACCCGTGAG	CACGTTCTTC	TTGCTCGCCA	GGTTGGCGTT	CCTTACATCC	400
40	TCGTTGCTCT	TAACAAGTGC	GACATGGTTG	AGGATGAGGA	AATCATCGAG	450
	CTCGTCGAGA	TGGAAGTTTCG	TGAACTTCTT	GCTGAGCAGG	ACTACGACGA	500
	AGAGGCTCCA	ATTGTTTACA	TCTCCGCTCT	GAAGGCTCTT	GAGGGCGACG	550
	AGAAGTGGGG	CAAGCAGATC	CTTGAGCTCA	TGCAGGCTTG	CGATGACAAC	600
	ATCCCTGACC	CAGTTCGTGA	GACCGACAAG	CCATTCTCTCA	TGCCATATCGA	650
45	GGACATCTTC	ACCATCACCG	GTCGTGGCAC	CGTTGTTACC	GGTCGTGTTG	700
	AGCGCGGTAC	CCTGAACGTG	AACGATGATG	TTGACATCAT	CGGCATCAAG	750
	GAGAAGTCCA	CCTCCACCAC	CGTTACCGGT	ATCGAGATGT	TCCGTAAGCT	800
	TCTTGACTCC	GCTGAGGCTG	GCGACAACCTG	TGGTCTGCTT	CTCCGTGGTA	850
	TCAAGCGCGA	AGATGTTGAG	CGTGGCCAGG	TTATCGTTAA	GCCAGGCGCT	900
50	TACACCCCTC	ACACCGAGTT	CGAGGGCTCT	GTCTACGTTT	TGTCCAAGGA	950
	TGAAGGTGGC	CGCCACACCC	CATTCTTCGA	CAACTACCGT	CCTCAGTTCT	1000
	ACTTCCGCAC	CACCGACGTT	ACCGGTGTTG	TGAAGCTTCC	AGAGGGCACC	1050
	GAGATGGTCA	TGCCTGGCGA	CAACGTCGAC	ATGTCCGTCA	CCCTGATCCA	1100
	GCCTGTCGCT	ATGGACGAGG	GCCTGCGTTT	CGCTATCCGC	GAAGGCTCCC	1150
55	GCACCGTTGG	CGCTGGTCGT	GTCACCAAGA	TCATCAAGTA	A	1191

## 2) INFORMATION FOR SEQ ID NO: 669

60

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1383 bases  
(B) TYPE: Nucleic acid  
(C) STRANDEDNESS: Double  
(D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Escherichia coli*  
(C) ACCESSION NUMBER: extracted from V00267

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 669

```
15 ATGGCTACTG GAAAGATTGT CCAGGTAATC GGCGCCGTAG TTGACGTCGA      50
   ATTCCCTCAG GATGCCGTAC CGCGCGTGTA CGATGCTCTT GAGGTGCAAA      100
   ATGGTAATGA GCGTCTGGTG CTGGAAGTTC AGCAGCAGCT CGGCGGCGGT      150
   ATCGTACGTA CCATCGCAAT GGGTTCCTCC GACGGTCTGC GTCGCGGTCT      200
   GGATGTAAAA GACCTCGAAC ACCCGATTGA AGTCCCGGTA GGTAAAGCGA      250
20 CTCTGGGCGG TATCATGAAC GTACTGGGTG AACC GGTCGA CATGAAAGGC      300
   GAGATCGGTG AAGAAGAGCG TTGGGCGGATT CACCGCGCAG CACCTTCCTA      350
   CGAAGAGCTG TCAAAC TCTC AGGAACTGCT GGAAACCGGT ATCAAAGTTA      400
   TCGACCTGAT GTGTCCGTTT GCTAAGGGCG GTAAAGTTGG TCTGTTCCGGT      450
   GGTGCGGGTG TAGGTAAAC CGTAAACATG ATGGAGCTCA TTCGTAACAT      500
25 CGCGATCGAG CACTCCGGTT ACTCTGTGTT TGCGGGCGTA GGTGAACGTA      550
   CTCGTGAGGG TAACGACTTC TACCACGAAA TGACCGACTC CAACGTTATC      600
   GACAAAGTAT CCCTGGTGTA TGGCCAGATG AACGAGCCGC CGGGAACCG      650
   TCTGCGCGTT GCTCTGACCG GTCTGACCAT GGCTGAGAAA TTCCGTGACG      700
   AAGGTCGTGA CGTTCTGCTG TTCGTTGACA ACATCTATCG TTACACCCTG      750
30 GCCGGTACGG AAGTATCCGC ACTGCTGGGC CGTATGCCTT CAGCGGTAGG      800
   TTATCAGCCG ACCCTGGCGG AAGAGATGGG CGTTCTGCAG GAACGTATCA      850
   CCTCCACCAA AACTGGTTCT ATCACCTCCG TACAGGCAGT ATACGTACCT      900
   GCGGATGACT TGA CTGACCC GTCTCCGGCA ACCACCTTTG CGCACCTTGA      950
   CGCAACCGTG G TACTGAGCC GTCAGATCGC GTCTCTGGGT ATCTACCCGG      1000
35 CCGTTGACCC GCTGGACTCC ACCAGCCGTC AGCTGGACCC GCTGGTGGTT      1050
   GGTCAGGAAC ACTACGACAC CGCGCGTGGC GTTCAGTCCA TCCTGCAACG      1100
   TTATCAGGAA CTGAAAGACA TCATCGCCAT CCTGGGTATG GATGAACTGT      1150
   CTGAAGAAGA CAAACTGGTG GTAGCGCGTG CTCGTAAGAT CCAGCGCTTC      1200
   CTGTCCCAGC CGTTC TTCGT GGCAGAAAGTA TTCACCGGTT CTCCGGGTAA      1250
40 ATACGTCTCC CTGAAAGACA CCATCCGTGG CTTTAAAGGC ATCATGGAAG      1300
   GCGAATACGA TCACCTGCCG GAGCAGGCGT TCTACATGGT CGGTTCCATC      1350
   GAAGAAGCTG TGGAAAAAGC CAAAAA ACTT TAA      1383
```

## 2) INFORMATION FOR SEQ ID NO: 670

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1410 bases  
(B) TYPE: Nucleic acid  
(C) STRANDEDNESS: Double  
(D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*  
(B) STRAIN: NCTC 11638  
(C) ACCESSION NUMBER: extracted from AF004014

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 670

	ATGAAAGCGA	TGGAAGGTAA	AATCATTCAG	GTTTTAGGCC	CGGTGGTAGA	50
	TGTGGAGTTT	GAATCCTATC	TGCCGGCGAT	TTTTGAAGCA	CTAGACATTA	100
5	ATTTTGAAGT	TAATGGCGTT	CAAAAATCTT	TAGTTTTAGA	GGTGGCAGCC	150
	CATTTGGGTG	GTAATCGGGT	GCGAGCGATT	GCTATGGATA	TGACAGAAGG	200
	CTTAGTGCGT	AACCAAGCCG	TCAAAGCTCG	TGGCAAAATG	ATTGAAGTGC	250
	CTGTGGGCGA	AGAAGTGTTA	GGGCGTATTT	TTAATGTTGT	GGGCGAGAGC	300
	ATTGATAATT	TAGAGCCGCT	TAAGCCGTCC	TTAACTTGCC	CCATTACAG	350
10	AAAAGCCCCT	AGTTTTGAGC	AGCAAAGCAC	TAAAACAGAA	ATGTTTGAAA	400
	CCGTATTAA	AGTCATTGAC	TTGCTCGCGC	CTTATTCTAA	GGGCGGTAAA	450
	GTAGGCTTGT	TTGGTGGGGC	TGGCGTAGGC	AAAACGGTGA	TCATTATGGA	500
	GCTTATCCAC	AATGTGGCTT	ATAAGCATAA	CGGGTATTCTG	GTGTTTGCAG	550
	GTGTGGGGGA	GCGCACCAGA	GAAGGGAACG	ATCTGTATTT	TGAGATGAAA	600
15	GAAGGGGGCG	TTTTAGACAA	AGTTGCGTTG	TGCTATGGGC	AAATGAATGA	650
	GCCACCAGGT	GCAAGGAATC	GCATCGCATT	CACCGGCTTG	ACGATGGCGG	700
	AGTATTTCCG	TGATGAAAAG	GGCTTAGATG	TGTTGATGTT	TATTGATAAC	750
	ATCTTTAGAT	ACGCTCAAAG	CGGTGCGGAA	ATGAGCGCGC	TATTAGGCCG	800
	TATCCCTTCA	GCGGTGGGGT	ATCAGCCAC	GCTAGCCGGG	GAAATGGGGA	850
20	AACTTCAAGA	GCGTATCGCT	TCCACTAAAA	ATGGCTCTAT	CACTTCGGTT	900
	CAAGCGGTGT	ATGTGCCAGC	AGACGACTTG	ACTGACCCAG	CCCCTGCTTC	950
	GGTGTTTGCG	CATTTAGATG	CGACTACGGT	GTTGAATAGA	AAGATCGCTG	1000
	AAAAAGGGAT	TTATCCGGCG	GTGGATCCTT	TGGATTCCAC	TTCAAGGATT	1050
	TTAAGCCCTC	AAATGATTGG	CGAGAAGCAC	TATGAAATCG	CCACCGGTAT	1100
25	CCAGCAAGTT	TTGCAAAAAT	ACAAGGATTT	GCAAGATATT	ATTGCGATTT	1150
	TGGGATTGGA	CGAATTGAGC	GAAGAGGATA	AAAAAACGGT	TGAAAGGGCC	1200
	AGAAAAATTG	AGAAGTTTTT	ATCCCAGCCG	TTTTTTGTGG	CTGAAGTGTT	1250
	TACAGGAAGT	CCCGGTAAGT	ATGTGACTCT	CCAAGAGACT	TTAGAGGGCT	1300
	TTGGAGGGAT	TTTAGAGGGC	AAATACGATC	ACATTCTCTGA	AAACGCGTTT	1350
30	TACATGGTGG	GCAGCATTCA	AGAGGTTTTA	GAAAAAGCTA	AAAACATGAA	1400
	AAATTCCTAA					1410

## 35 2) INFORMATION FOR SEQ ID NO: 671

## (i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 1401 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

## 45 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Clostridium acetobutylicum*  
 (B) STRAIN: DSM 792  
 (C) ACCESSION NUMBER: extracted from AF101055

## 50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 671

	ATGCCAGAAC	ATGTAGGTAA	AATTGTTCAG	GTAATAGGAC	CTGTTGTGGA	50
	TATTAAATTT	GATGCAGAGA	ACCTTCCTGA	CATCTATAAT	TCCATAGAAA	100
	TAGATATGGG	AGATAATAAA	AAACTCATTG	CTGAAGTTGA	ACAACATGTA	150
55	GGAGATGACA	TAGTAAGAAC	AATAGCAATG	GAAGGTACTG	ACGGATTAAA	200
	AAGAGGAATG	GAAGCAGTTA	ACACTGGTAA	ACCAATATCT	GTACCAGTTG	250
	GAGAAAAATG	TTTAGGACGT	CTTTTAAATG	TTTTAGGTCA	GACAATAGAT	300
	GAAGCAGGAG	ACATGAATGC	TGATAAGTAT	TATCCAATTC	ATAGACCAGC	350
	TCCAACCTTT	GAAGAACAAT	CAGTTCAACC	AGAAATGTTT	GAAACAGGTA	400
60	TTAAGGTTAT	AGATTTACTT	GCTCCATATC	AAAAGGGTGG	AAAAATCGGT	450

	TTGTTCCGGTG	GTGCCGGTGT	TGGTAAAACA	GTTCTTATTC	AGGAACTTAT	500
	AAATAATATA	GCAAAAGAAC	ACGGTGGATT	ATCAGTATTC	ACAGGTGTTG	550
	GAGAAAGAAC	AAGAGAAGGT	AATGACCTTT	ATTATGAAAT	GAAAGATTCA	600
	GGAGTTATAA	ATAAAACAGC	TCTAGTATTT	GGTCAGATGA	ATGAACCACC	650
5	TGGCGCTAGA	ATGAGAGTTG	CTTTAACAGG	ACTTACAATG	GCTGAATATT	700
	TTAGAGACAA	AGGTCAAGAT	GTGCTTCTAT	TTATAGATAA	TATATTCAGA	750
	TTTACACAAG	CTGGTTCAGA	GGTTTCAGCT	TTACTTGGTA	GAATACCTAG	800
	TGCCGTTGGT	TATCAGCCAA	CAC TTGCAA	TGAAATGGGT	GCTCTTCAAG	850
	AGAGAATAAC	ATCAACAAAA	CAGGGTTCAA	TCACATCCGT	TCAGGCTGTA	900
10	TATGTTTCCTG	CTGATGACCT	TACAGACCCA	GCTCCAGCAA	CAACATTTAC	950
	GCATCTTGAT	GCAACAACAG	TTCTTTCAAG	AGAAATATCA	AACTTAGGAA	1000
	TATATCCTGC	AGTTAGTCCT	CTTGAATCAA	CTTCAAGAAT	ACTTGATCCA	1050
	AGAATTGTTG	GAGAAGAGCA	TTATGAAGTT	GCTAACAAGG	TTAAACATAT	1100
	ACTTGAAAGA	TATCAAGAAC	TTCAAGATAT	CATAGCTATA	CTTGGTGTTG	1150
15	ATGAACTTTC	AGATGAGGAT	AGATTGT TAG	TTGGAAGAGC	AAGAAGAGTA	1200
	CAGAGATTCT	TATCTCAAGC	TTTTAGTGTT	GCTGAACAAT	TTACAGGAAT	1250
	GAAAGGTCAG	TTTGTACCTG	TAAAAGATAC	TATAAGAAGT	TTTAAAGAAA	1300
	TATTAGATGG	TAAGTGTGAT	GATCTTCCAG	AAGCTGCATT	TTTATTTGCA	1350
	GGAACAATAG	AAGATGTAAA	AGAAAAAGCT	AAAAAAATGA	TGGAAAGCTA	1400
20	A					1401

## 2) INFORMATION FOR SEQ ID NO: 672

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1509 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Cytophaga lytica*  
 (B) STRAIN: DSM 2039  
 (C) ACCESSION NUMBER: M22535

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 672

	ATGTCTAAAG	TTACAGGTAA	AGTTTCCCAA	ATTATTGGCC	CAGTTATAGA	50
	TGTGGAGTTC	CAAGCAGGGG	TAGATCTTCC	AAAAATTTAT	GATTCATTAG	100
	AAATTAAAAA	AGCAGATGGA	TCAATTTTGG	TTTGGGAAGT	ACAATCACAC	150
	ATTGGTGAGA	ACACAGTAAG	AACTATATCT	ATTGATTCTT	CTGATGGTTT	200
45	AAGTCGTGGA	GCAGAGGTTA	ATGCAACAGG	AAGCGCTATA	CAAATGCCAG	250
	TTGGAGATGA	CGTTTACGGA	CGTTTATTTA	ACGTAATTGG	AGACGCTATT	300
	GATGGTCTTG	GGAATTTACC	AAAATCTGGT	AAAGATGGTT	TGCCAATACA	350
	CAGAGAGGCA	CCAAAATTG	AAGACTTATC	TACTTCTACA	GAAGTATTAT	400
	TTACAGGTAT	TAAAGTAATT	GACCTTATTG	AGCCTTATGC	AAAAGGTGGT	450
50	AAGATTGGTT	TATTTGGAGG	TGCCGGAGTA	GGTAAAACAG	TATTAATTCA	500
	GGAATTAATT	AACAACATTG	CAAAGGTCA	CGGTGGACTT	TCTGTATTTG	550
	CTGGTGTAGG	TGAGCGTACT	CGTGAGGGTA	ACGATTTACT	ACGTGAGATG	600
	TTAGAGTCTG	GTATTATTAA	ATACGGAGAT	GACTTTATGC	ACTCTATGGA	650
	AGAAGGTGGT	TGGGATTTAT	CTAAAGTTGA	TAAATCTGTA	ATGAAAGATT	700
55	CTAAAGCAAC	CTTTGTATTT	GGACAAATGA	ATGAGCCACC	AGGAGCACGT	750
	GCACGTGTTG	CATTATCTGG	TTTAACTATT	GCAGAATATT	TCCGTGATGG	800
	AGCAGGTGAA	GGTCAAGGTA	AAGATGTACT	TTTCTTTGTG	GATAACATTT	850
	TCCGTTTAC	ACAAGCTGGT	TCTGAGGTAT	CTGCATTACT	TGGTCGTATG	900
	CCATCTGCGG	TAGGTTACCA	ACCAACATTA	GCAACAGAAA	TGGGTGCTAT	950
60	GCAAGAGCGT	ATTACATCAA	CAAAAAGAGG	TTCTATTACA	TCTGTACAGG	1000

	CGGTTTACGT	ACCTGCGGAT	GATTTAACGG	ATCCAGCACC	GGCAACTACC	1050
	TTTGCTCACT	TAGATGCAAC	AACGGTATTG	TCTCGTAAAA	TTGCAGAGTT	1100
	AGGTATTTAC	CCAGCGGTAG	ATCCATTAGA	TTCTACTTCT	AGAATCTTAG	1150
	CTCCAGAAAT	TTTAGGAAAA	GATCACTACT	CTTGTGCACA	ACGTGTAAAA	1200
5	GAGTTGTTAC	AACGTTATAA	AGAATTACAA	GATATTATTG	CTATCCTTGG	1250
	TATGGAAGAA	TTATCTGAGG	AAGATAAAAT	GGCAGTTGGT	AGAGCAAGAC	1300
	GTGTACAACG	TTTCTTATCT	CAGCCTTTCC	ACGTAGCAGA	GCAATTTACA	1350
	GGTCTTAAAG	GTGTTTTAGT	AGATATCAAG	GATACTATTA	AAGGATTTAA	1400
	TATGATTATG	GATGGTGAAT	TAGATCACTT	ACCAGAATCT	GCATTTAACC	1450
10	TTAAAGGTAC	TATTGAAGAA	GCTATAGAAG	CAGGAGAAAA	AATGCTTGCT	1500
	GAAGCATAA					1509

## 15 2) INFORMATION FOR SEQ ID NO: 673

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 819 bases  
 (B) TYPE: Nucleic acid  
 20 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

## 25 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Ehrlichia risticii*  
 (B) STRAIN: HRC-IL

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 673

30	CCTAAAATAT	ATGATGCATT	ATATGTAAAA	CTAGATAATG	AAAATTTGTG	50
	TTTAGAAGTT	TCACAAATTA	TTGGAGATAA	TGTTGTTAGA	TGTATTGCAA	100
	TGGGAGCTAC	TTATGGATTA	AATCGTGGTT	TAGAAGTAGT	TTGTTTCAGGA	150
	AATCCAATTC	AGGTTCCCTGT	AGGTGAACAA	GTTTTAGGTA	GAATGTTTAA	200
35	TGTTGTTGGT	AAAACAATTG	ACAATCTTGA	ATCTTTAGAT	GATAAAAATA	250
	TAAAAATGAT	GCCAATTCAT	CGAAATCCAC	CATCATTTGA	AGAGCAATCC	300
	AATGAAATTG	AAATTTTTGA	AACAGGCATT	AAAGTTATTG	ATTTATTAAT	350
	TCCATATGCT	AAAGGTGGTA	AGATTGGATT	ATTTGGTGGA	GCAGGGGTTG	400
	GGAAAACGGT	TCTTGTTCAA	GAATTAATTC	ACAATATCGC	AAAAGGTCAT	450
40	GGTGGTCTAT	CTGTTTTTGC	TGGAGTTGGT	GAAAGAACTC	GTGAAGGTAA	500
	TGACTTGAT	TATGAAATGA	TTGAAGGTGG	AGTTATAGAT	AAAACAGCCT	550
	TAGTGTTTGG	GCAAATGAAT	GAACCTCCTG	GCGCAAGAAT	GCGCGTAGCA	600
	TTAACTGCTT	TAACAATGGC	TGAATATTTT	CGTGATGTTT	AAAACCAAGA	650
	TGTTTTGTTA	TTTATTGATA	ATATCTTTAG	ATTTACACAA	GCTGGTAGTG	700
45	AAGTTTCAGC	ATTATTAGGA	AGAATGCCAT	CTGCTGTTGG	TTATCAACCA	750
	ACTTTGGCAT	ATGAAATGGG	ATTGTTACAA	GAAAGAATCA	CTTCCACTAA	800
	AAGTGTTTCT	ATAACATCT				819

## 50 2) INFORMATION FOR SEQ ID NO: 674

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 840 bases  
 55 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

60

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Vibrio cholerae*  
 (B) STRAIN: ATCC 25870

## 5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 674

	AGAGCGAAGT	ACCAAGTGTT	TACGATGCTC	TGAATGTTGT	GGATTCCAAA	50
	GAACGTCTGG	TTCTGGAAGT	TCAACAGCAG	CTAGGCGGTG	GCGTGATTCTG	100
	CGCTATCGTT	ATGGGTAGCT	CGGATGGTTT	ACGTCGTGGA	ATGACAGTAC	150
10	AAAACACTGG	CGCTCCAATT	TCAGTACCAG	TAGGTACTAA	AACCCTAGGT	200
	CGTATCATGA	ACGTGCTTGG	TGATGCGATT	GACGAACGTG	GCGACATTGG	250
	CGCAGAAGAG	GTGTACTCGA	TTCACCGTCC	TGCTCCAAGC	TACGAAGAAC	300
	AGTCTAGTGC	AACTGAACTT	TTGGAAACGG	GTGTAAAGGT	TATCGACCTG	350
	ATCTGTCCGT	TTGCGAAAGG	CGGTAAAATC	GGTCTGTTCG	GTGGTGCGGG	400
15	TGTAGGTAAG	ACCGTTAACA	TGATGGAACT	TATCAACAAC	ATCGCGCTAC	450
	AGCACTCAGG	TTTGTCTAGT	TTTGCTGGGG	TAGGTGAGCG	TACTCGTGAG	500
	GGTAACGACT	TCTACCACGA	AATGCAGGAA	GCGGGCGTTG	TAAACGTTGA	550
	ACAACCAGAA	CTGTCGAAAG	TAGCGATGGT	TTACGGTCAG	ATGAACGAGC	600
	CACCAGGCAA	CCGTCTGCGT	GTAGCACTGA	CTGGTCTGAC	TATGGCGGAA	650
20	AAGTTCCTGT	ATGAAGGCCG	TGACGTACTG	CTGTTTATCG	ACAACATCTA	700
	CCGTTACACC	CTAGCGGGAA	CGGAAGTATC	TGCTCTGCTT	GGCCGTATGC	750
	CTTCAGCGGT	AGGTTACCAA	CCAACACTGG	CTGAAGAGAT	GGGTGTTCTG	800
	CAAGAACGTA	TCACGTCAAC	CAAAAAGGT	TCTATCACCT		840

25

## 2) INFORMATION FOR SEQ ID NO: 675

## (i) SEQUENCE CHARACTERISTICS:

30 (A) LENGTH: 828 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

## 35 (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Vibrio cholerae*  
 (B) STRAIN: ATCC 25870

40

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 675

	CGGCGGTATC	CTAGTTGTAG	CGGCAACTGA	CGGTCCAATG	CCACAAACTC	50
	GTGAGCACAT	CCTGCTGGGT	CGCCAAGTAG	GTATTCCTTA	CATCATCGTA	100
45	TTCATGAACA	AGTGTGACAT	GGTTGACGAT	GAAGAGCTTC	TAGAGCTGGT	150
	AGAGATGGAA	GTTCGTGAGC	TGCTGTCTGA	GTACGATTTC	CCAGGTGATG	200
	ACCTGCCAGT	AATCCAAGGT	TCAGCACTAG	GCGCGCTAAA	CGGCGAAGCA	250
	CAGTGGGAAG	CGAAGATTGT	TGAGCTAGCA	GAAGCACTGG	ATACTTAYAT	300
	TCCAGAGCCA	GAGCGTGCA	TAGACATGGC	ATTCCTGATG	CCAATCGAAG	350
50	ACGTATTCTC	AATCCAAGGT	CGTGGTACAG	TAGTAACTGG	CCGTATCGAG	400
	CGCGGCATCC	TGAAAGTGGG	TGACGAAGTA	GCGATCGTTG	GTATCAAAGA	450
	GACAGTAAAA	ACGACCTGTA	CAGGTGTAGA	GATGTTCCGT	AAGCTGCTTG	500
	ACGAAGGTCG	TGCAGGTGAG	AACGTAGGTG	CACTRCTACG	TGGTACTAAG	550
	CGTGAAGAAG	TAGAGCGTGG	TCAAGTACTG	GCGAAGCCAG	GTTCAATCAC	600
55	ACCACACACT	AAGTTCGAAT	CAGAAGTATA	CGTACTGTCA	AAAGATGAAG	650
	GTGGCCGTC	TACTCCATTC	TTCAAAGGTT	ACCGTCCACA	GTTCTACTTC	700
	CGTACAACCTG	ACGTAACAGG	CAGCATTGAG	CTACCAGARG	GCGTAGAAAT	750
	GGTAATGCCA	GCGGACAACG	TGAAGATGGT	TGTAGACCTG	ATTGCACCAA	800
	TCGCGATGGA	CGAAGGTCTA	CGCTTCGC			828

60.

## 2) INFORMATION FOR SEQ ID NO: 676

## 5 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1298 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

## 10 (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Leishmania enriettii*  
 (B) STRAIN: ATCC 50120

## 15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 676

	CTTCTCGGAT	GGCGTGCCGC	CGGTGCTGAC	GGCGCTGGAC	GTGACGGAGG	50
20	AACTCGGGCG	CGACGAGCCG	CTGACGCTAG	AGATCGTGCA	ACACTTGGAC	100
	GCGCACACCG	GCCGCTGCAT	TGCGATGCAG	ACGACGGACC	TACTGAAGCT	150
	GAAGTCGAAG	GTCGTGTCGA	CCGGCGGGAA	CATCTCTGTG	CCTGTGGGCC	200
	GCGAGACGCT	TGGCCGCATC	TTCAACGTAC	TGGGCGACGC	GATTGACCAG	250
	CGCGGCCCCG	TGGGCGAGAA	GATGCGCATG	GCGATCCACG	CGGAGGCGCC	300
25	GAAGCTGGCG	GACCAGGCGG	CGGAGGACAC	GATCCTGACG	ACCGGCATCA	350
	AAGTGATCGA	TCTGATCCTG	CCGTACTGCA	AGGGCGGCAA	GATCGGTCTG	400
	TTCGGCGGTG	CCGGTGTGGG	GAAGACTGTG	ATCATCATGG	AGCTGATCAA	450
	CAACGTCGCG	AAGGGCCACG	GTGGCTTCTC	CGTGTTGCGC	GGCGTTGGGG	500
	AGCGCACCCG	CGAGGGGACG	GATCTGTACC	TGGAGATGAT	GCAATCGAAG	550
30	GTGATCGACC	TGAAAGGTGA	GTCGAAGTGT	GTGCTTGTGT	ACGGGCAGAT	600
	GAACGAGCCC	CCGGGTGCGC	GCGCGCGCGT	TGCGCAGTCT	GCGCTGACGA	650
	TGGCCGAGTA	CTTCCGCGAC	GTGGAGGGCC	AGAACGTGCT	GCTGTTTCATC	700
	GACAACATCT	TCCGCTTCAC	GCAGGCGAAC	TCCGAGGTGT	CAGCGCTGCT	750
	GGGCCGCGATC	CCCGCCGCTG	TGGGCTACCA	ACCGACGCTT	GCGGAGGATC	800
35	TCGGCATGTT	GCAGGAGCGC	ATCACGTCGA	CGACGAAGGG	GTCGATCACG	850
	TCTGTGCAGG	CGGTGTACGT	GCCTGCGGAT	GATATCACGG	ATCCC GCGCC	900
	GGCGACGACA	TTCTCGCACC	TGGACGCGAC	GACGGTGCTG	GACCGCGCGG	950
	TGGCGGAGTC	TGGCATCTAC	CCCGCGGTCA	ACCCACTGGA	GTGCGCGTCG	1000
	CGTATCATGG	ACCCTGATGT	GATCGACGTG	GATCACTACA	ACGTTGCGCA	1050
40	GGACATTGTT	CAGATGCTGA	CCAAGTACAA	GGAGCTGCAG	GATATCATTG	1100
	CGGTGCTTGG	TATCGACGAG	CTGAGCGAGG	AGGACAAGGT	TGTGGTGGAC	1150
	CGTGCGCGCA	AGGTGACCCG	GTTCTTGTC	CAGCCGTTCC	AGGTTGCGGA	1200
	GGTGTTTACT	GGCATGACAG	GCCATTACGT	ACAGCTGAGC	GACACGGTGG	1250
45	AGTCGTTCTC	CGGTTTGCTG	ATGGGGTTCG	ACGACCAGAT	TCCGGAGA	1298

## 2) INFORMATION FOR SEQ ID NO: 677

## 50 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1083 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

## 55 (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Babesia microtti*  
 (B) STRAIN: Persing-1



## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 677

5	CAAGCTCAAG	TCTGAGCGTG	AGAGAGGTAT	TACTATTGAC	ATTACTCTCT	50
	GGAAATTTGA	GACCCAGAAA	TACGAGTACA	CTGTCATAGA	CGCACCTGGT	100
	CATCGTGACT	TTATCAAAAA	TATGATTACT	GGGACTTCAC	AAGCCGACGT	150
	TGCTATGCTT	GTCGTTCCCTG	CTGAATCTGG	CGGATTCGAG	GCTGCTTTTT	200
	CCAAAGAAGG	TCAGACCCGT	GAACACGCCT	TACTAGCCTT	CACACTTGGC	250
	GTCAAACAGA	TGATTGTTGC	TATTAACAAA	ATGGATTCTT	GTCAGTACAA	300
10	GGAGGATCGT	TATATGGAAA	TTTTCAAGGA	AGTACAGCAG	TACTTGAAGA	350
	AGGTGGGTTA	CAAAGTTGAA	AGCGTGCCGT	TTGTTGCTAT	TTCAGGATTC	400
	CACGGTGACA	ACATGGTTGA	AAAATCTACT	AACATGCCTT	GGTATAAGGG	450
	TAAGACCCTC	GTAGAGGCAC	TTGATCAAAT	GGAGCCTCCA	AAACGTCCGG	500
	TCGAAAAACC	TCTTAGATTG	CCCCTGCAGT	CAGTCTATAA	AATTGGAGGT	550
15	ATTGGTACGG	TACCAGTCGG	AAGGGTCGAA	ACAGGACAAC	TGAAAGCAGG	600
	AATGATCATT	ACTTTTGCCC	CCACTGGTTT	GACCACTGAA	TGTAAATCTG	650
	TTGAAATGCA	TCACGAGGTT	GTGGAAGTGG	CTAGCCCCGG	TGATAACGTT	700
	GGATTTAATG	TCAAGAATGT	GTCTGTTAAG	GATATTAAGA	GAGGAAATGT	750
	GGCTTCGGAT	TCGAAAAATG	ACCCAGCCAA	GGAAGCTACC	TCTTTCTCTG	800
20	CACAAGTCAT	TGTACTCAAT	CACCCTGGTA	CCATCAAGGC	CGGTTACTCA	850
	CCTGTGGTTG	ATTGCCATAC	TGCCCCACATT	GCTTGCAAAT	TCGAATCTCT	900
	AGACACTAGG	ATTGACAAGC	GTACTGGCAA	GACTTTGGAA	GAAAATCCTA	950
	AGACTATTAA	GAATGGTGAC	GCTGCCATGG	TGACTATGAA	ACCAAATAAA	1000
	CCCATGGTTG	TGGAAACTTT	CACCGACTAC	GCCCCGTTGG	GCCGGTTCGC	1050
25	CGTGCGTGAT	ATGCGCCAAA	CCGTTGCCGT	CGG		1083

## 2) INFORMATION FOR SEQ ID NO: 678

30

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 551 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

35

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

40

- (A) ORGANISM: *Cryptococcus neoformans*
- (B) STRAIN: Lev-12

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 678

45	TGTGCTCATT	CAGGAGCTCA	TTAACAACAT	TGCCAAGGCT	CACGGTGGTT	50
	ACTCTGTCTT	CACTGGTGTC	GGTGAGCGAA	CTCGTGAGGG	TAACGACTTG	100
	TACCACGAAA	TGAGGGAGAC	TGGTGTTATC	AACCTTGAGG	GTGACTCCAA	150
	GGTCGCTCTT	GGTGAGTTCT	TTTTTTTCTT	CAGGCTAATT	AGTCGATGAC	200
	GTGGGCCCTG	ACTAAAACCTG	TTTCTTCCAG	TCTTCGGTCA	GATGAACGAG	250
50	CCCCCTGGAG	CCCGTGCCCG	AGTTGCCCTT	ACTGGTTTGA	CCATTGCCGA	300
	GTAATTCCGT	GACGAGGAAG	GCCAGGATGT	GTTGCTTTTC	ATTGACAACA	350
	TTTTCCGATT	CACCCAGGCC	GGTCCGAGG	TGTCTGCCCT	GCTCGGTCGT	400
	ATCCCCTCTG	CCGTCGGTTA	CCAGCCCACT	CTTTCACCG	ACATGGGTGG	450
	TATGCAGGAG	CGAATGTAGG	TTGCATTCTC	TGTGATTTTA	CGGCAAGCCT	500
55	TGACTTTTTT	TTTCTAGTAC	CACCACCAAG	AAGGGTTCCA	TTACCTCCGT	550
	C					551

## 60 2) INFORMATION FOR SEQ ID NO: 679

## (i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 552 bases  
(B) TYPE: Nucleic acid  
(C) STRANDEDNESS: Double  
(D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- 10 (A) ORGANISM: *Cryptococcus neoformans*  
(B) STRAIN: ATCC 44104

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 679

15 TGTGCTCATT CAGGAGCTCA TTAACAACAT TGCCAAGGCC CACGGTGGTT 50  
ACTCCGTCTT CACCGGTGTC GGTGAGCGAA CTCGTGAGGG TAACGACTTG 100  
TACCACGAAA TGAGGGAGAC TGGTGTTATC AACCTTGAGG GTGACTCCAA 150  
GGTCGCTCTT GGTGAGTTCT TTTTTTTGGG AGCTAATTAG TCGATGACGT 200  
20 GGGCCCTGAC CAAAACCGTT TCTTTCAGTC TTCGGTCAGA TGAACGAGCC 250  
CCCTGGAGCC CGTGCCCGAG TTGCTCTTAC TGGTTTGACC ATTGCCGAGT 300  
ACTTCCGTGA CGAGGAAGGC CAGGATGTGT TGCTTTTCAT TGACAACATT 350  
TTCCGATTCA CCCAGGCCGG TTCCGAGGTG TCTGCCTTGC TCGGTCGTAT 400  
CCCCTCTGCC GTCGGTTACC AGCCCACTCT TTCCACCGAT ATGGGTGGTA 450  
25 TGCAAGAGCG AATGTAAGTT GCATTTTTTG TGATTTTACG GCAAGTCTTG 500  
ACTTACATTT TTTTCTAGCA CCACCACCAA GAAGGGTTCC ATTACCTCCG 550  
TC 552

## 2) INFORMATION FOR SEQ ID NO: 680

## (i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 1018 bases  
(B) TYPE: Nucleic acid  
(C) STRANDEDNESS: Double  
(D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- 40 (A) ORGANISM: *Cunninghamella bertholletiae*  
(B) STRAIN: ATCC 42115

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 680

45 TCTCCCTGCT ATTTTAAACG CTCTTGAAGT TAAGGATCAT GCTGGTGGTC 50  
GTCTTGTTCT TGAAGTTGCT CAACACTTGG GTGAAAACAC TGTACGTACT 100  
ATTGCTATGG ATGGTACTGA AGGTAAGTTT ATTTT TAGAT GATCATAAAT 150  
50 AATTGATCAT AATGATAAAA AAAAAAGAAG AAGAAGAACA GGATGTATAT 200  
AATGGTTAAT AAATAATATT TTCATATTGK ATATAACTAT TTAATCTGTT 250  
TTTTTTTCTT CATGATTATA TATATATATG TMCTAATATC TAATATGAAC 300  
CTTTTTTATA AAATTAATCA GGTCTTGTCG GTGGTCAAAA GGTTGTTGAT 350  
ACTGGTGCTC CTATTACCAT TCCTGTTGGT AAGGAAGTTC TTGGTCGTAT 400  
55 CATCAACGTT ATTGGTGAAC CCATTGATGA ACGTGGTCCT ATTAAGGCCA 450  
AGTCTCACCG TGCTATTCAC GCTGAAGCTC CAGAATTCGT TGATCAATCT 500  
CCTACTCCCG AAATTCTTGA AACTGGTATT AAGGTTGTCG ATTTATTAGC 550  
TCCTTATGCT CGTGGTGGTA AGATTGGTCT TTTCGGTGGT GCTGGTGTAG 600  
GTAAACTGT CTTGATTCAA GAACATTATTA ACAACATTGC TAAAGCCCAT 650  
60 GGTGGTTACT CTATTTTCTG TGGTGTGGT GAACGTACTC GTGAAGGTAA 700

	CGATTTATAC	CACGAAATGA	TGGAAACTGG	TGTCATTAAA	CTTGAAGGTG	750
	ACTCCAAGTG	TGCTCTTGTA	TTCGGTCAAA	TGAACGAACC	TCCTGGTGCT	800
	CGTGCCCGTG	TTGCTTTAAC	TGGTTTAACC	ATTGCTGAAT	ACTTCCGTGA	850
	TGAAGAAGGT	CAAGATGTGT	TACTTTTTCAT	TGATAACATT	TTCCGTTTCA	900
5	CTCAAGCTGG	TTCTGAAGTA	TCTGCCCTTT	TAGGTCGTAT	TCCATCTGCT	950
	GTAGGTTACC	AACCCACTTT	ATCTACTGAT	ATGGGTGGTA	TGCAAGAACG	1000
	TATTACTACT	ACCAAGAA				1018

10

2) INFORMATION FOR SEQ ID NO: 681

(i) SEQUENCE CHARACTERISTICS:

15

- (A) LENGTH: 23 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 681

GGISSITTYG GIISIGGIAA RAC

23

25

2) INFORMATION FOR SEQ ID NO: 682

(i) SEQUENCE CHARACTERISTICS:

30

- (A) LENGTH: 26 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 682

GTIACIGGYT CYTCRAARTT ICCICC

26

40

2) INFORMATION FOR SEQ ID NO: 683

(i) SEQUENCE CHARACTERISTICS:

45

- (A) LENGTH: 26 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 683

GTIACIGGIT CISWIAWRTC ICCICC

26

55

2) INFORMATION FOR SEQ ID NO: 684

60

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3267 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Candida tropicalis*  
 (C) ACCESSION NUMBER: M64984

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 684

15	ATGGCTGGTG	CTTTAGAAAA	CGCAAGAAAA	GAAATTAAAC	GTCTTTCATT	50
	AGATGACACC	AATGAATCCC	AATATGGTCA	AATCTATTCT	GTTTCCGGTC	100
	CGGTTGTTAT	TGCCGAAAAC	ATGATTGGAT	GTGCCATGTA	CGAATTGGTT	150
	AAAGTTGGTC	ATGATAATTT	AGTTGGGGAA	GTTATTAGAA	TTAATGGTGA	200
	TAAAGCAACC	ATTCAAGTTT	ATGAAGAAAC	TGCAGGGGTC	ACTGTTGGTG	250
20	ATCCAGTTTT	AAGAACTGGT	AAACCATTAT	CTGTTGAATT	AGGTCCTGGT	300
	TTAATGGAAA	CTATTTATGA	TGGTATTCAA	AGACCTTTAA	AAGCCATTAA	350
	AGATGAATCC	CAATCTATTT	ATATCCCAAG	AGGTATTGAT	GTTCTTGCTT	400
	TATCAAGAAC	TGTTCAATAT	GATTTCACTC	CAGGTCAATT	GAAAGTTGGT	450
	GATCATATCA	CTGGTGGGGA	CATTTTGGT	TCTATTTATG	AAAACCTCTT	500
25	ATTGGATGAC	CATAAGATTT	TGTTACCTCC	AAGAGCAAGA	GGTACTATTA	550
	CTTCTATTGC	TGAAGCCGGT	TCTTATAATG	TTGAAGAACC	AGTTTGGGAA	600
	GTTGAATTTG	ATGGTAAGAA	ACATAAATAC	TCTATGATGC	ATACATGGCC	650
	AGTTAGAGTT	CCAAGACCAG	TTGCTGAAAA	ATTGACTGCT	GATCATCCAT	700
	TGTTGACCGG	TCAAAGAGTC	TTGGATTCTT	TATTCCTCATG	TGTTCAAGGT	750
30	GGTACTACTT	GTATCCCAGG	GGCTTTTGGT	TGTGGTAAAA	CTGTTATTTC	800
	TCAATCTTTG	TCCAAATTCT	CCAACCTCTGA	TGTTATTATC	TATGTTGGTT	850
	GTTTCACTAA	AGGTACTCAA	GTCATGATGG	CTGATGGTGC	CGACAAATCT	900
	ATTGAATCTA	TTGAAGTTGG	TGACAAAGTC	ATGGGTAAAG	ATGGTATGCC	950
	AAGAGAAGTT	GTTGGCTTAC	CAAGAGGTTA	TGATGATATG	TACAAGGTTT	1000
35	GTCAACTTTC	TAGTACTAGA	CGTAATGCTA	AATCCGAAGG	CTTGATGGAT	1050
	TTCACTGTTT	CTGCTGATCA	TAAACTTATC	TTGAAACTA	AACAAGATGT	1100
	CAAGATTGCT	ACACGTAAAA	TTGGTGGCAA	CACCTATACT	GGTGTTACTT	1150
	TCTATGTTTT	GGAAAAGACT	AAGACTGGTA	TTGAATTAGT	TAAAGCCAAG	1200
	ACTAAAGTTT	TCGGTCATCA	TATCCATGGT	CAAAATGGCG	CTGAAGAAAA	1250
40	AGCTGCTACT	TTTGCTGCTG	GCATTGACTC	TAAAGAATAC	ATTGATTGGA	1300
	TCATTGAAGC	TAGAGATTAT	GTACAAGTTG	ATGAAATTGT	CAAGACCAGC	1350
	ACCACTCAA	TGATCAACCC	AGTTCATTTT	GAATCTGGTA	AACTCGGTAA	1400
	CTGGTTACAC	GAACACAAGC	AAAACAAATC	ACTTGCTCCA	CAATTGGGTT	1450
	ACTTGTTGGG	TACTTGGGCT	GGTATTGGAA	ATGTTAAATC	TTCTGCTTTC	1500
45	ACCATGAACT	CCAAAGATGA	TGTTAAATTA	GCTACAAGAA	TTATGAACTA	1550
	CTCTTCAAAA	TTGGGCATGA	CTTGTTCTTC	TACTGAATCC	GGTGAATCA	1600
	ATGTCGCTGA	AAACGAAGAA	GAATTTTTCA	ATAACCTTGG	TGCTGAAAAG	1650
	GATGAAGCTG	GTGATTTTAC	TTTTGATGAA	TTTACCGATG	CTATGGATGA	1700
	ATTGACTATC	AATGTTTCATG	GTGCAGCTGC	AAGCAAGAAG	AACAATTTGT	1750
50	TGTGGAATGC	TTTGAAATCT	CTTGGTTTCA	GAGCCAAGTC	TACTGATATT	1800
	GTCAAGAGTA	TTCTCAACA	TATTGCTGTT	GATGATATTG	TTGTCAGAGA	1850
	ATCTTTGATT	GCCGGTTTAG	TTGATGCTGC	TGGTAATGTT	GAAACCAAAT	1900
	CCAATGGTTC	TATTGAAGCT	GTTGTTAGAA	CTTCTTTCAG	ACATGTCGCT	1950
	AGAGGTCTTG	TCAAGATTGC	TCATTCTTTG	GGTATTGAAT	CATCTATTAA	2000
55	TATTAAAGAT	ACTCACATTG	ATGCTGCTGG	TGTTAGACAA	GAATTTGCTT	2050
	GTATTGTCAA	TTTGACTGGT	GCTCCACTTG	CTGGTGTTC	TTCTAAATGT	2100
	GCACTTGCAA	GAAACCAAAC	TCCAGTTGTC	AAATTTACCA	GAGACCCAGT	2150
	TTTGTTCAAC	TTTGATTTGA	TCAAATCTGC	AAAAGAAAAC	TATTATGGTA	2200
	TTACTTTGGC	TGAAGAAACT	GATCATCAAT	TCCTTTTATC	CAACATGGCC	2250
60	TTGGTGACAC	ACTGTGGTGA	ACGTGGTAAT	GAGATGGCTG	AAGTTTTGAT	2300

	GGAATTCCCA	GAATTGTTTA	CTGAAATTTT	TGGTAGAAAA	GAACCAATTA	2350
	TGAAACGTAC	CACTTTGGTT	GCCAATACTT	CTAATATGCC	AGTCGCTGCC	2400
	AGAGAAGCTT	CTATTTATAC	TGGTATTACA	TTGGCTGAAT	ATTTTCAGAGA	2450
	TCAAGGTAAG	AATGTTTCTA	TGATTGCTGA	TTCTTCTTCA	CGTTGGGCTG	2500
5	AAGCTTTGAG	AGAAATTTCT	GGTAGATTGG	GTGAAATGCC	TGCTGATCAA	2550
	GGTTTCCCAG	CTTATTTGGG	TGCTAAATTG	GCTTCTTTCT	ATGAGCGTGC	2600
	CGGTAAAGCC	ACTGCTTTGG	GTTCAACCAGA	TAGAGTTGGT	TCAGTTTCTA	2650
	TTGTTGCTGC	TGTTTCTCCA	GCTGGTGGTG	ATTTCTCTGA	TCCAGTTACT	2700
	ACTTCTACTT	TGGGTATTAC	TCAAGTTTTT	TGGGGGTTGG	ATAAGAAATT	2750
10	GGCCCAAAGA	AAACATTTCC	CATCTATTAA	CACCAGTGT	TCTTATTCTA	2800
	AATACACCAA	TGTTTTGAAC	AAATACTATG	ATTCCAACCTA	TCCAGAATTC	2850
	CCACAATTGA	GAGACAAAAT	TAGAGAAATT	TTATCTAATG	CTGAAGAATT	2900
	GGAACAAGTT	GTTCAATTAG	TTGGTAAATC	TGCATTGTCT	GATTCTGATA	2950
	AGATTACTTT	AGATGTTGCT	ACCTTGATTA	AAGAAGATTT	CTTGCAACAA	3000
15	AATGGTTATT	CTTCATATGA	TGCATTCTGT	CCAATTTGGA	AGACTTTTGA	3050
	TATGATGAGA	GCATTTATTT	CATATTATGA	TGAAGCACAA	AAAGCAATTG	3100
	CCAATGGTGC	TCAATGGTCT	AAATTAGCTG	AAAGTACTAG	TGATGTTAAA	3150
	CATGCTGTTT	CTTCAGCTAA	ATTCTTTGAA	CCATCAAGAG	GTCAAAAAGA	3200
	AGGTGAAAAA	GAATTTGGAG	ATTTATTAAC	CACTATCTCC	GAAAGATTTG	3250
20	CTGAAGCTTC	AGAATAA				3267

## 2) INFORMATION FOR SEQ ID NO: 685

25

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1782 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

30

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus hirae*  
 (B) STRAIN: ATCC 9790  
 (C) ACCESSION NUMBER: D17462

35

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 685

40

	TTGCAAATTG	GAAAAATCAT	AAAAGTCTCC	GGTCCTCTCG	TTATGGCAGA	50
	AAATATGTCA	GAAGCAAGTA	TTCAAGACAT	GTGTTTAGTG	GGAGATTTAG	100
	GATCATCGG	CGAAATCATT	GAGATGCGTC	AAGATGTGGC	GTCTATTCAA	150
	GTATATGAAG	AAACTTCAGG	AATTGGTCCC	GGAGAACCTG	TTCGTTCCAC	200
45	TGGGGAAGCA	CTATCTGTTG	AGCTAGGACC	AGGAATCATT	TCACAAATGT	250
	TTGACGGGAT	TCAAAGACCA	CTGGATACAT	TTATGGAAGT	GACTCAAAGT	300
	AACTTCTTAG	GACGTGGGGT	CCAATTACCA	GCTTTAGATC	ATGAGAAACA	350
	ATGGTGGTTT	GAAGCGACAA	TCGAAGAAGG	AACAGAAGTA	AGTGCTGGAG	400
	ACATCATTGG	GTACGTGGAT	GAAACGAAGA	TCATTGAGCA	CAAAATCATG	450
50	GTCCCTAATG	GTATCAAAGG	AACTGTACAA	AAAATTGAAT	CTGGATCATT	500
	TACGATCGAT	GATCCGATTT	GTGTGATCGA	AACGGAACAA	GGCTTAAAAG	550
	AGCTGACGAT	GATGCAAAAA	TGGCCAGTAC	GTCGTGGTCG	ACCAATCAAA	600
	CAAAAATTAA	ATCCAGATGT	ACCGATGATC	ACCGGTCAAA	GGGTCATTGA	650
	CACGTTTTTC	CCAGTAACTA	AAGGAGGAGC	GGCAGCCGTT	CCAGGTCCGT	700
55	TTGGTGCAGG	GAAGACAGTT	GTGCAACACC	AGATTGCTAA	GTGGTCGGAC	750
	GTAGATCTAG	TGGTTTACGT	TGGTTGTGGG	GAACGAGGAA	ATGAAATGAC	800
	GGATGTCGTC	AATGAATTTT	CTGAACTGAT	CGATCCAAAT	ACAGGCGAGT	850
	CTTTGATGGA	ACGAACTGTG	TTGATCGCTA	ATACATCGAA	CATGCCAGTA	900
	GCTGCTCGAG	AAGCTTCTAT	TTATACGGGA	ATCACGATTG	CCGAGTACTT	950
60	CCGTGACATG	GGGTATGATG	TAGCAATCAT	GGCAGATTCC	ACTTCTCGTT	1000

	GGGCAGAAGC	ACTGCGTGAA	ATGAGCGGAC	GTTTAGAAGA	AATGCCTGGT	1050
	GATGAAGGTT	ATCCCGCTTA	TCTGGGCTCT	CGTCTAGCTG	AATACTATGA	1100
	ACGTTCAAGG	CGTGTCATTG	CTCTAGGCTC	TGACCAACGT	GAGGGCAGTA	1150
	TCACTGCCAT	CAGTGCGGTT	TCTCCTTCTG	GTGGAGATAT	CTCTGAACCA	1200
5	GTGACTCAAA	ATACCTTACG	TGTGGTGAAG	GTTTTCTGGG	GATTAGATTC	1250
	TAGTCTTGCT	CAAAAAAGAC	ATTTTCCATC	GATTAACTGG	ATCCAAAGTT	1300
	ACTCATTATA	TTCAACAGAA	GTTGGCAGAT	ATATGGATCA	AATCTTACAA	1350
	CAGGATTGGT	CTGATATGGT	AACTGAAGGC	ATGCCGATCT	TGCAAGAAGA	1400
	AGAACAATTA	AATGAAATCG	TGCGCTTGGT	AGGGATCGAT	TCGCTTTCTG	1450
10	ATAACGATCG	CTTGACCCTT	GAAGTAGCAA	AATCGATTCT	AGAAGACTAT	1500
	TTACAACAAA	ATGCTTTTGA	TGATGTAGAT	ACGTTTACTT	CAAGAGAAAA	1550
	ACAATTCAAC	ATGTTGAAAG	TTATTTTGAC	TTTTGGGAAA	GAAGCTCGAA	1600
	AAGCCTTATC	GTTGGGAGCG	TACTTCAATG	AAATCATGGA	AGGTACAGTA	1650
	GCGGTCAGAG	AACGCATTAG	TCGGAGCAAG	TATATTCCAG	AAGAAGAGTT	1700
15	AGCCAAAATT	AGTAGTATAA	ATGAAGAAAT	CAAAGAAACG	ATCCAATTGA	1750
	TTGTTTCAGA	AGGAGGGATG	ACCGATGATT	AA		1782

## 20 2) INFORMATION FOR SEQ ID NO: 686

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1781 bases  
 (B) TYPE: Nucleic acid  
 25 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

## 30 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Chlamydia pneumoniae*  
 (B) STRAIN: CWL 029  
 (C) ACCESSION NUMBER: Genome project

## 35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 686

	CAGGGACATG	TTATAGAAGC	TTATGGAAAC	TTGTTACGTG	TACGCTTTGA	50
	CGGATATGTT	AGACAAGGTG	AAGTTGCATA	TGTC AACGTA	GATAATACCT	100
	GGTTAAAAGC	AGAAGTGATT	GAAGTTGCTG	ATCAAGAAGT	CAAGGTTTCA	150
40	GTATTTGAAG	ATACACAAGG	CGCGTGTCGA	GGAGCTCTTG	TTACGTTTTT	200
	AGGACATCTT	TTAGAAGCCG	AGTTAGGGCC	TGGCTTGCTT	CAGGGCATT	250
	TCGATGGACT	TCAAAATCGT	CTTGAGGTGC	TAGCTGAAGA	TAGTTCTTTC	300
	TTGCAGAGAG	GCAAGCATGT	TAATGCTATT	TCTGATCATA	ATTTATGGAA	350
	TTATACTCCC	GTAGCTTCTG	TTGGGGATAC	TTTAAGACGA	GGAGATCTTC	400
45	TAGGAACAGT	ACCTGAAGGA	CGATTTACTC	ATAAGATTAT	GGTTCCTTTT	450
	TCTTGCTTTC	AAGAGGTTAC	CCTGACTTGG	GTAATTTCTG	AAGGAACCTA	500
	TAATGCTCAT	ACTGTGGTCG	CAAAAGCTCG	AGATGCTCAG	GGTAAAGAAT	550
	GTGCCTTTAC	TATGGTGCAA	AGATGGCCGA	TCAAACAAGC	TTTTATTGAA	600
	GGAGAGAAGA	TCCCTGCGCA	TAAGATTATG	GATGTGGGTT	TGCGAATCTT	650
50	AGATACGCAA	ATTCCAGTAT	TGAAGGGGGG	AACTTTCTGT	ACCCAGGAC	700
	CTTTTGGTGC	AGGGAAAACA	GTCTTACAAC	ACCATCTTTC	TAAGTACGCT	750
	GCTGTAGATA	TTGTGATTTT	GTGTGCGTGC	GGAGAGCGTG	CTGGTGAAGT	800
	TGTTGAGGTA	TTACAAGAGT	TCCCTCATCT	TATCGACCCC	CATACCGGAA	850
	AGTCTTTAAT	GCACAGAACA	TGTATTATTT	GTAACACATC	ATCCATGCCT	900
55	GTGGCTGCCC	GAGAGTCTTC	GATCTATTTA	GGAGTGACGA	TTGCAGAATA	950
	CTATCGCCAG	ATGGGACTAG	ATATTCTGCT	TTTAGCTGAT	TCTACATCCC	1000
	GATGGGCACA	AGCCCTTAGA	GAGATTTCGG	GACGTCTTGA	AGAAATCCCT	1050
	GGAGAGGAAG	CATTTCTGCT	ATACCTGTCT	TCTAGAATAG	CTGCTTTTTA	1100
	TGAGCGAGGA	GGAGCTATCA	CCACGAAAGA	TGGTTCTGAA	GGATCTTTAA	1150
60	CTATATGTGG	TGCGGTGTCT	CCTGCAGGAG	GAAACTTTGA	AGAACCAGTC	1200

	ACTCAATCTA	CATTAGCTGT	AGTCGGAGCG	TTCTGTGGTC	TTTCAAAAGC	1250
	ACGAGCTGAC	GCACGTAGGT	ATCCTTCAAT	AGACCCTTTG	ATTTCTTGGT	1300
	CAAAATATTT	GAACCAGGTA	GGACAAATTT	TAGAAGAGAA	GGTTTCAGGC	1350
	TGGGGTGGTG	CTGTGAAAAA	AGCAGCACAG	TTTCTAGAGA	AAGGTTTCTA	1400
5	AATCGGCAAG	CGTATGGAAG	TTGTCAGTGA	AGAAGGGGTT	TCTATGGAAG	1450
	ACATGGAAAT	CTACTTAAAG	GCAGAACTTT	ATGATTTTTG	TkATCTCCAG	1500
	CAGAACGCAT	TCGATCCTGT	GGACTGTTAT	TGTCCTTTTG	AGAGACAGAT	1550
	AGAGTTATTT	TCATTAATCA	GTCGTATTTT	TGATGCTAAA	TTTGTTTTTG	1600
	ATAGTCCTGA	TGATGCAAGA	AGCTTTTTTC	TTGAGCTGCA	GAGCAAGATT	1650
10	AAGACATTAA	ATGGCCTGAA	ATTTCTTTTC	GAGGAATATC	ATGAGAGTAA	1700
	AGAGGTCATA	GTTAGACTGT	TGGAAAAAAC	AATGGTACAA	ATGGCGTAAG	1750
	GATATGCAAA	CAATCTACAC	AAAAATAACT	G		1781

15

## 2) INFORMATION FOR SEQ ID NO: 687

## (i) SEQUENCE CHARACTERISTICS:

	(A) LENGTH: 1758 bases
20	(B) TYPE: Nucleic acid
	(C) STRANDEDNESS: Double
	(D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

25

## (vi) ORIGINAL SOURCE:

(A)	ORGANISM: <i>Halobacterium salinarum</i>
(C)	ACCESSION NUMBER: S56356

## 30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 687

	ATGAGTCAAG	CTGAAGCAAT	CACTGACACC	GGCGAAATCG	AGAGCGTGAG	50
	CGGTCCGGTC	GTGACCGCCA	CGGGCCTCGA	CGCGCAGATG	AACGACGTCG	100
	TCTACGTGGG	CGACGAGGGT	CTGATGGGCG	AGGTCATCGA	GATCGAAGGC	150
35	GACGTAACCA	CCATCCAGGT	CTACGAGGAG	ACGTCCGGCA	TCGGGCCCGG	200
	CCAGCCCGTC	GACAACACGG	GCGAACCCT	CACCGTGGAC	CTGGGCCCGG	250
	GGATGCTGGA	CTCCATCTAC	GATGGTGTGC	AGCGTCCACT	GGACGTCCTC	300
	GAAGACGAGA	TGGGGGCGTT	CCTCGATCGC	GGTGTGACG	CACCCGGCAT	350
	CGACCTCGAC	ACCGACTGGG	AGTTCGAGCC	CACCGTCGAG	GCGGGCGACG	400
40	AGGTCGCGGC	CGGCGATGTC	GTCGGCACCG	TCGACGAAAC	GGTCAGCATC	450
	GAACACAAGG	TTCTGGTGCC	CCCCCGCAGT	GACGGCGGCG	AAGTCGTCGC	500
	CGTCGAATCC	GGCACGTTCA	CCGTCGACGA	CACGGTCGTC	GAGTTGGACA	550
	CCGGCGAGGA	GATCCAGATG	CACCAAGGAGT	GGCCGGTCCG	CCGCCAGCGC	600
	CCCACCGTCG	ACAAGCAGAC	GCCGACGGAG	CCGCTGGTGT	CCGGCCAGCG	650
45	CATCCTCGAC	GGCCTGTTCC	CGATCGCGAA	AGGCGGGACG	GCCGCGATCC	700
	CGGGGCCGTT	CGGGTCCGGG	AAGACGGTCA	CCCAGCAGTC	CCTCGCGAAG	750
	TTCGCCGACG	CGGACATCGT	TGTCTACATC	GGCTGTGGTG	AGCGCGGCAA	800
	CGAGATGACG	GAAGTCATCG	AGGACTTCCC	GGAGCTGCCC	GACCCCCAGA	850
	CCGGGAACCC	GCTGATGGCC	CGCACCACGC	TCATCGCGAA	CACGTCGAAC	900
50	ATGCCGGTTG	CCGGGCGTGA	GTCCTGCATT	TACACGGGAA	TCACCATCGC	950
	GGAGTACTAC	CGCGACATGG	GCTACGACGT	GGCGCTGATG	GCCGACTCCA	1000
	CCTCGCGGTTG	GGCGGAGGCC	ATGCGGGAGA	TCTCCTCGCG	ACTCGAGGAG	1050
	ATGCCCCGGCG	AGGAGGGGTA	TCCCGCGTAC	CTGGCCGCCC	GCCTCTCGGA	1100
	GTTCTACGAG	CGCGCCGGCT	ACTTCGAGAA	CTTCAACGGG	ACCGAGGGCT	1150
55	CCATCTCGGT	CATCGGTGCG	GTGTCGCCGC	CCGGCGGGGA	CTTCTCCGAG	1200
	CCGGTCACCC	AGAACACGCT	GCGCATCGTG	AAGACGTTCT	GGGCGCTTGA	1250
	CTCGGACCTC	GCCGAGCGCC	GGCACTTCCC	GGCGATCAAC	TGGGACGAGT	1300
	CCTACAGCCT	GTACAAGGAC	CAACTCGACC	CGTGGTTCAC	GGACAACGTC	1350
	GTCGACGACT	GGCCCGAGCA	GCGCCAGTCG	CCGGTCGACA	TCCTCGACGA	1400
60	GGAATCCGAA	CTCGAAGAGA	TCGTGCAGCT	CGTCGGGAAG	GACGCGCTGC	1450

CCGAGGACCA	GCAGCTCACG	CTGGAAGTCG	CGCGGTACAT	CCGCGAGGCG	1500
TGGCTCCAGC	AGAACGCGCT	CCACGACGTG	GATCGCTACT	GCCCGCCCGA	1550
GAAGACGTAC	GCCATCCTCT	CCGGCATCAA	GACGCTTCAC	GAGGAGTCCT	1600
TTGAGGCGTT	GGACGCCGGT	GTGCCAGTCG	AGGAGATCAC	GTCGATCGAC	1650
5 GCCGCGCCGC	GCCTGAATCG	TCTCGGCACG	ACGCCCACG	ACGAGCACGA	1700
GGCGGAGGTC	GCGGAGATCA	AACAGCAGAT	TACCGAGCAG	CTTCGGGAGC	1750
TCTACTGA					1758

10

## 2) INFORMATION FOR SEQ ID NO: 688

## (i) SEQUENCE CHARACTERISTICS:

15

- (A) LENGTH: 3118 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

20

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Human
- (C) ACCESSION NUMBER: L09234

25

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 688

GAATTC	CCGGC	AGCTG	ACTAG	TCTTG	TGATT	GGGGT	CCTGG	GCTGA	TAAAA	50
TCATT	CCAAA	TGACG	AGCAC	ATTGA	TAAAG	ACGTC	CGATG	AGGAC	CGGGA	100
GTCCA	AATTC	GGCTT	TGTTT	TTGCC	GTATC	TGGAC	CTGTG	GTGAC	AGCTG	150
30 AACGA	ATGGC	CGGTT	CTGCT	ATGTA	CGAAC	TGGTG	CGTGT	CGGTT	TATTAT	200
GAAC	TGGTC	GAGAG	ATCAT	CCGTT	TGGAG	GGTG	ACATG	CAACA	ATCCA	250
AGTAT	ACGAA	GACAC	CTCAG	GTGTG	ACAGT	AGGCG	ATCCC	GTGCT	GCGCA	300
CAGGC	AAAGC	GCTGT	CCGTG	GAAC	TGGGAC	CCGGA	ATCAT	GGGC	AGCATC	350
TTGAC	CGGTA	TCCAG	CGACC	GCTGA	AAGGAT	ATCA	ATGAAC	TGTCA	AATAG	400
35 TATCT	ACATC	CCGAA	AAGGT	TCAAT	GTGCC	TGCC	CTGAGT	CGACT	GCAC	450
AGTGG	GA	CAGT	CCCCG	TC	AGG	TTGGA	AAGCCA	CATT	ACTGGT	500
GGTG	ACCTGT	ACGGT	TTGGT	CCACG	AAAAAT	ACTCT	GGTGA	AACAC	AAAGTT	550
GCTG	CTGCCG	CCCCG	TGCCA	AGGGA	AACTGT	CACGT	ACATT	GCAGA	AACCTG	600
GAAAC	TACAC	AGTTG	ATGAT	GTTGT	CCTGG	AGACA	GAAAT	TGACG	GCGAG	650
40 CGATC	AAAGT	TCACC	ATGCT	GCAAG	TGTGG	CCTGT	ACGTC	AGCCC	AGGCC	700
TGTTA	CAGAA	AAGTT	GCCAG	CTAAC	TACCC	CCTC	CTTACT	GGCC	AGCGTG	750
TGCTC	GACTC	CCTAT	TCCC	TGTGT	CCAGG	GTGGA	ACAAC	AGCTA	TTCCT	800
GGGCG	CTTCG	GATGT	GCCAA	GACTG	TAATA	TCAC	AGTCTT	TGTCA	AAAATA	850
CTCAA	AATCC	GATGT	AATTA	TCTAT	GTAGG	TTGT	GGTGAG	CGAGG	TAATG	900
45 AAATG	TCAGA	AGTAC	TCAGG	GATTT	CCCCG	AGTTG	TCGTT	GGAG	ATTGAT	950
GGTGT	GACTG	AATCA	ATCAT	GAAGA	GAACA	GCCCT	TGGTC	CAAAC	ACATC	1000
AAAC	ATGCCT	GTGG	CTGCT	GAGA	AGCAT	TATCT	ACACA	GGTAT	TACAC	1050
TGTC	AGAATA	CTTC	AGGGAC	ATGGG	TTACA	ATGT	ATCCAT	GATGG	CTGAC	1100
TCAAC	TTTAC	GATGG	GCCGA	AGCT	CTTCGA	GAAAT	CTCAG	GTCGA	TTGGC	1150
50 TGAA	ATGCCT	GCCG	ACAGCG	GTTAT	CCCCG	CTAC	CTAGGT	GCAC	GACTTG	1200
CCAGT	TTTCTA	CGAG	CGTGCC	GGCCG	TGTGA	AGTG	CTTGGG	TAACC	CAGAC	1250
AGGG	AGGGCT	CCGT	GAGTAT	AGTGG	GCGCC	GTGT	CGCCG	CCGGT	TGGAGA	1300
CTTCT	TCAGAT	CCCG	TGACGA	CGGC	CACACT	AGGT	ATCGTC	CAGGT	GTTCT	1350
GGGG	TCTCGA	CAAGA	AACTT	GCCC	AGCGAA	AGCA	TTCCC	ATCCA	TCAAC	1400
55 TGGC	TCATCT	CGTAC	AGTAA	ATAC	ATGCGT	GCTCT	TGGATG	ACTT	CTACGA	1450
CAAGA	ATTTT	CCAG	AGTTT	TCCC	ACTGCG	TACAA	AGGTG	AAGG	AGATTT	1500
TGCAG	GAGGA	AGA	AGACCTG	TCTG	AAATTG	TGCAG	TTGGT	CGGT	AAAGCT	1550
TCATT	TGGCAG	AAAC	TGACAA	GATCA	CACACT	GAGGT	TGCCA	AACT	ATTAAA	1600
GGATG	ATTTT	CTGC	AACAGA	ACAG	CTATTC	ACCAT	TATGAC	CGTTT	CTGCC	1650
60 CATT	CTACAA	GACAG	TAGGA	ATGCT	GAAAA	ATATG	ATTGC	TTTCT	ACGAT	1700



	ATGTCTCGGC	ATGCAGTTGA	ATCTACTGCT	CAGAGCGAGA	ACAAGATCAC	1750
	TTGGAATGTT	ATTAGAGATT	CTATGGGCAA	TATTCTGTAT	CAGCTTTCCT	1800
	CCATGAAATT	CAAGGATCCA	GTCAAGGATG	GAGAAGCGAA	GATCAAGGCA	1850
	GACTTTGAGC	AGCTTCATGA	AGACATTGAG	CAAGCCTTCA	GGAACCTGGA	1900
5	GGATTAAAGT	GGTAGCTGCC	AGTGGTTCTC	TCGGTGCAGT	TGTCACATTT	1950
	GGCAAGCTCT	GTAGGGTTGC	CGAGTGGCAT	CGGTGCTAGA	CACCTGAGCA	2000
	TTCCTTTGCC	ACATAAAGAC	TAAAGCAGGT	GGAATTTTCA	TTGTAAAAAG	2050
	CTGGTTCCAT	TGGTGCTAAG	ATTATGTTGT	GCCCTTTTCT	GCTTCTCACA	2100
	TTCCAACAGA	GGAATTTACT	TCCAGTTTTT	TTCCATTTTC	CTCCTCATTT	2150
10	TAAGTGTCGG	TACAGAGGCA	ATAATCTGAT	AACCTCTGTAC	CGTCACTTAC	2200
	AAGCAGGGAG	AATTTGTAAAT	TATTACAAAT	CCCATTATCT	CTGTGCACCA	2250
	CAGCCTTGTA	AATTCATTTG	TCCCAGGACT	CCCTCTTGTT	TGTACGTGAG	2300
	ATTGCCGTCT	GTATGTATGT	ACACACCGTA	CTGCAGTATT	TGAAGTCAGT	2350
	CAGAAGGTGA	ATTACACCAC	TTACTCATTG	TGTCACGTAG	CAAGTGTGCA	2400
15	AACTGCCATC	CATTGTCCTA	TTTATTCACA	TAACTAGTTT	TCTTTGCATT	2450
	TCCAGTGTTG	CAAATTGTGT	TTAGAAAATT	ATGCCATCGA	GACTGGTCGA	2500
	ACCTCACATT	GTAATCAGT	ATTTACACAC	ACGTTTACTT	GCTACAGAAA	2550
	TGTAGAAAAA	ATAATTGTTG	TATATTGAAA	GTACAAGTGA	CAAAGTTGCA	2600
	TTTAAAATGG	TGAATGTATT	TTATATTTCT	TTTGTAGACA	CAAGAGTTAA	2650
20	TGCATTTTGC	TTAATGGAGA	TGTATGTAAA	CCTAAAATAG	CAGTTTGTGC	2700
	ACAAATTATG	TATATGTGAA	ATGGAGATGG	TTTCTAATTT	GCTGATTGAT	2750
	TGCCAGTATT	AATTTAAACA	ACTGTAGTTG	TGGGATGTAG	TGGGAAGATT	2800
	TTTTTTTTTCC	TATAAAATTG	GTGGATGTAT	GTGTCGGAGA	TTTTGATTGT	2850
	ATGTGTAAAA	TAGTGATCCC	AGTAACTGTA	AAGCTTTAGA	ATACAGTTAC	2900
25	TGACTGTATA	GTTGTACAGG	TGTTGTTACT	TTTAAAGAATT	TATTGACACA	2950
	AAGGTGAAAG	TCTATTATTG	TATTGTAATG	TTTAAAGCAT	TTAAGGTTTA	3000
	AAAATCCTAC	TTCTGTGTAT	AAATGTTACC	ATTCTTCATA	TAACATAACT	3050
	GTGTAGAAAT	ACAGTCAACT	TCATGTTTCAT	TAGCATTTCA	CTGTTGTCAC	3100
30	ATAAATTATG	CCCGGAAT				3118

## 2) INFORMATION FOR SEQ ID NO: 689

- 35 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1836 bases
  - (B) TYPE: Nucleic acid
  - (C) STRANDEDNESS: Double
  - (D) TOPOLOGY: Linear
- 40 (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
- (A) ORGANISM: *Plasmodium falciparum*
  - 45 (B) STRAIN: 3D7
  - (C) ACCESSION NUMBER: L08200

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 689

50	ATGACAAAAG	TTGCTGTTGA	AAAAGAGGAA	CCAGGAGTTG	TTTATAAGGT	50
	GGCTGGTTCA	TTAGTTATTG	CTGAGAATAT	GAGTGGAAC	CGTATGTACG	100
	AGTTAGCTAA	AGTAGGATGG	AATAAATTGG	TTGGAGAAAT	TATTAGATTA	150
	GAAGGGAATT	ATGCATATAT	ACAAGTTTAT	GAAGATACTT	CAGGTTTATC	200
	TGTAGGAGAC	CCTGTTATAA	AAACAGGAAA	TGCTTTATCA	GTCGAATTGG	250
55	GTCCTGGTAT	TTTAGATAAT	ATTTATGATG	GTATTCAAAG	ACCATTAGAA	300
	AGAATAGCAA	ATGTGTGTGG	TGATGTATAT	ATATATAAAG	GTATTGATAT	350
	GACATCTTTA	GATCATGATA	AACAATGGCA	ATTTTATGCT	GATAAGAAAT	400
	TAAAATTAAA	TGATATTGTT	ACTGGTGGAG	ATATCTTTGG	ATTTGTTGAT	450
	GAAAATAAAT	TATTTAAAGA	ACACAAAATT	ATGGCTCCAC	CTAATGCTAA	500
60	AGGGAGGCTT	ACATATATTG	CTCCAGATGG	ATCATATACT	TTAAAAGATA	550

	AAATATTTGA	ATTAGAATAT	CAAGGAAAAA	AATATACATA	TGGTTTATCT	600
	CATTTATGGC	CTGTTTCGTGA	TCCTAGACCT	GTTTTAGAAA	AGGTAACAGG	650
	GGATACTTTA	TTATTAACAG	GGCAAAGAGT	TTTAGATTCTG	TTATTTCCAA	700
	CAGTTCAAGG	AGGTAAGTGT	GCTATTCCTG	GTGCATTGG	TTGTGGAAAA	750
5	ACTTGTGTTT	CTCAGGCCTT	ATCAAAATAT	TCTAATAGTG	AAGTTATTAT	800
	ATATGTAGGA	TGTGGTGAAA	GAGGTAATGA	AATGGCTGAA	ATTTTATCCG	850
	ACTTTCCTGA	ATTAAGTACT	AAAGTAGATA	ATGAAGATGT	AGGTATTATG	900
	CAAAGAACGT	GTTTAGTTGC	TAATACTTCT	AACATGCCTG	TCGCTGCAAG	950
	AGAAGCTAGT	ATTTATACAG	GTATTACTTT	ATGTGAATAT	TTCCGTGATA	1000
10	TGGGTTATAA	TGCTACCATG	ATGGCTGATA	GTACAAGTAG	ATGGGCAGAA	1050
	GCCTTAAGAG	AAATTTTCAGG	ACGTTTAGCT	GAAATGCCTG	CAGATAGTGG	1100
	TTATCCAGCT	TATTTAGGTG	CTAGATTAGC	TTCTTTTAT	GAACGTGCAG	1150
	GAAAAGTCAA	ATGTATTGGT	TCTCCATCTC	GTATAGGATC	CATTACAATT	1200
	GTGGGTGCTG	TGTCTCCACC	AGGTGGTGAT	TTCTCTGACC	CTGTAACTAC	1250
15	AGCAACCATG	TCTATTGTTC	AAGCATTTTG	GGGGTTAGAT	AAAAAACTAG	1300
	CTCAAAGAAA	ACATTTCCCT	TCTGTTAATT	GGTCTACATC	CTTTTCAAAG	1350
	TATGTCAGAC	AATTAGAACA	ATACTTTGAT	AATTTTGATC	AAGATTTCTT	1400
	ATCTTTAAGA	CAAAAATTA	GTGATATTTT	ACAACAAGAA	AGTGACTTGA	1450
	ATGATATTGT	TCAACTAGTA	GGAAAGGATT	CATTATCAGA	AGACCAAAAA	1500
20	GTTGTTATGG	AAGTAGCCAA	AATTATTAGA	GAAGATTTTC	TTCAACAAAA	1550
	TGCATTTAGC	GATTATGATT	ATATGTGCCC	ATTACAAAAA	ACAGTTGGTA	1600
	TGATGAGAAT	TATTTGCCAC	TTTTATGCTC	AATGCTTAAG	AACATTACAA	1650
	GAATATGACT	CAAGAGAAAG	AAAAATTGGT	TGGGGATCTA	TATATAATAC	1700
	ATTAAGACCA	ACTATAAATA	AAATTACACA	TATGAAATTT	GAAAACCCAA	1750
25	AAAATTCAGA	TGAATATTTT	AAAAGGTATT	TTAAGGCACT	TGAAGAAGAA	1800
	ATAACAGTAG	GTTTAAGAAA	CTTGATGGAA	AAATGA		1836

## 30 2) INFORMATION FOR SEQ ID NO: 690

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3216 bases  
 (B) TYPE: Nucleic acid  
 35 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

## 40 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Saccharomyces cerevisiae*  
 (B) STRAIN: X2180-1A  
 (C) ACCESSION NUMBER: J05409

## 45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 690

	ATGGCTGGTG	CAATTGAAAA	CGCTCGTAAG	GAAATAAAAA	GAATCTCATT	50
	AGAAGACCAT	GCTGAATCTG	AATATGGTGC	CATCTATTCT	GTCTCTGGTC	100
	CGGTCGTCAT	TGCTGAAAAT	ATGATTGGTT	GTGCCATGTA	CGAATTGGTC	150
50	AAGGTCGGTC	ACGATAACCT	GGTGGGTGAA	GTCATTAGAA	TTGACGGTGA	200
	CAAGGCCACC	ATCCAAGTTT	ACGAAGAAAC	TGCAGGCCTT	ACGGTCGGTG	250
	ACCCTGTTTT	GAGAACAGGT	AAGCCTCTGT	CGGTAGAATT	GGGTCCTGGT	300
	CTGATGGAAA	CCATTTACGA	TGGTATTCAA	AGACCTTTGA	AAGCCATTAA	350
	GGAAGAATCG	CAATCGATT	ATATCCCAAG	AGGTATTGAC	ACTCCAGCTT	400
55	TGGATAGGAC	TATCAAGTGG	CAATTTACTC	CGGGAAAGTT	TCAAGTCGGC	450
	GATCATATTT	CCGGTGGTGA	TATTTACGGT	TCCGTTTTTG	AGAATTGCT	500
	AATTTCAAGC	CATAAGATTC	TTTTGCCACC	AAGATCAAGA	GGTACAATCA	550
	CTTGGATTGC	TCCAGCTGGT	GAGTACACTT	TGGATGAGAA	GATTTTGGAA	600
	GTTGAATTTG	ATGGCAAGAA	GTCTGATTTC	ACTCTTACC	ATACTTGCC	650
60	TGTTCTGTGT	CCAAGACCAG	TTACTGAAAA	GTTATCTGCT	GACTATCCTT	700

	TGTTAACAGG	TCAAAGAGTT	TTGGATGCTT	TGTTTCCTTG	TGTTCAAGGT	750
	GGTACGACAT	GTATTCCAGG	TGCTTTTGGT	TGTGGTAAGA	CCGTTATCTC	800
	TCAATCTTTG	TCCAAGTACT	CCAATTCTGA	CGCCATTATC	TATGTCGGGT	850
	GCTTTGCCAA	GGGTACCAAT	GTTTTAATGG	CGGATGGGTC	TATTGAATGT	900
5	ATTGAAAACA	TTGAGGTTGG	TAATAAGGTC	ATGGGTAAAG	ATGGCAGACC	950
	TCGTGAGGTA	ATTAAATTGC	CCAGAGGAAG	AGAACTATG	TACAGCGTCG	1000
	TGCAGAAAAG	TCAGCACAGA	GCCCACAAAA	GTGACTCAAG	TCGTGAAGTG	1050
	CCAGAATTAC	TCAAGTTTAC	GTGTAATGCG	ACCCATGAGT	TGGTTGTTAG	1100
	AACACCTCGT	AGTGTCGGCC	GTTTGTCTCG	TACCATTAAAG	GGTGTCAAT	1150
10	ATTTTGAAGT	TATTACTTTT	GAGATGGGCC	AAAAGAAAGC	CCCCGACGGT	1200
	AGAATTGTTG	AGCTTGTCAA	GGAAGTTTCA	AAGAGCTACC	CAATATCTGA	1250
	GGGGCCTGAG	AGAGCCAACG	AATTAGTAGA	ATCCTATAGA	AAGGCTTCAA	1300
	ATAAAGCTTA	TTTTGAGTGG	ACTATTGAGG	CCAGAGATCT	TTCTCTGTTG	1350
	GGTTCCCATG	TTCGTAAAGC	TACCTACCAG	ACTTACGCTC	CAATTCTTTA	1400
15	TGAGAATGAC	CACTTTTTTCG	ACTACATGCA	AAAAAGTAAG	TTTCATCTCA	1450
	CCATTGAAGG	TCCAAAAGTA	CTTGCTTATT	TACTTGTTTT	ATGGATTGGT	1500
	GATGGATTGT	CTGACAGGGC	AACTTTTTTCG	GTTGATTCCA	GAGATACTTC	1550
	TTTGATGGAA	CGTGTTACTG	AATATGCTGA	AAAGTTGAAT	TTGTGCGCCG	1600
	AGTATAAGGA	CAGAAAAGAA	CCACAAGTTG	CCAAAACGTG	TAATTTGTAC	1650
20	TCTAAAGTTG	TCAGAGGTAA	TGGTATTCGC	AATAATCTTA	ATACTGAGAA	1700
	TCCATTATGG	GACGCTATTG	TTGGCTTAGG	AFTCTTGAAG	GACGGTGTCA	1750
	AAAATATTCC	TTCTTTCTTG	TCTACGGACA	ATATCGGTAC	TCGTGAAACA	1800
	TTTCTTGCTG	GTCTAATTGA	TTCTGATGGC	TATGTTACTG	ATGAGCATGG	1850
	TATTAAAGCA	ACAATAAAGA	CAATTCATAC	TTCTGTCAGA	GATGGTTTGG	1900
25	TTTCCCTTGC	TCGTTCTTTA	GGCTTAGTAG	TCTCGGTAA	CGCAGAACCT	1950
	GCTAAGGTTG	ACATGAATGG	CACCAAACAT	AAAATTAGTT	ATGCTATTTA	2000
	TATGTCGTGT	GGAGATGTTT	TGCTTAACGT	TCTTTCGAAG	TGTGCCGGCT	2050
	CTAAAAAATT	CAGGCCGTGT	CCCCGCCGTG	CTTTTGCACG	TGAGTGCCGC	2100
	GGATTTTATT	TCGAGTTACA	AGAATTGAAG	GAAGACGATT	ATTATGGGAT	2150
30	TACTTTATCT	GATGATTCTG	ATCATCAGTT	TTTGCTTGCC	AACCAGGTTG	2200
	TCGTCCATAA	TTGCGGAGAA	AGAGGTAATG	AAATGGCAGA	AGTCTTGATG	2250
	GAATCCCAG	AGTTATATAC	TGAAATGAGC	GGTACTAAAG	AACCAATTAT	2300
	GAAGCGTACT	ACTTTGGTCG	CTAATACATC	TAACATGCCG	GTTGCAGCCA	2350
	GAGAAGCTTC	TATTTACACT	GGTATCACTC	TTGCAGAATA	CTTCAGAGAT	2400
35	CAAGGTAAAA	ATGTTTCTAT	GATTGCAGAC	TCTTCTTCAA	GATGGGCTGA	2450
	AGCTTTGAGA	GAAATTTCTG	GTCGTTTGGG	TGAGATGCCT	GCTGATCAAG	2500
	GTTTCCCAGC	TTATTTGGGT	GCTAAGTTGG	CCTCCTTTTA	CGAAAGAGCC	2550
	GGTAAAGCTG	TTGCTTTAGG	TTCCCCAGAT	CGTACTGGTT	CCGTTTCCAT	2600
	CGTTGCTGCC	GTTTCGCCAG	CCGGTGGTGA	TTTCTCAGAT	CCTGTTACTA	2650
40	CTGCTACATT	GGGTATCACT	CAAGTCTTTT	GGGGTTTAGA	CAAGAAATTG	2700
	GCTCAAAGAA	AGCATTTCCC	ATCTATCAAC	ACATCTGTTT	CTTACTCCAA	2750
	ATACACTAAT	GTCTTGAACA	AGTTTTATGA	TTCCAATTAC	CCTGAATTTT	2800
	CTGTTTTAAG	AGATCGTATG	AAGGAAATTC	TATCAAACGC	TGAAGAATTA	2850
	GAACAAGTTG	TTCAATTAGT	TGGTAAATCG	GCCTTGCTGT	ATAGTGATAA	2900
45	GATTACTTTG	GATGTTGCCA	CTTTAATCAA	GGAAGATTTT	TTGCAACAAA	2950
	ATGGTTACTC	CACTTATGAT	GCTTTCTGTC	CAATTTGGAA	GACATTTGAT	3000
	ATGATGAGAG	CCTTCATCTC	GTATCATGAC	GAAGCTCAAA	AAGCTGTTGC	3050
	TAATGGTGCC	AACTGGTCAA	AACTAGCTGA	CTCTACTGGT	GACGTTAAGC	3100
	ATGCCGTTTC	TTCATCTAAA	TTTTTTTGAAC	CAAGCAGGGG	TGAAAAGGAA	3150
50	GTCCATGGCG	AATTCGAAAA	ATTGTTGAGC	ACTATGCAAG	AAAGATTTGC	3200
	TGAATCTACC	GATTAA				3216

55 2) INFORMATION FOR SEQ ID NO: 691

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1860 bases

(B) TYPE: Nucleic acid

60 (C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

5 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Schizosaccharomyces pombe*

(B) STRAIN: 972 h-

(C) ACCESSION NUMBER: S47814

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 691

	ATGGCGGGAG	GAATTGAACT	GGCCAAGAAG	GCTATCAGGA	GCCTCAAAAA	50
	TTACGACGAG	CATGAAAACC	GATATGGATC	TATTTTCAGC	GTTTCTGGTC	100
	CTGTCGTTGT	TGCAGCCAAT	ATGCTTGGAT	GTTTCGATGT	CGAACTCGTT	150
15	CGCGTTGGTC	ATGAAGAACT	AGTTGGTGAA	GTAATTCGTA	TCCATCAAGA	200
	TAAATGTACT	ATTCAAGTAT	ACGAAGAGAC	GTCCGGTCTC	ACTGTTGGTG	250
	ATCCTGTCCA	ACGCACTGGA	AAGCCATTAT	CTGTTGAATT	AGGTCCTGGT	300
	TTAGCTGAGA	CTATTTATGA	TGGTATCCAA	CGTCCGTTAA	AGCAAATTTT	350
	CGACAAATCT	CAAAGTATTT	ATATTCCTAG	AGGTATTAAT	ACAGAATCAC	400
20	TTAATCGTGA	GCATAAGTGG	GATTTACAC	CAAATAAGGA	TTTACGCATT	450
	GGCGATCATG	TATCCGGTGG	TGATGTTTTC	GGTCTGTAT	TTGAAAACCTC	500
	TCTTTTCAAT	GATCATAAAA	TTATGTTACC	CCCTAGAGCC	CGTGGTACCG	550
	TCACATATAT	TGCTGAAGCT	GGATCATACC	ATGTTGATGA	AAAACCTTCTT	600
	GAAGTCGAGT	TTAATGGCAA	GAAACATTCT	TTTAGTATGT	TGCATACTTG	650
25	GCCTGTCCGT	GCTGCTCGTC	CAGTTGCGGA	CAACTTAACT	GCTAATCAAC	700
	CTTTATTGAC	TGGTCAACGT	GTTTTGGATG	CGTTATACCC	CTGTGTTCAA	750
	GGTGGCACTA	CTGCTATCCC	CGGTGCCTTT	GGTTGTGGTA	AAACAGTTAT	800
	TTCAACAATCT	CTTCTAAGT	ACTCTAATC	TGATTTGATT	GTTTACGTCG	850
	GTTGTGGTGA	ACGTGGAAAC	GAAATGGCAG	AAGTGTTAAT	GGATTTCCCA	900
30	GAACATAACAA	TTGATATTAA	TGGTAAACCA	GAGCCCATTA	TGAAGCGTAC	950
	TACATTGGTA	GCCAACACTT	CTAACATGCC	TGTCGCTGCT	CGTGAAGCTT	1000
	CCATTTATAC	CGGTATTACA	CTTGCTGAAT	ATTATCGTGA	TCAAGGTAAG	1050
	AACGTTTCAA	TGATGGCTGA	TTCTACATCT	CGTTGGGCTG	AAGCTTTGCG	1100
	TGAAATTTCT	GGTCGTTTGG	CTGAGATGCC	TGCCGATTCT	GGTTATCCCG	1150
35	CTTATTTGGG	TGCCAAATTG	GCTTCTTTTT	ACGAACGTGC	TGGTCGTGCT	1200
	CGTTGCTTGG	GAAGTCCTGA	CCGTGAAGGA	ACAGTTTCAA	TTGTTGGAGC	1250
	TGTTTCTCCT	CCGGGTGGTG	ATTTTCTTGA	TCCTGTTACT	AGTGCAACCT	1300
	TGGGAATTGT	TCAAGTCTTC	TGGGGTTTGG	ACAAGAAATT	GGCCCAACGT	1350
	AAACACTTTC	CCTCAATCAA	CACCTCTCTT	TCCTATTCTA	AATACATCAA	1400
40	TGCTTTGCAA	CCTTGGTATG	AGGAAAGAGT	TCCAGGCTTT	AATACTCTTC	1450
	GTGATCAAA	CAAACAGATC	ATTCAACAAG	AAGATTCCAT	GTTGGAAATT	1500
	ATTCAGTTGG	TTGGTAAGTC	GGCTCTTTCT	GAAACGGATA	AAGTTACTTT	1550
	GGACATAGCC	GGTATTATTA	AGAATGACTT	CTTACAACAA	AACGGTTATT	1600
	CTGATTACGA	TCGCTGTTGC	CCTCTTTACA	AGACTTATCA	TATGATGCGA	1650
45	AACATGATTG	CTTACTACAC	AAAGGCTAAA	AGTGCCGTTG	AAACTGGTAG	1700
	CGTTCCTTGG	TCAAAGATTA	AAGAAAGTAC	TTCAGATATC	TTTTATGAGT	1750
	TAACCTCGAT	GAAATTCGAA	AACCCTAATG	AAGGCGAGAA	GGAAATAGTC	1800
	GAACACTATG	AAACTCTGCA	CAAGAAGATT	GAGGACAAGT	TTCACACTCT	1850
	GACTGAGTAA					1860

50

2) INFORMATION FOR SEQ ID NO: 692

55 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1833 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

60

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 5 (A) ORGANISM: *Trypanosoma congolense*  
 (B) STRAIN: IL3000  
 (C) ACCESSION NUMBER: Z25814

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 692

```

10 ATGACGAGCG ATAAAAACCC TTACAAAACA GAGCAGCGCA TGGGGGCCGT      50
   GAAGGCCGTC TCCGGGCCAG TTGTCATTGC TGAAAACATG GGCGGTAGCG      100
   CTATGTATGA GCTTGTGCAG GTAGGTTTCT TCCGGTTAGT GGGCGAGATC      150
   ATTCGTCTAG AGGGCGATAC CGCCACTATT CAGGTCTATG AGGAAACAGG      200
   TGGCCTCACT GTCGGAGACC CGGTGTACTG TACGGGTAAG CCTCTTTTCG      250
15 TTGAGCTTGG ACCTGGAATC ATGTCTGAAA TATTTGACGG TATCCAGCGG      300
   CCTCTTGACA CCATCTACCG CATGGTGGAA AACGTGTTTA TCCCCAGGGG      350
   CGTTCAGGTG AAGTCACTCA ATGACCAGAA ACAGTGGGAC TTAAAGCCAT      400
   GCCTGAAGGT TGGAGATCTT GTGTCTGGTG GTGATATCAT TGGCTCAGTG      450
   GTGGAGAACT CTCTCATGTA CAATCACAGC ATTATGATTC CGCCCAATGT      500
20 GCGGGGCCGT GTTACTTCCA TTGTTCTTTC AGGAAATTAC ACCCTCCAAG      550
   ATGACATTAT TGAATTGGAA TATAATGGGA CAGTGAAATC ACTAAACTT      600
   ATGCATCGCT GGCCAGTACG GACCCCGCGT CCTGTGGCGT CAAAAGAATC      650
   CGGCAATCAT CCGCTTCTCA CCGGACAGCG TGTGCTCGAT GCTCTCTTTC      700
   CATCCGTCCA GGGTGGAAAC TGCGCCATCC CTGGCGCGTT TGGATGCGGA      750
25 AAGACGGTTA TCAGTCAGGC TCTTTCGAAG TTCTCCAACA GCGACGCTGT      800
   TATCTATGTC GGCTGCGGCG AGCGTGGGAA TGAGATGGCA GAGGTGCTCA      850
   TGGACTTCCC CACACTCACC ACCGTTATTG ATGGTCGTGA GGAGTCCATC      900
   ATGAAGCGTA CCTGCCTGGT GCCAAACACC TCAAAATATG CTGTCGCTGC      950
   TCGTGAGGCG TCTATTTACA CTGGCATCAC TTTAGCTGAG TATTATCGTG      1000
30 ATATGGGCAA GCACATTGCT ATGATGGCCG ACTCTACCTC TCGATGGGCT      1050
   GAGGCTCTCC GTGAGATCTC TGGGCGTCTC GCTGAAATGC CCGCTGATGG      1100
   TGGTTACCCT GCGTACCTCA GTGCGCGTCT TGCTTCCTTC TACGAGCGTG      1150
   CGGGGCGCGT GACATGCATC GGTGGGCCAA AACGCGAGGG CTCAGTAACC      1200
   ATCGTTGGTG CCGTTTCTCC TCCTGGAGGT GACTTTTCTG ACCCAGTGAC      1250
35 GTCCGCTACG CTTGGTATTG TGCAAGTCTT TTGGGGTCTT GAGAAGCGTC      1300
   TTGCGCAACG TAAACACTTT CCTTCTGTTA ATTGGCTCAT TTCCTATTCA      1350
   AAATACCTTA ATGCTTTGGA GCCCTTCTTC AACACGCTTG ACCCTGACTA      1400
   CATGCGCCTG CGGTCAGTTG CTGCGGAGAT CCTTCAGCGT GAGGAAGAGT      1450
   TGCAAGAAAT TGTTCAACTT GTCGGTAAGG ACTCACTTTC GGAGTCTGAC      1500
40 AAAATTATTC TAGAAACGGC TAAGGTTATT CGTGAAGAGT TTCTCCAGCA      1550
   GAATGCCTTT ACGCCGTACG ACAAGTATTG CCCGCCGTAC AAGACCTGCT      1600
   GGATGCTACG TAACATTGTC GCGTTCTACG AGGAGAGCCA GCGCGTTGTA      1650
   GCTGAGTCCG CTGGGGAAC TTAAGATTAC TGGAAGTTC TTCGTGAAAT      1700
   GATTCCTCAT ATTTACACGG GTTTAACTGA GATGAAGTTC CGTGATCCTC      1750
45 AGGAGGGTGA GGAGGCCAAC GTAGAATTCT ACAGAAAACA AAATGAGGAA      1800
   ATTGTCAGCG CATTCGCCTC GCTGCTGCAA TAA                      1833

```

50 2) INFORMATION FOR SEQ ID NO: 693

(i) SEQUENCE CHARACTERISTICS:

- 55 (A) LENGTH: 1758 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

60 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Thermus thermophilus*  
 (B) STRAIN: HB8  
 (C) ACCESSION NUMBER: D63799

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 693

	ATGATCCAAG	GGGTGATCCA	GAAGATCGCG	GGCCCGGCGG	TGATCGCCAA	50
	GGGCATGCTC	GGGGCCCGCA	TGTACGACAT	CTGCAAGGTG	GGCGAAGAGG	100
	GCCTCGTG	GGG	CGAGATCATC	CGCCTGGACG	GGGACACGGC	150
10	GTCTACGAGG	ACACCTCGGG	CCTAAAGGTG	GGGGAGCCCG	TGGTCTCCAC	200
	GGGCCTTCCC	TTGGCGGTGG	AGCTCGGCCC	CGGGATGCTG	AACGGCATCT	250
	ACGACGGCAT	CCAGCGCCCC	CTGGAGCGCA	TCCGGGAGAA	GACGGGGATC	300
	TACATCACCC	GGGGCGTGGT	GGTCCACGCC	CTGGACCGGG	AGAAGAAGTG	350
	GGCCTGGACG	CCCATGGTCA	AGCCCCGGGA	CGAGGTGCGG	GGGGGTATGG	400
15	TCCTGGGCAC	GGTGCCCGAG	TTCGGCTTCA	CCCACAAGAT	CCTGGTACCC	450
	CCGGACGTGC	GGGGCCGGGT	CAAGGAGGTG	AAGCCCGCCG	GGGAGTACAC	500
	CGTGAGGAG	CCGGTGGTGG	TCCTCGAGGA	CGGCACCGAG	CTCAAGATGT	550
	ACCACACCTG	GCCCGTTCGC	CGGGCGAGGC	CCGTGCAAAG	GAAGCTTGAC	600
	CCCAACACCC	CCTTCCTCAC	GGGGATGCGC	ATCCTGACG	TCCTCTTCCC	650
20	CGTGGCCATG	GGGGGCACCG	CCGCCATCCC	TGGGCCCTTC	GGCAGCGGCA	700
	AGACCGTGAC	CCAGCAGTCC	CTGGCCAAAGT	GGTCCAACGC	CGACGTGGTG	750
	GTCTACGTGG	GCTGCGGGGA	GCGGGGGAAC	GAGATGACCG	ACGTGCTCGT	800
	GGAGTTCCCC	GAGCTCACCG	ACCCCAAGAC	GGGTGGGCCC	TTGATGCACC	850
	GCACCGTCCT	CATCGCCAAC	ACCTCCAACA	TGCCCCGTGGC	CGCCCCGCGAG	900
25	GCCAGCATCT	ACGTGGGCGT	GACCATCGCC	GAGTACTTCC	GCGACCAGGG	950
	TTTCTCCGTG	GCCCTCATGG	CCGACTCCAC	GAGCCGCTGG	GCCGAGGCTT	1000
	TGCGCGAGAT	CTCTAGCCGC	CTCGAGGAGA	TGCCCCGCCGA	GGAGGGCTAC	1050
	CCGCCCTACC	TCGCCGCCAG	GCTCGCCGCC	TTCTACGAGC	GGGCGGGCAA	1100
	GGTCATCACC	CTGGGCGGCG	AGGAGGGGGC	GGTGACCATC	GTGGGGGCGG	1150
30	TCTCCCCGCC	GGGCGGCGAC	ATGTCCGAGC	CCGTGACCCA	GTCCACCTTG	1200
	AGGATCGTGG	GGGCCTTCTG	GCGGCTTGAC	GCCTCCCTGG	CCTTCCGCCG	1250
	CCACTTCCCC	GCCATCAACT	GGAACGGCTC	CTACAGCCTC	TTCACCTCCG	1300
	CCCTTGACCC	CTGGTACCGG	GAGAACGTGG	CCGAGGACTA	CCCCGAGCTC	1350
	CGCGACGCCA	TCTCCGAGCT	TTTGACGCGG	GAGGCGGGCC	TCCAGGAGAT	1400
35	CGTCCAGCTC	GTGGGGCCGG	ACGCCCTCCA	GGACGCCGAG	CGCCTCGTCA	1450
	TTGAGGTGGG	CCGGATCATC	CGCGAGGACT	TCCTGCAGCA	GAACGCCTAC	1500
	CACGAGGTGG	ACGCCTACTG	CTCCATGAAG	AAGGCCTACG	GGATCATGAA	1550
	GATGATCCTC	GCCTTCTACA	AGGAGGCGGA	GGCGGCCATC	AAGCGGGGGG	1600
	TTTCCATAGA	CGAGATCCTG	CAGCTCCCCG	TTCTGGAGCG	CATCGGCCGC	1650
40	GCCCCGTACG	TGAGCGAGGA	GGAGTTCCCC	GCCTACTTTG	AGGAGGCCAT	1700
	GAAGGAGATC	CAGGGGGCCT	TCAAGGCTGG	CCTAAAGGGG	GAGAGATGGA	1750
	CCTTCTGA					1758

45

2) INFORMATION FOR SEQ ID NO: 694

(i) SEQUENCE CHARACTERISTICS:

50 (A) LENGTH: 21 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Single  
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 694

CGGCGCIATC YTS GTT GTTG C

60

21

## 2) INFORMATION FOR SEQ ID NO: 695

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: DNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 695

GTTTCACGTG ATGACGTACA

20

## 2) INFORMATION FOR SEQ ID NO: 696

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: DNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 696

ATIGGICAYR TIGAYCAYGG IAARAC

26

## 2) INFORMATION FOR SEQ ID NO: 697

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: DNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 697

CCIACIGTIC KICCRCCYTC RCG

23

## 2) INFORMATION FOR SEQ ID NO: 698

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1185 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

398

(A) ORGANISM: *Escherichia coli*

(C) ACCESSION NUMBER: extracted from J01690

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 698

```

5      GTGTCTAAAG AAAAATTGTA ACGTACAAAA CCGCACGTTA ACGTTGGTAC      50
      TATCGGCCAC GTTGACCACG GTAAAACTAC TCTGACCGCT GCAATCACCA      100
      CCGTACTGGC TAAAACCTAC GGCGGTGCTG CTCGTGCATT CGACCAGATC      150
      GATAACGCGC CGGAAGAAAA AGCTCGTGGT ATCACCATCA ACACTTCTCA      200
10     CGTTGAATAC GACACCCCGA CCCGTCACTA CGCACACGTA GACTGCCCGG      250
      GGCACGCCGA CTATGTTAAA AACATGATCA CCGGTGCTGC TCAGATGGAC      300
      GGCGCGATCC TGGTAGTTGC TGCGACTGAC GGCCCGATGC CGCAGACTCG      350
      TGAGCACATC CTGCTGGGTC GTCAGGTAGG CGTTCCGTAC ATCATCGTGT      400
      TCCTGAACAA ATGCGACATG GTTGATGACG AAGAGCTGCT GGAAGTGGTT      450
15     GAAATGGAAG TTCGTGAACT TCTGTCTCAG TACGACTTCC CGGGCGACGA      500
      CACTCCGATC GTTCGTGGTT CTGCTCTGAA AGCGCTGGAA GGCGACGCAG      550
      AGTGGGAAGC GAAAATCCTG GAACTGGCTG GCTTCCTGGA TTCTTATATT      600
      CCGGAACCAG AGCGTGCGAT TGACAAGCCG TTCCTGCTGC CGATCGAAGA      650
      CGTATTCTCC ATCTCCGGTC GTGGTACCGT TGTTACCGGT CGTGTAAGAAC      700
20     GCGGTATCAT CAAAGTTGGT GAAGAAGTTG AAATCGTTGG TATCAAAGAG      750
      ACTCAGAAGT CTACCTGTAC TGGCGTTGAA ATGTTCCGCA AACTGCTGGA      800
      CGAAGGCCGT GCTGGTGAGA ACGTAGGTGT TCTGCTGCGT GGTATCAAAC      850
      GTGAAGAAAT CGAACGTGGT CAGGTACTGG CTAAGCCGGG CACCATCAAG      900
      CCGCACACCA AGTTCGAATC TGAAGTGATC ATTCTGTCCA AAGATGAAGG      950
25     CGGCCGTCAT ACTCCGTTCT TCAAAGGCTA CCGTCCGCAG TTCTACTTCC      1000
      GTACTACTGA CGTGACTGGT ACCATCGAAC TGCCGGAAGG CGTAGAGATG      1050
      GTAATGCCGG GCGACAACAT CAAAATGGTT GTTACCCTGA TCCACCCGAT      1100
      CGCGATGGAC GACGGTCTGC GTTTCGCAAT CCGTGAAGGC GGCCGTACCG      1150
      TTGGCGCGGG CGTTGTTGCT AAAGTTCTGG GCTAA      1185
30

```

## 2) INFORMATION FOR SEQ ID NO: 699

## 35 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 26 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

40

## (ii) MOLECULE TYPE: DNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 699

45 GTIACIGGYT CYTYRARRTT ICCICC

26

## 2) INFORMATION FOR SEQ ID NO: 700

50

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 24 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

55

## (ii) MOLECULE TYPE: DNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 700

60



TIRTIGAYGT CGARTTCCCT CARG

24

## 5 2) INFORMATION FOR SEQ ID NO: 701

## (i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 21 bases  
(B) TYPE: Nucleic acid  
(C) STRANDEDNESS: Single  
(D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: DNA

## 15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 701

GTGTTACGA TCATCGATGC G

21

## 20 2) INFORMATION FOR SEQ ID NO: 702

## (i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 20 bases  
(B) TYPE: Nucleic acid  
(C) STRANDEDNESS: Single  
(D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: DNA

## 30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 702

CTCTCGATAT CCGCGAAGCG

20

## 35 2) INFORMATION FOR SEQ ID NO: 703

## (i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 20 bases  
(B) TYPE: Nucleic acid  
(C) STRANDEDNESS: Single  
(D) TOPOLOGY: Linear

## 45 (ii) MOLECULE TYPE: DNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 703

TATGGAAATT CGAAACATCT

20

## 50 2) INFORMATION FOR SEQ ID NO: 704

## (i) SEQUENCE CHARACTERISTICS:

- 55 (A) LENGTH: 20 bases  
(B) TYPE: Nucleic acid  
(C) STRANDEDNESS: Single  
(D) TOPOLOGY: Linear

60

400

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 704

5 AGTGCTCCAA TTAATGTTGG

20

2) INFORMATION FOR SEQ ID NO: 705

10

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

15

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 705

20

GTACAGTTCC AATACCTGAA

20

2) INFORMATION FOR SEQ ID NO: 706

25

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 bases

(B) TYPE: Nucleic acid

30

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 706

35

TGAAATCTTC ACATCCAACA

20

2) INFORMATION FOR SEQ ID NO: 707

40

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 25 bases

45

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 707

TWACCATTTC AGTACCTTCT GGTA

25

2) INFORMATION FOR SEQ ID NO: 708

55

(i) SEQUENCE CHARACTERISTICS:

60

(A) LENGTH: 26 bases

401

- (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Single  
 (D) TOPOLOGY: Linear

5 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 708

TCRTCCATIC CIARIATIGC IATIAT

26

2) INFORMATION FOR SEQ ID NO: 709

15 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1656 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

20

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Borrelia burgdorferi*  
 25 (C) ACCESSION NUMBER: extracted from AE001122

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 709

	ATGAATGAAG	TTTTATTTGT	AAAGACTGCT	GGTAGGAATT	TAAAAGCAGA	50
30	AGTAATTCGT	ATTAGGGGCA	ATGAAGTTGA	TGCACAGGTT	TTTGAATTGA	100
	CAAAAGGGAT	ATCTGTTGGA	GACCTAGTTG	AATTTACAGA	CAAACCTTTA	150
	ACAGTTGAAC	TCGGACCAGG	GCTTTTAACT	CAAGTATATG	ATGGGCTTCA	200
	AAATCCTTTG	CCTGAATTGG	CTATTCAATG	TGGATTTTTT	TTAGAAAGGG	250
	GAGTATATTT	AAGGCCCTTG	AATAAGATA	AAAAGTGGAA	TTTTAAAAAA	300
35	ACCTCCAAAG	TTGGAGATAT	CGTTATTGCA	GGAGATTTTT	TAGGTTTTGT	350
	AATTGAGGGA	ACTGTTCCAC	ATCAAATAAT	GATTCCATTT	TATAAAAGGG	400
	ATTCTTATAA	AATTGTGGAG	ATTGTAAGTG	ATGGCGACTA	TTCGATTGAT	450
	GAGCAAATTG	CTGTAATTGA	AGATGATTCT	GGTATGAGGC	ATAATATTAC	500
	AATGTCTTTT	CATTGGCCTG	TTAAAGTTCC	TATTACTAAT	TATAAGGAAC	550
40	GCCTTATTCC	TAGTGAACCT	ATGTTGACTC	AAACTAGAAT	TATAGATACA	600
	TTTTTCCCAG	TTGCCAAAGG	TGGAACTTTT	TGCATTCCGG	GTCCTTTTGG	650
	AGCAGGAAAA	ACGGTCTTTC	AGCAGGTTAC	AAGTCGAAAT	GCTGATGTTG	700
	ATGTAGTGAT	TATTGCAGCT	TGTGGTGAGC	GAGCAGGAGA	AGTGGTAGAA	750
	ACTCTTAAAG	AATTTCCCGA	ATTAATGGAT	CCAAAAACCG	GCAATCTTTT	800
45	AATGGACAGG	ACTTGTATTA	TTTGTAATAC	ATCTTCAATG	CCAGTTGCAG	850
	CTAGAGAAGC	TTCTGTTTAT	ACTGCTATTA	CTATTGGTGA	GTATTACAGG	900
	CAAATGGGCC	TTGATATTCT	TCTTTTGGCA	GATTCAACTT	CAAGATGGGC	950
	TCAAGCAATG	AGAGAAATGT	CTGGACGCCT	TGAGGAAATT	CCTGGCGAGG	1000
	AGGCTTTTCC	GGCATATCTT	GAGTCTGTTA	TTGCTTCCTT	TTATGAAAGG	1050
50	GCAGGTATTG	TAGTTCCTTA	TAATGGGGAT	ATTGGATCTG	TAACAGTTGG	1100
	TGGCTCTGTA	AGTCCTGCTG	GTGGTAATTT	TGAAGAGCCA	GTTACTCAAG	1150
	CAACTTTAAA	AGTTGTAGGA	GCATTTACAG	GGCTTACAAG	AGAAAGGTCT	1200
	GATGCTAGGA	AATTTCCAGC	TATTAGTCCT	CTTGAATCTT	GGAGTAAATA	1250
	TAAAGGCGTT	ATTGATCAAA	AAAAGACTGA	ATATGCAAGA	TCTTTTTTGG	1300
55	TGAAAGGTAA	TGAAATTAAT	CAAATGATGA	AAGTTGTTGG	AGAAGAAGGC	1350
	ATAAGTAACG	ATGATTTTTT	AATTTATTTA	AAATCCGAGC	TACTTGATTC	1400
	GTGCTATTTG	CAGCAAAATT	CATTTGATTG	TATTGATGCT	GCTGTTAGTT	1450
	CAGAGCGTCA	AAATTATATG	TTTGATATAG	TTTATAACAT	TCTTAAACT	1500
	AACCTTTGAGT	TTTCTGATAA	ACTTCAAGCA	AGAGATTTTA	TAAATGAGTT	1550
60	AAGGCAAAAT	CTTTTAGACA	TGAATCTTTC	TTCTTTTAAG	GATCATAAGT	1600

TTAATAAATT GGAGCATGCT TTGGGTGAAT TGATAAATTT TAAAAAGGTA 1650  
ATTTAG 1656

5

## 2) INFORMATION FOR SEQ ID NO: 710

## (i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 1818 bases  
(B) TYPE: Nucleic acid  
(C) STRANDEDNESS: Double  
(D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

15

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Treponema pallidum*  
(B) STRAIN: Nichols  
(C) ACCESSION NUMBER: extracted from AE000520

20

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 710

GTGATCAAAG ACGATGTGGT TACAGGCCGT GTAGTGAGGG TGTCTGGTCC 50  
CATTGTGTAT GCCGAGGGCC TCTCTGCGTG CAGCGTATAC GATGTTGTCTG 100  
25 ACGTAGGGGA AGCATCGCTC ATCGGAGAAA TTATCCGGTT GGATGAGAGC 150  
AAGGCGGTCTG TGCAAGTATA CGAGGATGAC ACAGGTATGC GAGTCGGGGA 200  
GAAGGTGACA AGCTTGCGTC GACCACTCTC AGTCCGCTTA GGGCCTGGAT 250  
TAATCGGCAC CATTTATGAC GGTATTACAG GCCCACTTGA GCGCCTCTTC 300  
CAAGAAGACG GCGCCTTCTT GCGTCCTGGT GCGCGTTCAC AACCGCTTGA 350  
30 TGGCTCCGTA CGCTGGGATT TTCGTCCTCA TTGTAACGAG CGCGGTGAGG 400  
CCCTGTGCGC GGGGATTCCG ATTGCACCTG GGTCAGTGTT AGGGACCGTG 450  
CAGGAGACTC CTTCTGTTGT GCACACTATC ATGGTTCCTC CTGACATCCG 500  
GGGGAGCGTG CTATCTTCGT TCAAGGGCGC AGGTGCTTAC ACAATAGATG 550  
AAGAAATTGG ACGCACTGAT CTTGGTGAGC CGCTTTTTCT ATCCCAGTAC 600  
35 TGGCCAGTGC GTCGTGCGCG TCCTTTTCAGC AAAAACTTG CAGTGTGTGA 650  
GCCACTAGTT ACTGGACAGC GGGCGATTGA TGTTTTCTTC CCCCTATCAA 700  
AGGGAGGAAC GGCGGCTATT CCAGGGGGAT TTGGAAGTGG GAAGACAATG 750  
ACGCAGCATG CCGTTGCCAA GTGGTGTGAT GCAGATATTA TCGTGTACAT 800  
CGGCTGCGGA GAGCGGGGCA ACGAGATGAC AGACGTGCTC TCTGAATTTT 850  
40 CCAAACATCAT CGATCCGCGC ACAGGACGCT CTCTTATGGA GCGGACGATT 900  
TTGATCGCAA ATACGTCAA TATGCCTGTG TCCGCACGCG AGGTGTCGCT 950  
GTATTACAGG ATTACCCTTG CGGAATACTA CCGTGATATG GGTATGCATG 1000  
TGGCCATCAT GGCTGATTCT ACCAGCCGCT GGGCGGAGGC GCTGCGTGAA 1050  
TTGTCTGGGC GCATGGAAGA AATGCCCTGC GAGGAGGGAT TCCCTGCGTA 1100  
45 CCTTCCGACG CGTCTTGACG AATTTTATGA GCGCGCAGGA CGCGTGGA 1150  
CCTGTGTGCG GCGCGAGGGC TCTGTGAGCA TCATTGGTGC TGTTTCTCCC 1200  
CTGGGTGGAG ATTTCTCTGA GCCGGTGACG CAGCACACAA AGCGCTTCAT 1250  
CCGTTGCTTT TGGGCCCTTG ATCGTGAAC TGCACACGCG CGTCATTACC 1300  
CTGCCATTGG GTGGATAGAT TCATACTCTG AATATGCGCA GGAAGTAAGT 1350  
50 GCATGGTGGA GTAAGTATGA CCCGCGCGCA GGCGCGTTGC GCGCCGACG 1400  
CTTGGAATTT CTGAGAAAGG AACAGCGGTT ACAGCAAATT GTCAGGCTTG 1450  
TCGGTCCTGA TGCCTGCTC GGAGAAGATC GTCTGGTGCT AATGGTGTGT 1500  
GAAATGATCA AAGGTGGCTT TCTGCAGCAG AACGCTTTTG ATCCGACGGA 1550  
TGTGTTCTCC TGTCCCGAAA AGCAGGTGCA GATCTTGCGT ACCATAGTGG 1600  
55 ATTTTCACGA ACGTGCCGTG GTGCTGCTGC GTGCAGGTAT TTCGCTTTCT 1650  
GCGCTGTCCC AGCTTTCGTG CCGGGAGCTC ATCGTACGTA TGAAAACCTAC 1700  
GTACGGGAAT GAGGATGTAC ACAAGATGCA GAAAGTGTAC GACACGATGT 1750  
GCACTGAGTT TGACCAACTG AGTGTGTGTG CTGCCGCGCG CACACAAGGG 1800  
GGGGAGAAAG TCGAATGA 1818

60

## 2) INFORMATION FOR SEQ ID NO: 711

- 5 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 1779 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear
- 10 (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: *Chlamydia trachomatis*  
 15 (B) STRAIN: MoPn

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 711

20	CAGGGCTATG	TCGTAGAAGC	TTACGGAAAT	TTATTGCGGG	TGCATTTTGA	50
	TGGGCATGTG	CGTCAAGGAG	AAGTGGCCTA	TGTCAGCGTG	GATGATACTT	100
	GGTTGAAAGC	GGAAATTATA	GAAGTTGTGG	GAGATGAGGT	TAAAGTCCAA	150
	GTTTTTTGAGG	AAACTCAAGG	AATTTCTCGA	GGCGCTTTGG	TAACCTTTTTC	200
	CGGGCATTTA	TTAGAAGCGG	AACTTGGGCC	CGGTCTATTG	CAAGGTATTT	250
	TTGACGGACT	TCAGAATCGC	TTAGAGGTAT	TGGCAGATAC	AAGCTTGTTT	300
25	TTGAAAAGAG	GGGAGTATGT	TAATGCCATT	TGTCGGGAAA	CTGTATGGGC	350
	TTATACGCAA	AAGGCTTCTG	TCGGGGATGT	TCTATCTCGG	GGAGATGTGC	400
	TTGGTACAGT	AAAGGAAGGG	CGGTTTGATC	ATAAAATCAT	GGTTCCTTTC	450
	TCTTGTTTTG	AGGAAGTGAC	TATCACTTGG	GTCATTTCTT	CAGGAGATTA	500
	CACTGTTGAT	ACCGTTATTG	CTAAAGGACG	TACTGCTTCA	GGAGCCGAGC	550
30	TTGAATTTAC	AATGGTTCAG	AAATGGCCCA	TTAAACAGGC	TTTTTTAGAA	600
	GGGAAAAGG	TACCGTCTCA	TGAAATTATG	GATGTTGGGT	TACGAGTATT	650
	AGATACTCAG	ATCCCCGTCT	TAAAGGGAGG	AACTTTTTGT	ACTCCAGGGC	700
	CTTTTGGTGC	AGGAAAGACC	GTTTTACAGC	ACCATTTATC	TAAGTATGCA	750
	GCTGTAGATA	TCGTAGTTTT	GTGTGCTTGT	GGAGAGCGAG	CTGGAGAGGT	800
35	TGTAGAAATT	CTTCAGGAGT	TCCCGCATT	GACAGATCCT	CATACGGGGC	850
	AGTCTTTGAT	GCATAGGACC	TGTATTATTT	GTAATACATC	TTCCATGCCT	900
	GTAGCAGCTA	GAGAGTCCTC	CATTTATTTG	GGTATTACTA	TAGCAGAATA	950
	TTACCGTCAA	ATGGGGTTGC	ATGTTTTGTT	ATTGGCTGAC	TCGACATCTA	1000
	GATGGGCTCA	AGCTTTAAGG	GAAATTTCAG	GGCGATTAGA	AGAAATCCCT	1050
40	GGAGAAGAAG	CTTTCCCAGC	CTATTTGGCG	TCTCGAATAG	CAGCTTTTTTA	1100
	TGAGCGAGGC	GGGGCTGTGA	AAATGAAAGA	TGGATCGGAA	GGCTCCTTGA	1150
	CTATCTGTGG	AGCGGTTTCT	CCCGCAGGAG	GAAATTTTGA	AGAGCCTGTT	1200
	ACACAAGCAA	CTTTATCTGT	TGTTGGGGCT	TTCTGTGGGC	TTTCTAAGGC	1250
	TAGAGCAGAT	GCTAGACGGT	ATCCTTCTAT	TGATCCGATG	ATTTTCATGGT	1300
45	CTAAGTACTT	GGATTCTGTG	GCGGAGATTT	TAGAGAAAAA	AGTTCCAGGA	1350
	TGGGGAGATT	CCGTTAAAAA	AGCTTCTCGT	TTCTTAGAAG	AAGGAGCAGA	1400
	AATTGGTAAG	CGAATAGAAG	TTGTTGGGGA	AGAAGGGATT	TCTATGGAAG	1450
	ATATAGAAAT	CTTTTGTGAA	TCAGAGTTGT	ATGATTTCTG	TTACTTACAG	1500
	CAAAACGCTT	TCGATGCAGA	GGACTGTTAT	TGTCCTTTTG	ATCGTCAAAT	1550
50	AGAGCTTTTT	TCTTTAATGA	GTCATATTTT	TAGCTCTAGA	TTCTGTTTTG	1600
	ATTGTCCAGA	TAATGCTCGG	AGTTTCTTTT	TAGAGCTTCA	AAGTAAATTT	1650
	AAAACGCTGA	ATGGTCAAAA	ATTCCTTTCT	GAAGACTATC	AGAAGGGGCT	1700
	AGAAGTGATC	TATAAACTAT	TAGAAAGCAA	AATGGTGCAG	ACGGCGTAGG	1750
55	TATGCAAACA	ATATATACAA	GAATTACGG			1779

## 2) INFORMATION FOR SEQ ID NO: 712

- 60 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 965 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

5

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

10

- (A) ORGANISM: *Enterococcus faecalis*  
 (B) STRAIN: V583

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 712

	GTGCAAATTG	GAAAAATTGT	CAAAGTTTCA	GGTCCTTTGA	TTTTAGCTGA	50
15	AAACATGTCA	GATGCTAGTA	TCCAAGACAT	TTGTCAATGTA	GGAGATTTAG	100
	GCGTTATCGG	AGAGATTATT	GAAATGCGAG	GCGACGTTCG	TTCGATTCAA	150
	GTATATGAAG	AAACAACAGG	CATTGGACCA	GGAGAACCAG	TTATTTCAAC	200
	AGGAGAACCA	TTATCTGTTG	AATTAGCCCC	AGGTTTAATT	GCCGAAATGT	250
	TTGATGGTAT	TCAACGACCA	TTGGATACAT	TTCAAGAAGT	AACCCACAGT	300
20	AACTTTTTAG	GCCGTGGCGT	TAAAATTGAT	GCGTTAGATC	GTGAGAAAAA	350
	ATGGACGTTT	GAACCAACTG	TGGCAGTTGG	TGAAGAAGTG	TCGGCAGGTG	400
	ACATCGTCGG	TGTGGTTCAA	GAAACACCGA	TTATTCAACA	TAAAATTATG	450
	GTGCCTTTTCG	GCGTTTCAGG	AACGATTGCC	GAAATTAAG	CAGGTGACTT	500
	TGCCATTGAT	GAAACAGTTT	ACTCAGTGGA	AACGGCTAAA	GGAACGGAAA	550
25	GTTTTAGCAT	GATGCAAAAA	TGGCCCGTTC	GGCGGGGACG	TCCCATTTTA	600
	GAAAAACTAA	GTCCCAAGT	ACCGATGGTG	ACCGGACAAC	GCGTAATTGA	650
	TACCTTTTTT	CCAATTACGA	AAGGCGGAGC	GGCAGCAGTT	CCAGGACCAT	700
	TTGGCGCTGG	AAAAACAGTC	GTTCAGCACC	AAATTGCTAA	GTGGGCCGAT	750
	GTGACTTAG	TCGTTTACGT	TGGTTGTGGG	GAACGCGGGA	ATGAAATGAC	800
30	AGATGTTTTA	AATGAATTTT	CAGAATTAAT	TGACCCAACA	ACTGGTGAGT	850
	CTTTGATGAA	TCGGACGATT	TTAATTGCGA	ATACGTCAAA	TATGCCGGTA	900
	GCGGCACGGG	AAGCCTCGAT	TTATACAGGG	ATTACCATTG	CAGAATATTT	950
	CCGTGATATG	GGTTA				965

35

2) INFORMATION FOR SEQ ID NO: 713

(i) SEQUENCE CHARACTERISTICS:

40

- (A) LENGTH: 1737 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

45

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Methanosarcina barkeri*  
 (C) ACCESSION NUMBER: extracted from J04836

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 713

	GTGGAAGTAA	AAGGTGAAAT	TTATCGTGTG	TCTGGGCCTG	TCGTCACCGC	50
	CATCGGCTTG	CAGGCAAAAA	TGTATGACCT	GGTCAAAGTC	GGTAATGAAG	100
55	GTTTAATGGG	TGAAGTCATT	CAGATATTAG	GGCCCAAGAC	CATCATCCAG	150
	GTATATGAAG	AGACCGCAGG	TATCAAGCCA	GGGGAACCCT	GTGTATCTAC	200
	AGGGTCGTCT	CTGTCCGTAG	AACTTGGTCC	GGGTCTTCTT	TCCAGTATTT	250
	ATGACGGGGT	TCAAAGGCCT	CTGCACGTCC	TGCTTGAAAA	AATGGGTAGC	300
	TTCATCCAGA	GAGGTGTCAG	CGCAGATGGG	CTTGATCATA	AGAAACTCTG	350
60	GGATTTCAAA	CCCATTGTCA	AGAAGGGCGA	TTCCGTAAAA	GGTGGAGACG	400

	TAATTGGTGT	TGTACAGGAA	ACCGTGAATA	TTGAACATAA	GATCATGGTG	450
	CCTCCTGATA	TCTCAGGTAC	AATTTCCGAC	ATAAAGAGCG	GAAACTTTAC	500
	GGTAGTAGAC	ACAATCTGTA	CTCTGACTGA	TGGGACCGAA	TTGCAGATGA	550
	TGCAGAGGTG	GCCTGTTCTGA	AGACCCAGAC	CTGTGAAGGC	AAAACCTTACT	600
5	CCAACCAGGC	CTCTGGTTAC	AGGAATGAGA	ATCCTTGATG	GGCTTTTCCC	650
	TGTGGCAAAA	GGCGGAACAG	CTGCAATCCC	CGGACCTTTC	GGATCGGGAA	700
	AGACCGTAAC	TCAGCAGTCG	CTTGCAAAAT	GGAGTGATAC	CGAAATTGTG	750
	GTCTACATCG	GTTGTGGTGA	GCGTGGA AAC	GAAATGGCAG	ATGTTCTGAG	800
	CGAATTCCCT	GAAGTCGAAG	ATCCGCAGAC	CGGGCGCCCA	CTTATGGAGC	850
10	GTACTGTTCT	TATCGCTAAC	ACTTCAAACA	TGCCTGTGGC	CGCAAGAGAA	900
	GCATCTGTGT	ATACCGGAAT	CACCATTTGCA	GAATACTACC	GTGACATGGG	950
	ATTAGATGTA	TCCCTTATGG	CAGACTCCAC	CTCAAGGTGG	GCAGAAGCCA	1000
	TGAGAGAAAT	CTCTTCCCGT	CTGGAAGAAA	TGCCTGGTGA	AGAAGGTTAC	1050
	CCAGCATACC	TGTCTGCAAG	ACTGGCCGAA	TTCTACGAGC	GTGCCGGGGT	1100
15	TGCGGAGAGT	CTTTGCGGCG	AAACAGGTTC	CATTACTGTT	ATTGGAGCAG	1150
	TATCTCCACC	TGGCGGTGAC	TTCTCAGAGC	CTGTTACACA	GAATACCCTG	1200
	CGTATCGTAA	AAGTGTTCCTG	GGCTCTCGAT	GCCAAACTAT	CTCAGAGGCG	1250
	TCACTTCCCG	GCCATCAACT	GGCTGAACAG	TTACAGTCTG	TATAAGGACA	1300
	GTCTTAATGA	CTGGTTTGCA	GATAATGTGG	CTCCTGATTA	TGTGCCTTTG	1350
20	AGGGAAAGAG	CAATGGAAAT	GCTCCAGACA	GAATCTGAAC	TGCAGGAAAT	1400
	CGTGCAGCTT	GTAGGTTCCG	ATGCTCTGCC	AGACGACCAG	CAGCTTCTGC	1450
	TTGAAATCAC	CCGTATGCTT	AGGGAAATTT	TCCTGCAGCA	GAATGCATTC	1500
	CACCCAGTAG	ATGCATACAG	CCCGTTTCGAT	CAGCAGTACA	AGATCCTTAA	1550
	GGCAATCATG	AAATGGGGAG	ACGCTGCGAT	GGATGCCTTG	AAATCAGGTG	1600
25	TTCCCGTAAC	TGAAATTATC	AAGCTTGAAT	CCAAAAATGT	GCTTGCTAAG	1650
	GTCAAGTACG	AAGAGAAGTT	TGATGAGTCT	ATGAATGCTG	TCCTGGCACA	1700
	GATGGATAAA	GAGTTTGCAT	CCCTGAGAGG	TAGGTAA		1737

30

## 2) INFORMATION FOR SEQ ID NO: 714

## (i) SEQUENCE CHARACTERISTICS:

35

- (A) LENGTH: 1785 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

40

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Methanosarcina jannaschii*
- (C) ACCESSION NUMBER: extracted from U67477

45

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 714

	ATGAAAAGAG	AGGTTGAGAA	TATGCCAGTT	GTTGGTAAGA	TTATTAAAAT	50
	CGCAGGGCCT	GTTGTAGTTG	CAGAGGGAAT	GAAAGGAGCT	CAGATGTATG	100
	AGGTCGTAA	AGTAGGAGAA	GAGAAATTGA	CTGGAGAAAT	CATTTCAGTTG	150
50	CACGATGATA	AAGCAGTTAT	TCAGGTTTAT	GAAGAAACAT	CTGGAATTAA	200
	ACCAGGAGAG	CCAGTTGTTG	GTAAGTGGAGC	TCCATTGTCT	GTTGAATTAG	250
	GGCCAGGGAT	GTTAAGAGCT	ATGTATGATG	GTATTCAGAG	GCCTTTAACA	300
	GCAATTGAAG	AGAAAACAGG	TTCAATCTTT	ATCCCAAGAG	GAGTTGATGT	350
	CCCTGCATTA	CCAAGAGATA	TAAAATGGGA	ATTTAAACCA	GTGGTAAATG	400
55	AAGGAGATTA	TGTTGAAGAA	GGAGACATAA	TTGGAAGTGT	TGATGAAACT	450
	CCTTCAATAG	TTCATAAAAT	CTTAGTTCCA	ATTGGTGTTA	AAGGAAAAAT	500
	TGTTGAAATA	AAAGAGGGTA	AATTTACAGT	TGAAGAGACA	GTTGCAGTTG	550
	TAGAAACAGA	AAATGGAGAA	AGGAAAGAAA	TTACAATGAT	GCAAAAATGG	600
	CCAGTAAGAA	AACCAAGACC	ATATAAAGAG	AACTACCTC	CAGAAATTCC	650
60	ATTAATTACA	GGGCAAAGAG	TTGAAGACAC	TTTCTTTACA	TTAGCAAAAG	700

	GAGGAACAGC	AGCAATTCCA	GGTCCATTCTG	G TTCAGGAAA	AACCGTTACT	750
	CAGCATCAGT	TGGCAAAGTG	GTCTGACGCT	GATGTCGTTG	TTTATATCGG	800
	ATGTGGAGAA	AGAGGAAACG	AGATGACAGA	GGTTATTGAA	GAGTTCCCAC	850
	ACTTAGAAGA	TATTAGAACT	GGAAACAAAT	TAATGGATAG	AACTGTATTA	900
5	ATAGCCAACA	CATCAAACAT	GCCTGTCTGCT	GCAAGGGAAG	CATCTGTCTA	950
	TACAGGAATT	ACAATTGCAG	AGTACTTCAG	AGATATGGGT	TATGGAGTTT	1000
	TATTAACAGC	AGATTCAACA	TCAAGATGGG	CAGAGGCAAT	GAGAGAAATT	1050
	TCAGGTAGAT	TGGAAGAAAT	GCCAGGGGAA	GAAGGGTATC	CAGCATACTT	1100
	AGCTTCAAGA	TTGGCTCAGT	TCTATGAAAG	AGCTGGAAGA	GTTATAACCT	1150
10	TAGGGAAAGA	TAACAGACAA	GGATTTCGTTT	GTATCGTTGG	AGCTGTTTCA	1200
	CCACCAGGAG	GGGACTTCTC	AGAACCAGTT	ACATCAAACA	CACTAAGGAT	1250
	AGTTAAGGTA	TTCTGGGCGT	TAGATGCAAA	CTTGGCAAGA	AGAAGACACT	1300
	TCCCAGCTAT	CAACTGGTTG	CAGAGTTATT	CATTATACAT	TGATGATGTT	1350
	ACAGAGTGGT	GGAACACAAA	TACTGGTCCA	GATTGGAGAC	AATTAAGAGA	1400
15	TGAAGCAATG	AGCTTATTAC	AAAAAGAGGC	AGAGTTGCAA	GAGATTGTTC	1450
	AGTTAGTTGG	GCCTGATGCA	TTGCCAGATA	GGGAGAGAGT	TATTTTAGAA	1500
	GTTGCAAGAA	TGTTGAGGGA	GGATTTCTTA	CAGCAAGATG	CGTTTGATGA	1550
	GGTAGATACC	TACTGTCCTC	CAATGAAACA	GTACTTAATG	TTAAAGATAA	1600
	TTATGACATT	CTACCAAGAA	GCATTGAAGG	CAGTTGAAAG	AGGAGTTGAA	1650
20	CCAGCTAAGA	TTTTAGGAGT	TTCAGTTAAG	CAAGATATTG	CAAGAATGAA	1700
	ATACATCCCA	CACGATGAGT	TTATAAATGT	TAAATCAAAA	GAAATAATGG	1750
	AGAAAATTAA	GAATGAATTA	GGTTCATTAA	ACTAA		1785

25

## 2) INFORMATION FOR SEQ ID NO: 715

## (i) SEQUENCE CHARACTERISTICS:

30

- (A) LENGTH: 1354 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

35

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Porphyromonas gingivalis*
- (B) STRAIN: W83

40

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 715

	TGAGCGAGGT	GATCAAGGTG	ATCGGCAAAA	ATGCTTATGT	GCAGGTTTTTC	50
	GAAAGTACTC	GCGGTATGCA	CGTAGGAGAT	GAGGCAGAGT	TTACCGGCAG	100
	TATGCTTGAG	GTAACGCTCG	GCCCCGGTAT	GCTTTCGAAG	AACTACGACG	150
45	GTCTGCAACA	CGACTTGGAC	AAGATGGACG	GGATCTTCCT	CAAACGAGGC	200
	GATTATACTC	CCGCTCTCGA	TGACGACAAG	CTGTGGGACT	TCAAGCCTTT	250
	GGCCAATGTG	AACGACAATG	TGATCGCAGG	CTCATGGCTC	GGAGAGGTGA	300
	CGGAAAATTT	CCAACCGCAC	AAGATCATGG	TACCTTTTCGT	TTTCGAAGGC	350
	AATTACAAGG	TGAAGAGTCT	GGCCAAAGCC	GGTTCGTACA	AAGTGAACGA	400
50	TGTGATCGCT	GTGGTAACGG	ATCAGGACGG	GAAAGACCAC	AATGTAACCA	450
	TGGTGACAGAA	ATGGCCGGTG	AAACGTGCTA	TCACTTGCTA	TCGCGAGAAG	500
	CCGCGTCCTT	TCAAACCTGCT	CGAAACGGGT	ATCCGTATCA	TCGACACTTT	550
	CAACCCCATC	GTAGAGGGTG	GTACGGGATT	TATCCCCGGT	CCTTTCGGTA	600
	CGGGAAAGAC	GGTGCTCCAG	CATGCTATCT	CGAAGCAGGC	GGAAGCCGAT	650
55	ATCGTGATCA	TTGCAGCCTG	TGGCGAGCGT	GCAAACGAGG	TTGTGGAGAT	700
	CTTTGCGGAA	TTCCCCCACC	TGAATGACCC	CCACACGGGA	CGTAAATTGA	750
	TGGAACGTAC	CATTATTATT	GCTAATACGT	CGAATATGCC	TGTGGCTTCG	800
	CGTGAGGCAT	CCGTATATAC	GGCCATGACG	ATAGCCGAGT	ACTATCGCTC	850
	CATGGGCCTT	CGCGTGCTGA	TGATGGCAGA	CTCCACTTCG	CGTTGGGCAC	900
60	AGGCTCTGCG	TGAGATGTCT	AACCGTCTGG	AAGAGCTTCC	CGGACCGGAT	950



	GCTTTCCCGA	TGGACTTGTC	AGCTATCGTA	GCCAACTTCT	ACGCTCGTGC	1000
	AGGATACGTT	TACCTGAACA	ACGGTTCGGC	CGGTTTCGGTA	ACGTTTCATCG	1050
	GTACGGTATC	TCCCGCCGGT	GGTAACCTCA	AAGAGCCTGT	GACGGAAAAC	1100
	ACCAAGAAAG	TGGCTCGCTG	CTTCTATGCT	TTGGAGCAGA	ATCGTGCCGA	1150
5	CCGCAAACGT	TATCCGGCTG	TAAACCCCAT	CGATAGTTAC	TCGAAGTACA	1200
	TCGAATATCC	CGAATTCGAG	AGCTATATAT	CGAACCACAT	CAGTTTACTC	1250
	ATTATATTCA	ACAGAAGTTG	GCAGATATAT	GGATCAAATC	TTACAGCAGA	1300
	CTGGACTACT	AAGGTGAATG	AGCTGAAGAT	GCGCTTGCAT	CAGGGTAAAG	1350
	AAAT					1354

## 2) INFORMATION FOR SEQ ID NO: 716

## 15 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1788 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

## 20 (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*  
 (B) STRAIN: Type 4

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 716

	TTTGACTCAA	GGGAAGATTA	TAAAAGTATC	GGGACCTCTA	GTTATTGCAT	50
30	CAGGTATGCA	GGAGGCTAAT	ATTCAAGATA	TTTGCCGTGT	AGGTAAGCTA	100
	GGGTTAATCG	GTGAAATTAT	TGAAATGAGA	AGAGATCAGG	CATCTATCCA	150
	AGTCTATGAA	GAAACATCTG	GTCTTGGTCC	GGGAGAACCT	GTTGTTACAA	200
	CTGGAGAACC	TCTCTCGGTT	GAATTAGGGC	CAGGATTGAT	TTCTCAAATG	250
	TTTGATGGCA	TACAACGCCC	ATTAGATCGA	TTTAAATTGG	CTACTCATAA	300
35	TGATTTTCTA	GTTTCGTGGG	TAGAAGTTCC	AAGTTTGGAT	AGAGATATTA	350
	AGTGGCATT	TGATTCCACT	ATAGCAATTG	GTCAAAAAGT	GAGTACGGGT	400
	GATATTCTTG	GAACGTGCAA	GGAAACCGAG	GTAAGTTAATC	ATAAAATTAT	450
	GGTTCCTTAT	GGAGTATCTG	GAGAAGTCGT	TTCTATTGCA	TCTGGCGATT	500
	TTACAATTGA	TGAAGTTGTA	TATGAAATAA	AAAAATTGGA	CGGTAGTTTC	550
40	TATAAAGGAA	CGCTTATGCA	AAAATGGCCT	GTCCGCAAGG	CGCGTCCTGT	600
	TTCTAAACGT	TTAATTCCAG	AAGAACCATT	AATCACAGGT	CAACGAGTTA	650
	TTGATGCATT	CTTTCAGTA	ACCAAAGGGG	GAGCTGCAGC	AGTTCCTGGA	700
	CCGTTTGGAG	CAGGAAAGAC	AGTTGTACAA	CACCAAGTAG	CTAAATTTGC	750
	CAATGTTGAT	ATTGTTATTT	ATGTCGGTTG	TGGAGAACGT	GGAAATGAAA	800
45	TGACGGATGT	ACTGAATGAG	TTTCCTGAGT	TGATTGACCC	TAATACCGGA	850
	CAATCAATTA	TGCAACGGAC	AGTTCTGATT	GCTAATACTT	CAAATATGCC	900
	TGTTGCTGCT	CGTGAGGCTT	CAATTTATAC	AGGAATTACC	ATGGCTGAGT	950
	ATTTTCGTGA	TATGGGCTAC	TCTGTCGCCA	TTATGGCTGA	TTCAACTTCA	1000
	CGTTGGGCAG	AAGCGCTACG	TGAAATGTCA	GGACGTCTAG	AAGAAATGCC	1050
50	TGGTGATGAG	GGTTATCCTG	CTTATCTGGG	AAGTCGTATC	GCTGAATATT	1100
	ATGAAAGAGC	AGGACGTTCT	CAGGTTCTAG	GGCTTCAGAG	ACGTGAAGGA	1150
	ACGATTACTG	CTATTGGAGC	TGTATCGCCA	CCTGGTGGAG	ATATTTTCAG	1200
	ACCAGTTACT	CAAAACACTT	TACGGATTGT	GAAAGTTTTT	TGGGGGCTTG	1250
	ATGCTCCGTT	GGCACAGCGA	CGTCATTTTC	CTGCAATTAA	CTGGCTTACA	1300
55	TCTTATTAC	TATATAAAGA	CAGTGTGGGC	ACTTATATAG	ATGGTAAAGA	1350
	GAAGACAGAT	TGGAATAGTA	AAATAACTCG	TGCGATGAAC	TACTTACAAC	1400
	GGGAATCTAG	TTTAGAGGAA	ATTGTTTCGT	TTGTTGGAAT	TGATTCTCTG	1450
	TCTGATAATG	AACGACTAAC	GATGGAAATT	GCTAAACAAA	TTTCGAGAAGA	1500
	TTATTTGCAA	CAGAACGCTT	TTGATTCCGT	AGATACATTC	ACTTCGTTTG	1550
60	CAAAACAAGA	AGCAATGCTA	AGTAATATTC	TCACTTTTGC	TGATCAGGCA	1600

AATCATGCTT	TAGAGTTGGG	TTCTTACTTT	ACAGAGATTA	TGGAAAGGTAC	1650
CGTGGCAGTT	CGAGACCGTA	TGGCGAGAAG	TAAATATGTT	TCAGAAGATA	1700
GATTAGATGA	AATCAAAATT	ATATCAAATG	AGATTACACA	TCAAATTCAT	1750
TTGATATTAG	AAACAGGAGG	TCTATAAATG	AGTGTTAT		1788

5

## 2) INFORMATION FOR SEQ ID NO: 717

## 10 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 823 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

15

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Burkholderia mallei*  
 (B) STRAIN: GB8

20

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 717

CGATCCTGGT	GTGCTCGGCC	GCTGACGGCC	CGATGCCGCA	AACGCGTGAG	50
25 CACATCCTGC	TGGCGCGTCA	GGTCGGTGTG	CCGTACATCA	TCGTGTTTCT	100
GAACAAGTGC	GACATGGTGG	ACGACGCGGA	GCTGCTCGAG	CTGGTCGAAA	150
TGGAAGTGCG	CGAACTGCTG	TCGAAGTACG	ACTTCCCGGG	CGACGACACG	200
CCGATCATCA	AGGGTTCGGC	GAAGCTGGCG	CTGGAAGGCG	ACAAGGGCGA	250
GCTGGGCGAA	GTGGCGATCA	TGAACCTGGC	CGACGCGCTG	GACACGTACA	300
30 TCCCGACGCC	GGAGCGTGCG	GTCGACGGCG	CGTTCCCTGAT	GCCGGTGGAA	350
GACGTGTTCT	CGATCTCGGG	CCGTGGTACG	GTGGTGACGG	GTCGTGTCGA	400
GCGCGGCGTG	ATCAAGGTTG	GCGAGGAAAT	CGAAATCGTC	GGTATCAAGG	450
CGACGGCGAA	GACGACCTGC	ACGGGCGTGG	AAATGTTCCG	CAAGCTGCTG	500
GACCAGGGTC	AGGCGGGCGA	CAACGTCGGT	ATCCTGCTGC	GCGGCACAAA	550
35 GCGTGAAGAC	GTGGAGCGCG	GCCAGGTTCT	GGCGAAGCCG	GGTTCGATCA	600
CGCCGCACAC	GCACTTCACG	GCAGAAGTGT	ACGTGCTGAG	CAAGGACGAA	650
GGCGGCCCGC	ACACGCCGTT	CTTCAACAAC	TACCGTCCGC	AGTTCTACTT	700
CCGTACGACG	GACGTGACGG	GCTCGATCGA	GCTGCCGAAG	GACAAGGAAA	750
TGGTGATGCC	GGGCGACAAC	GTGTCGATCA	CGGTGAAGCT	GATCGCGCCG	800
40 ATCGCGATGG	AAGAAGGTCT	GCG			823

## 2) INFORMATION FOR SEQ ID NO: 718

45

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 824 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

50

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Burkholderia pseudomallei*  
 (B) STRAIN: 1026B

55

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 718

60 GCGATCCTGG	TGTGCTCGGC	CGCTGACGGC	CCGATGCCGC	AAACGCGTGA	50
---------------	------------	------------	------------	------------	----

	GCACATCCTG	CTGGCGCGTC	AGGTCGGTGT	GCCGTACATC	ATSGTGTTC	100
	TGAACAAGTG	CGACATGGTG	GACGACGCGG	AGCTGCTCGA	GCTGGTCGAA	150
	ATGGAAGTGC	GCGAACTGCT	GTCGAAGTAC	GACTTCCCGG	GCGACGACAC	200
	GCCGATCATC	AAGGGTTCGG	CGAAGCTGGC	GCTGGAAGGC	GACAAGGGCG	250
5	AGCTGGGCGA	AGTGGCGATC	ATGAACCTGG	CCGACGCGCT	GGACACGTAC	300
	ATCCCGACGC	CGGAGCGTGC	GGTCGATGGC	GCGTTCCTGA	TGCCGGTGGA	350
	AGACGTGTTT	TCGATCTCGG	GCCGTGGTAC	GGTGGTGACG	GGTCGTGTCT	400
	AGCGCGGCGT	GATCAAGGTT	GGCGAGGAAA	TCGAAATCGT	CGGTATCAAG	450
	GCGACGGCGA	AGACGACCTG	CACGGGCGTG	GAAATGTTCC	GCAAGCTGCT	500
10	GGATCAGGGT	CAGGCGGGCG	ACAACGTCGG	TATCCTGCTG	CGCGGCACGA	550
	AGCGTGAAGA	CGTGGAGCGC	GGCCAGGTTC	TGGCGAAGCC	GGGTTTCGATC	600
	ACGCCGCACA	CGCACTTCAC	GGCTGAAGTG	TACGTGCTGA	GCAAGGACGA	650
	AGGCGGCCGC	CACACGCCGT	TCTTCAACAA	CTACCGTCCG	CAGTTCTACT	700
	TCCGTACGAC	GGACGTGACG	GGCTCGATCG	AGCTGCCGAA	GGACAAGGAA	750
15	ATGGTGATGC	CGGGCGACAA	CGTGTCGATC	ACGGTGAAGC	TGATCGCGCC	800
	GATCGCGATG	GAAGAAGGTC	TGCG			824

## 20 2) INFORMATION FOR SEQ ID NO: 719

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 800 bases  
 (B) TYPE: Nucleic acid  
 25 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

## 30 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Clostridium beijerincki* (deposited as  
*Clostridium butyricum*)  
 (B) STRAIN: ATCC 8260

## 35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 719

	TGTATCAGCA	GCAGATGGTC	CAATGCCACA	AACAAGAGAA	CATATACTAC	50
	TAGGATCAAG	AGTTGGTATC	CAATATATCG	TAGTATTCTT	AAATAAAGCA	100
	GATATGGTAG	ACGATCCAGA	ATTATTAGAA	TTAGTAGAAA	TGGAAGTAAG	150
40	AGAATTATTA	AGCGAATATG	ACTTCCCAGG	AGACGATATT	CCAGTAATAA	200
	CAGGATCAGC	ATTAAAAGCA	TTAGAAAATC	CAACAGATGA	AGAAGCAATT	250
	AAGCCAATCA	TGGATTTAAT	GGAAGCAGTA	GATAGCTATA	TCCCAACTCC	300
	AGAAAGAGCA	ACAGATAAGC	CATTCTTAAT	GCCAATCGAA	GATGTATTCA	350
	CAATTACAGG	AAGAGGAACA	GTTGCAACAG	GAAGAGTTGA	AGCTGGAGTA	400
45	CTTCATGTAG	GAGATGAAGT	AGAAATCGTT	GGATTAACAG	AAGAAAAGAA	450
	GAAAGTTGTA	GTAACGGAA	TGAAATGTT	CAGAAAGTTA	TTGGATGAAG	500
	CACAAGCTGG	AGATAACATC	GGAGCATTAT	TAAGAGGAGT	TCAAAGAAGT	550
	GATATTGAAA	GAGGTCAAGT	TTTATCAAAA	CCAAATTCAG	TACACCCTCA	600
	CACTAAATTT	GTAGGTCAAG	TATACGTACT	TAAAAAAGAA	GAAGGTGGAA	650
50	GACATACTCC	ATTCTTTGAT	GGATACAGAC	CACAATTCTA	TTTCAGAACA	700
	ACAGACGTTA	CAGGRTCAAT	CAAGTTACCA	GATGGAATGG	AAATGGTAAT	750
	GCCTGGAGAT	CACATTGATA	TGAATGTTGA	ATTAATCACT	CCAATCGCAA	800

55

## 2) INFORMATION FOR SEQ ID NO: 720

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 799 bases  
 60 (B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double  
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

5

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Clostridium innocuum*

(B) STRAIN: ATCC 14501

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 720

	GGTGCTATCC	TGGTTGTTGC	TGCATCTGAT	GGTCCTATGC	CTCAGACTCG	50
	TGAGCACATC	CTGCTTGCTC	GTCAGGTAGG	TGTTCCCTTAC	ATCGTTGTAT	100
	TCCTGAACAA	ATGCGACATG	GTTGATGACG	AAGAACTGAT	CGACCTTGTT	150
15	GAAATGGAAG	TACGTGAGCT	GTTAAGCGAG	TACGGATTTCG	ACGGAGATAA	200
	CGCTCCGGTT	ATCCGTGGTT	CTGCACTGAA	GGCTCTGGAA	GGTGACGACA	250
	AATACGTTGG	CGCTATCAAA	GAAGTATGG	ATGCAGTTGA	TGAATTCATC	300
	CCAGATCCAA	CTCGTGAAAC	TGACAAACCA	TTCTGATGT	CTGTAGAAGA	350
	CGTTATGACA	ATCACAGGAC	GTGGTACAGT	TGCTACAGGA	CGTGTTGAGC	400
20	GTGGGGTAGT	AAAAGTGGGA	GAAGAAGTTG	AAATCGTTGG	TATCAAGGAT	450
	ACTCAGAAAA	CTGTTGTTAC	CGGACTGGAA	ATGTTCCGTA	AGCAGCTGGA	500
	CTTCGCAGAA	TCCGGAGACA	ACATCGGTGC	TCTGCTGCGT	GGTATCAACC	550
	GTGACCAGAT	TCAGCGTGGA	CAGGTTCTTG	CTAAACCAGG	ATCCGTACAT	600
	CCACACACAA	AGTTCAAGGC	TCAGGTTTAT	GTATTAACAA	AAGAAGAAGG	650
25	TGGACGTCAC	ACTCCATTCC	TTTCTAACTA	CCGTCCTCAG	TTCTACTTCC	700
	GTACAACTGA	CGTAACTGGT	GTTATTACAT	TACCGGAAGG	AACTGAAATG	750
	GTTATGCCTG	GTGACAACGT	TGAAATGAAC	GTTGAGCTGA	TTGCTCCAA	799

30

2) INFORMATION FOR SEQ ID NO: 721

(i) SEQUENCE CHARACTERISTICS:

35 (A) LENGTH: 789 bases  
(B) TYPE: Nucleic acid  
(C) STRANDEDNESS: Double  
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

40

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Clostridium novyi*

(B) STRAIN: ATCC 19402

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 721

	TTGTATCAGC	AGCAGATGGT	CCAATGCCAC	AAACAAGAGA	ACACATCCTA	50
	TTAGCATCAA	GAGTAGGAGT	TAACCACATA	GTAGTATTCT	TAAACAAAGC	100
	AGACCAAGTA	GATGATCCAG	AATTACTAGA	ATTAGTAGAA	ATGGAAGTAA	150
50	GAGAATTATT	AAGCGAATAC	GGATTTGACG	GAGACGAATG	TCCAGTAGTA	200
	GTAGGATCAG	CATTAAAAGC	AATCGAAGAA	GGGGATGACC	AATGCATCCT	250
	AGACTTAATG	AAAGCTGTAG	ATGAATATAT	CCCAACTCCA	GAAAGAGCAA	300
	CAGATCAACC	ATTCTTAATG	CCTGTAGAAG	ATGTATTTAC	AATTACAGGA	350
	AGAGGAACAG	TTGCAACAGG	AAGAGTTGAA	AGAGGAGTAC	TACACGTAGG	400
55	AGATGAAGTA	CAAATCGTAG	GAATGAAAGA	AGAAATCGGA	AAGACAACAA	450
	TCACAGGAGT	AGAAATGTTC	AGAAAGATGT	TAGATGAAGC	AATGGCTGGA	500
	GATAACATCG	GAGCATTATT	AAGAGGAGTA	CAAAGAGACG	AAATCGAAAG	550
	AGGTCAAGTA	CTAGCAAAAC	CAGGTTCAAGT	AACACCTCAC	AAAAAATTCG	600
	TAGGTCAAGT	TTACGTATTA	AAGAAAGAAG	AAGGTGGAAG	ACACACTCCA	650
60	TTCTTTAACG	GATACAGACC	ACAATTCTAC	TTCAGAACAA	CAGACGTAAAC	700

AGGATCAATC GCTTTACCAG AAGGAGTAGA AATGGTAATG CCAGSAGACC 750  
 ATATAGACAT GAACGTAGAA TTAATCACAC CAGTAGCAA 789

5

## 2) INFORMATION FOR SEQ ID NO: 722

## (i) SEQUENCE CHARACTERISTICS:

10

- (A) LENGTH: 798 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

15

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Clostridium septicum*
- (B) STRAIN: ATCC 12464

20

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 722

	GTTCAGCAGC	AGACGGTCCA	ATGCCACAAA	CAAGAGAACA	TATACTACTA	50
	GCATCAAGAG	TTGGTGTTGA	CTATATCGTA	GTATTCTTAA	ACAAGGCAGA	100
	TATGGTAGAT	GACGAAGAAT	TATTAGAATT	AGTAGAAATG	GAAGTTAGAG	150
25	AATTATTATC	AGAATACAAC	TTCCCAGGAG	ATGATATTCC	AGTAATCAAG	200
	GGATCAGCTT	TAGTAGCATT	AGAAAACCCA	ACAGATGAAA	AATCAATCGC	250
	TCCAATCTTA	GAATTAATGG	AAGCAGTAGA	TAGCTACATT	CCAACACCAG	300
	AAAGAGCAAC	AGATAAGCCA	TTCTTAATGC	CAGTAGAAGA	TGTATTCAACA	350
	ATAACTGGTA	GAGGAACAGT	TGCAACAGGA	AGAGTTGAAA	GAGGAGTTCT	400
30	TCATGTAGGA	GACGAAGTAG	AAATCGTTGG	ATTATCAGAA	GAAAGCAGAA	450
	AAGTAGTAGT	AACAGGAATA	GAAATGTTCA	GAAAGTTACT	AGACGAAGCA	500
	CAAGCTGGAG	ATAATGTTGG	AGTACTTTTA	AGAGGTGTTC	AAAGAACAGA	550
	TATCGAAAGA	GGTCAAGTAT	TAGCAAAGAC	TGGATCAGTT	AAGCCACACA	600
	GCAAGTTCGT	AGGTCAAGTA	TACGTACTTA	AGAAAGAAGA	AGGTGGAAGA	650
35	CATACTCCAT	TCTTCGATGG	ATACAGACCA	CAATTCTACT	TCAGAACAAC	700
	AGACGTTACT	GGATCAATCA	AATTACCAGA	CGGAATGGAA	ATGGTTATGC	750
	CAGGAGACCA	CATTGATATG	AACGTTGAAT	TAATCACTCA	AGTAGCAA	798

40

## 2) INFORMATION FOR SEQ ID NO: 723

## (i) SEQUENCE CHARACTERISTICS:

45

- (A) LENGTH: 799 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

50

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Clostridium tertium*
- (B) STRAIN: ATCC 14573

55

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 723

	GTTCAGCAGC	AGATGGTCCA	ATGCCTCAAA	CAAGAGAACA	CATACTACTA	50
	GCTTCAAGAG	TTGGTGTTGA	CTACATAGTT	GTTTTCTTAA	ACAAGGCAGA	100
	TATGGTAGAT	GACGAAGAAT	TATTAGAATT	AGTTGAAATG	GAAGTAAGAG	150
60	AATTATTATC	AGAATACAAC	TTCCCAGGAG	ATGATATTCC	AGTAATAAAG	200

	GGTTCAGCTT	TACAAGCATT	AGAAAACCCA	ACAGATGAAA	AAGCAATCGC	250
	TCCAATCCTT	GAGTTAATGG	AAGCTGTAGA	TAGCTACATT	CCAACTCCAG	300
	AAAGAGCAAC	AGATAAGCCA	TTCTTAATGC	CAGTAGAAGA	TGTATTCCACA	350
	ATCACTGGTA	GAGGAACAGT	TGCTACAGGA	AGAGTTGAAA	GAGGAGTTCT	400
5	TCACGTAGGA	GACGAAGTAG	AAATCGTTGG	ATTATCAGAA	GACAGCAGAA	450
	AAGTAGTAGT	AACAGGAATA	GAAATGTTCA	GAAAGTTACT	AGACGAAGCG	500
	CAAGCTGGAG	ACAACGTAGG	AGTTCTTTTA	AGAGGAGTTC	AAAGAACTGA	550
	CATCGAAAGA	GGTCAAGTTT	TAGCAAAAGT	TGGATCAGTT	AAGCCACACA	600
	AGAAATTTGT	AGGTCAAGTA	TACGTACTTA	AAAAAGAAGA	AGGTGGAAGA	650
10	CATACTCCAT	TCTTCGATGG	ATACAGACCA	CAATTCTACT	TCAGAACCAAC	700
	AGAYGTTACT	GGTTC AATCA	AGTTACCAGA	TGGAATGGAA	ATGGTTATGC	750
	CAGGAGACCA	CATTGATATG	AACGTTGAAT	TAATCACTCA	AGTAGCTAT	799

15

## 2) INFORMATION FOR SEQ ID NO: 724

## (i) SEQUENCE CHARACTERISTICS:

20

- (A) LENGTH: 801 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

25

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Clostridium tetani*
- (B) STRAIN: ATCC 19406

30

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 724

	TAGTAAGTGC	AGCAGATGGT	CCAATGCCAC	AAACAAGAGA	ACACATACTA	50
	TTAGCATCCA	GAGTTGGAGT	TGAGCACATA	GTAGTATTCT	TAAATAAAGC	100
	AGACCAAGTA	GATGACGCAG	AGTTAATCGA	ATTAGTAGAA	ATGGAAGTAA	150
35	GGGAATTAAT	GAACGAATAC	GGATTCCCAG	GAGATGACGC	ACCAGTAGTA	200
	GTAGGATCCG	CATTAAAAGC	ATTAGAAAAT	CCAGAAGATG	ATGCAGCAAC	250
	ACAATGCATA	ATGGACTTAA	TGGCAGCAGT	AGATGAATAT	ATACCAACAC	300
	CAGAAAGAGC	AACAGATAAG	CCATTCTTAA	TGCCAGTAGA	AGATATCTTC	350
	ACAATCACAG	GAAGAGGAAC	AGTTGCAACA	GGAAGAGTAG	AAAGAGGAAT	400
40	TCTAAAAGTA	GGAGACGAAA	TAGAAATCGT	AGGATTAAGT	GATGAAAGCA	450
	AGAAATCAGT	AATCACAGGA	ATAGAAATGT	TCAGAAAAC	ATTAGATGAA	500
	GCACAAGCAG	GAGATAACAT	CGGAGCATTA	TTAAGAGGTG	TTCAAAGAGA	550
	TGAAATCCAA	AGAGGTCAAG	TATTAGCAGC	AACAGGATCA	GTAAAACCAC	600
	ATAAGAGTTT	TACAGGTCAA	GTATATGTAT	TAAAGAAAGA	AGAAGGAGGA	650
45	AGACACACTC	CATTCTTTAA	CGGATACAGA	CCACAATTCT	ACTTTAGAAC	700
	AACAGACGTA	ACAGGTTCAA	TCGCACTACC	AGAAGGAGTA	GAAATGGTAA	750
	TGCCAGGAGA	CCACATAGAC	ATGAAGGTAG	AATTAATAAC	AAGAGTAGCA	800
	A					801

50

## 2) INFORMATION FOR SEQ ID NO: 725

## (i) SEQUENCE CHARACTERISTICS:

55

- (A) LENGTH: 633 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

60

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Enterococcus malodoratus*

(B) STRAIN: ATCC 43197

5

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 725

	TATGCCTCAA	ACTCGTGAAC	ACATCTTGTT	ATCTCGTAAC	GTTGGTGTTT	50
	CTTACATCGT	TGTATTCTTA	AACAAAATGG	ATATGGTTGA	TGATGAAGAA	100
10	TTACTAGAAT	TAGTTGAAAT	GGAAGTTCGT	GACTTATTGT	CAGAATACGA	150
	CTTCCCAGGC	GACGACACTC	CAGTTATCGC	TGGTTCAGCT	TTGAAAGCTT	200
	TAGAAGGCGA	TGCTTCATAC	GAAGAAAAAA	TCTTAGAATT	AATGGCTGCT	250
	GTTGATGAAT	ATATCCCAAC	ACCACTTCGT	GATACTGACA	AACCATTGAT	300
	GATGCCAGTC	GAAGATGTAT	TCTCAATCAC	TGGTCGTGGA	ACTGTTGCAA	350
15	CTGGTCGTGT	TGAACGTGGA	CAAGTTCGCG	TTGGTGACGA	AGTTGAAATC	400
	GTTGGTATTG	CTGAAGCAAC	TGCTAAAACA	ACTGTTACAG	GTGTTGAAAT	450
	GTTCCGTAAA	TTGTTAGATT	ACGCTGAAGC	AGGCGATAAC	ATTGGTGCAT	500
	TGTTACGTGG	TGTTGCACGT	GAAGACATCC	AACGTGGACA	AGTATTGGCT	550
	AAACCAGCTT	CAATCACTCC	ACATACAAAA	TTCTCTGCAG	AAGTTTACGT	600
20	TTTAACTAAA	GAAGAAGGCG	GACGTCATAC	TCC		633

## 2) INFORMATION FOR SEQ ID NO: 726

25

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 623 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

30

(D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

35

(A) ORGANISM: *Enterococcus sulfureus*

(B) STRAIN: ATCC 49903

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 726

40	CACGTGAACA	CATCTTGTTA	TCTCGTAACG	TAGGTGTTCC	TTACATCGTT	50
	GTATTCTTAA	ACAAAATGGA	TATGGTTGAT	GACGAAGAAT	TATTAGAATT	100
	AGTAGAAATG	GAAGTTCGTG	ACTTATTATC	AGAATACGAT	TTCCCAGGCG	150
	ATGACACTCC	AGTTGTTGCA	GGTTCGTGCTT	TGAAAGCTTT	AGAAGGCGAC	200
	GCTTCTTACG	AAGAAAAAAT	CATGGAATTA	ATGGCTGCAG	TTGACGAGTA	250
45	CATCCCAACT	CCAACTCGTG	ACACTGACAA	ACCATTGATG	ATGCCAGTTG	300
	AGGATGTATT	CTCAATCACT	GGACGTGGTA	CTGTTGCTAC	AGGTCGTGTT	350
	GAACGTGGAC	AAGTTCGCGT	TGGTGACGTT	GTAGATATCG	TTGGTATCGC	400
	TGACGAAACT	GCTCAAACAA	CTGTAACAGG	TGTTGAAATG	TTCCGTAAAT	450
	TATTAGACTA	CGCTGAAGCA	GCGGATAACA	TCGGTGCTTT	ATTACGTGGT	500
50	GTTGCTCGTG	AAGACATCCA	ACGTGGACAA	GTTTTAGCTA	AACCAGCTTC	550
	AATCACTCCA	CATACAAAAT	TCTCTGCTGA	AGTATACGTA	TTAAGCAAAG	600
	AAGAAGGTGG	ACGTCATACT	CCA			623

55

## 2) INFORMATION FOR SEQ ID NO: 727

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 646 bases

60

(B) TYPE: Nucleic acid

- (C) STRANDEDNESS: Double  
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Lactococcus garvieae*  
(B) STRAIN: ATCC 49156

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 727

	CGGTCCTATG	CCTCAAACCTC	GTGAACACAT	CTTGTTATCA	CGTAACGTTG	50
	GCGTACCATA	CATCGTTGTT	TTCCTGAACA	AAATGGATAT	GGTTGATGAC	100
	GAAGAATTGC	TAGAATTAGT	TGAAATGGAA	GTTCTGACC	TATTGTCTGA	150
15	ATATGACTTC	CCAGGCGACG	ATGTTCTGT	AATCGCTGGT	TCTGCTTTGA	200
	AAGCTCTTGA	AGGAGATCCT	TCATACGAAG	AAAAAATCAT	GGAATTGATG	250
	GCTGCAGTTG	ACGAATACGT	TCCAACCTCA	GAACGTGATA	CTGACAAACC	300
	ATTCATGATG	CCAGTCGAAG	ACGTATTCTC	AATCACTGGA	CGTGGTACTG	350
	TTGCTACAGG	CCGTGTTGAA	CGTGGACAAG	TTCGCGTTGG	TGATGAAGTA	400
20	GAAATCGTTG	GTATTGCTGA	CGAAACTGCT	AAAACAACTG	TAACAGGTGT	450
	TGAAATGTTT	CGTAAATTGT	TAGACTATGC	TGAAGCAGGG	GATAACATTG	500
	GTGCATTGCT	ACGTGGGGTT	GCTCGTGAAG	ACATCCAACG	TGGACAAGTA	550
	TTGGCTAAAG	CTGGTACAAT	CACACCTCAT	ACAAAATTCA	AAGCTGAAGT	600
	TTATGTTTTG	ACAAAAGAAG	AAGGTGGACG	TCACACTCCA	TTCTTC	646

2) INFORMATION FOR SEQ ID NO: 728

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 823 bases  
(B) TYPE: Nucleic acid  
(C) STRANDEDNESS: Double  
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Mycoplasma pirum*  
(B) STRAIN: ATCC 25960D

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 728

	GAGCAATTTT	AGTTGTTTCT	GCAACTGATG	GTCCAATGCC	TCAAACCTCGT	50
	GAACATATCT	TATTAGCACG	CCAAGTTGGT	GTTCTTAAAA	TGGTTGTTTT	100
45	CTTAAACAAA	TGTGATGTTG	CTTCTGATCC	AGAAATGCAA	GAATTAGTTG	150
	CTGAAGAAGT	AAAAGACTTA	TTAAAATCTT	ATGGTTTTGA	TGGTGACAAT	200
	ACTCCAATTA	TTCGTGGTTC	AGCATTAGAA	GCATTAAATG	GTAAACCTGA	250
	ATGAGAAGAA	AAAATTAAAG	AATTAATGAA	GGCAGTGGAT	GACACTATTC	300
	CTGATCCAGT	TCGTGATACT	GAAAAGCCAT	TCTTGTTACC	AATTGAAGAC	350
50	GTAATGACAA	TTACAGGTCG	TGGTACTGTT	GTTACAGGTC	GTGTAGAACG	400
	TGGTACTCTA	AAATTAAATG	ATGAAGTTGA	AATTGTTGGT	TTAGGTGAAA	450
	CATTTAATC	TGTTGTAACA	GGTATTGAAA	TGTTCCGTAA	AGAATTAGAT	500
	GAAGCTCGTG	CTGGTGACAA	TGCTGGTATT	TTACTTCGTG	GTGTTGACCG	550
	TGGTCAAGTA	CAACGTGGTC	AAGTTCTTGC	TAAACCAGGT	TCTATTACTC	600
55	CTCATACTAA	ATTTAAAGCT	GAAATTTATG	CTTTGAAAAA	AGAAGAAGGT	650
	GGTCGTCATA	CTGCTTTCTT	AAACGGTTAT	CGTCCTCAAT	TCTATTTTCA	700
	AACAACTGAT	GTTACAGGTT	CTATTAAATT	AAAAGATGGA	ACTGAAATGG	750
	TTATGCCTGG	TGACAATACT	GAAATCACTG	TAGAATTAAT	TTCACCAATT	800
	GCTTGTAATA	AGGAAGTAAG	TTT			823



## 2) INFORMATION FOR SEQ ID NO: 729

- 5 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 826 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear
- 10 (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: *Mycoplasma salivarium*  
 15 (B) STRAIN: ATCC 23064

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 729

	GGAGCAATCT	TAGTTGTTGC	TGCAACTGAT	GGTGCGATGC	CTCAAACCTCG	50
20	TGAACACGTT	TTACTTGCAA	AACAAGTTGG	TGTTCCCTAAA	ATCGTTGTTT	100
	TCTTAAACAA	AATCGATATG	TTCAAGCCAG	AAGAAAGAGC	CGAAATGGTT	150
	GAAATGGTTG	AAATGGACAT	TCGTGACTTA	TTAAACAAAT	ACGACTTTGA	200
	TGGTGACAAT	ACTCCTATTA	TTGCTGGTTC	AGCATTAAAA	GCATTACAAG	250
	GTGATCCAGA	ATATGAAAAG	AATATTCTAG	AACTTATGGA	TGCAGTAGAC	300
25	ACATACATTG	ATGAACCTAC	TCGTGATAAA	GATAAACCAT	TCTTAATGGC	350
	TGTAGAAGAC	GTATTTACAA	TTACTGGTTCG	TGGAACCTGTT	GCTACTGGTA	400
	GAGTAGAACG	TGGTACATTA	CATCTAAATG	ATGAAGTTGA	AATCGTTGGT	450
	CTACGTCCAA	CAATTAAAAC	TGTTGTTACT	GGAATTGAAA	TGTTCCGTAA	500
	AAATTTAAAA	GAAGCTCAAG	CTGGAGATAA	TGCAGGACTT	TTACTACGTG	550
30	GAATTGATAG	AGATCAAGTA	GAACGTGGAC	AAGTTTTGGC	CAAACCAAAA	600
	AGTATTATTC	CTCACACAGA	ATTTGAAGCT	GCTGTGTATG	TTCTAAAAGC	650
	TGAAGAAGGT	GGACGTCACA	CTCCATTCTT	TGAACACTAT	AAACCACAAT	700
	TTTACTTTTCG	TACAACCGAC	GTTACTGGTG	GAATTAAATT	CAAACCTGGA	750
	CGTGAAATGG	TTATGCCTGG	CGAAAATGTT	GAATTTACAG	TTACTTTAAT	800
35	TGCTCCTATT	GCAGTTGAAG	AAGGAA			826

## 2) INFORMATION FOR SEQ ID NO: 730

- 40 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 810 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 45 (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:  
 50 (A) ORGANISM: *Neisseria polysaccharea*  
 (B) STRAIN: ATCC 43768

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 730

55	TGGTATGTTC	CGCAGCYGAY	GGYCCTATGC	CTCAAACCTCG	CGAACACATC	50
	CTGYTGGCTC	GCCAAGTAGG	YGTACCTTAC	ATCATCGTRT	TCATGAACAA	100
	ATGCGACATG	GTTGACGATG	CCGAGCTGTT	GGAACCTGGTT	GAAATGGAAA	150
	TCCGYGACCT	GYTGTCMAGC	TACGACTTCC	CMGGCGACGA	CTGCCCAATC	200
	GTACAAGGTT	CTGCACTGAA	AGCTTTGGAA	GGYGAYGCTG	GTTACGAAGA	250
60	GAAAATCTTC	GAAYTGGCTG	CTGCTTTGGA	CAGCTACATC	CCAACTCCTG	300

	AGCGTGCTGT	GGACAAACCK	TTCYTGYTGC	CTATCGAAGA	CGTRTTCTCT	350
	ATCTCTGGYC	GYGGTACMGT	AGTAACYGGY	CGTG TAGAGC	GCGGTRTCAT	400
	CCACGTTGGT	GACGAGATYG	AAATCGTAGG	TCTGAAAGAA	ACCCAAAAAA	450
	CCACTTG TAC	CGGCGTTGAA	ATGTTCCGCA	AACTGCTGGA	CGAAGGTCAA	500
5	GCWGGTGACA	ACGTAGGCGT	ATTGYTGCCT	GGTACCAARC	GTGAAGACGT	550
	AGAGCGTGGT	CAAGTATTGG	CYAAACCAGG	YACCATYACT	CCSCACACCA	600
	AATTCAAAGC	AGAAGTATAC	G TACTGAGCA	AAGAAGAGGG	TGGTCGYCAC	650
	ACTCCATTCT	TCGCYAACTA	CCGYCCMCAA	TTCTACTTCC	GTACYACTGA	700
	CGTAACYGGT	GCAGTTACTT	TGGAAGAAGG	TGTAGAAATG	GTAATGCCAG	750
10	GTGAGAACGT	AACCATTACY	GTAGAACTGA	TTGCGCCTAT	CGCTAGGAAG	800
	AAGGTCTGCG					810

## 15 2) INFORMATION FOR SEQ ID NO: 731

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 813 bases  
 (B) TYPE: Nucleic acid  
 20 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

## 25 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Salmonella choleraesuis* subsp. *choleraesuis*  
 serotype Enteritidis  
 (B) STRAIN: ATCC 13076

## 30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 731

	CTGGTTGTTG	CTGCGACTGA	CGGCCCGATG	CCGCAGACCC	GTGAGCACAT	50
	CCTGCTGGGT	CGTCAGGTAG	GCGTTC CGTA	CATCATCGTG	TTCCTGAACA	100
	AATGCGACAT	GGTTGATGAC	GAAGAGCTGC	TGGAAGTGGT	TGAAATGGAA	150
35	GTTTCGYGAAC	TGCTGTCTCA	GTACGACTTC	CCGGGCGACG	ACACTCCGAT	200
	CGTTCGTGGT	TCTGCTCTGA	AAGCGCTGGA	AGGCGACGCA	GAGTGGGAAG	250
	CGAAAATCAT	CGAACTGGCT	GGCTTCCTGG	ATTCTTACAT	CCCGGAACCA	300
	GAGCGTGCGA	TTGACAAGCC	GTTCTTGCTG	CCGATCGAAG	ACGTATTCTC	350
	CATCTCCGGT	CGTGGTACCG	TTGTTACCGG	TCGTGTAGAA	CGCGGTATCA	400
40	TCAAAGTGGG	CGAAGAAGTT	GAAATCGTTG	GTATCAAAGA	GA CTCAGAAG	450
	TCTACCTGTA	CTGGCGTTGA	AATGTTCCGC	AAACTGCTGG	ACGAAGGCCG	500
	TGCCGGTGAG	AACGTAGGTG	TTCTGCTGCG	TGGTATCAAA	CGTGAAGAAA	550
	TCGAACGTGG	TCAGGTACTG	GCTAAGCCGG	GCACCATCAA	GCCGCACACC	600
	AAGTTCGAAT	CTGAAGTGTA	CATTCTGTCC	AAAGATGAAG	GCGGCCGTCA	650
45	CACTCCGTTT	TTCAAAGGCT	ACCGTCCGCA	GTTCTACTTC	CGTACTACTG	700
	ACGTGACTGG	CACCATCGAA	CTGCCGGAAG	GCGTAGAGAT	GGTAATGCCG	750
	GGCGACAACA	TCAAATGGT	TGTTACCCTG	ATCCACCCGA	TCGCAATGGA	800
	CGACGGTCTG	CGT				813

50

## 2) INFORMATION FOR SEQ ID NO: 732

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 812 bases  
 (B) TYPE: Nucleic acid  
 55 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

## 60 (ii) MOLECULE TYPE: Genomic DNA